Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A9K7
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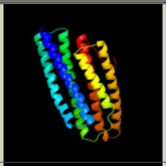
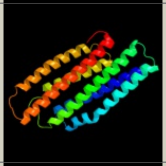
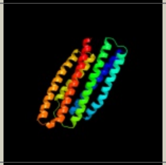
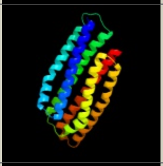
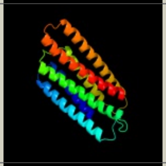
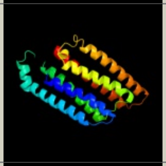
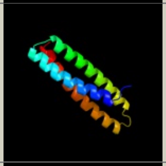
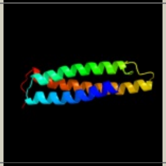
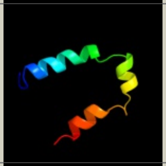
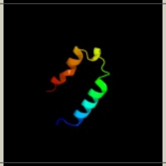
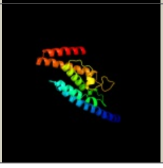
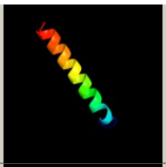
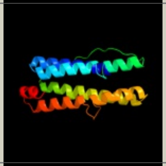
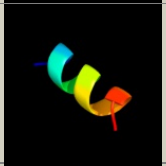
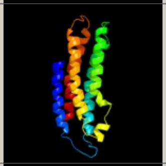
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sumb_	Alignment		100.0	26	**Fold:**Spectrin repeat-like **Superfamily:**PhoU-like **Family:**PhoU-like
2	d1xwma_	Alignment		100.0	30	**Fold:**Spectrin repeat-like **Superfamily:**PhoU-like **Family:**PhoU-like
3	d1t72a_	Alignment		100.0	31	**Fold:**Spectrin repeat-like **Superfamily:**PhoU-like **Family:**PhoU-like
4	c2i0mA_	Alignment		100.0	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phosphate transport system protein phou; **PDBTitle:** crystal structure of the phosphate transport system regulatory protein2 phou from streptococcus pneumoniae
5	c3l39A_	Alignment		99.9	8	**PDB header:**phosphate-binding protein **Chain:** A: **PDB Molecule:**putative phou-like phosphate regulatory protein; **PDBTitle:** crystal structure of putative phou-like phosphate regulatory2 protein (bt4638) from bacteroides thetaiotaomicron vpi-54823 at 1.93 a resolution
6	c2oltB_	Alignment		99.8	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a phou-like protein (so_3770) from shewanella2 oneidensis mr-1 at 2.00 a resolution
7	d1vcta1	Alignment		99.7	12	**Fold:**Spectrin repeat-like **Superfamily:**PhoU-like **Family:**PhoU-like
8	c2bknA_	Alignment		99.3	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein ph0236; **PDBTitle:** structure analysis of unknown function protein
9	d1cola_	Alignment		51.2	26	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
10	d1rh1a2	Alignment		36.0	18	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
11	c2qrxA_	Alignment		27.9	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**gm27569p; **PDBTitle:** crystal structure of drosophila melanogaster translin2 protein

12	d1zkea1	Alignment		26.6	14	**Fold:**ROP-like **Superfamily:**HP1531-like **Family:**HP1531-like
13	c3qd8M_	Alignment		25.9	17	**PDB header:**metal binding protein **Chain:** M: **PDB Molecule:**probable bacterioferritin bfrb; **PDBTitle:** crystal structure of mycobacterium tuberculosis bfrb
14	c1pq1B_	Alignment		22.0	50	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl2-like protein 11; **PDBTitle:** crystal structure of bcl-xl/bim
15	d1eq1a_	Alignment		19.3	7	**Fold:**Apolipophorin-III **Superfamily:**Apolipophorin-III **Family:**Apolipophorin-III
16	c3izcw_	Alignment		17.6	14	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein rpl22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
17	c1jqsB_	Alignment		16.9	38	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**elongation factor g; **PDBTitle:** fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
18	c3ci9B_	Alignment		16.4	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
19	d1seta1	Alignment		15.9	10	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Seryl-tRNA synthetase (SerRS)
20	c2k7wB_	Alignment		13.6	60	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** bax activation is initiated at a novel interaction site
21	d1krqa_	Alignment	not modelled	13.6	12	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
22	c2nl9B_	Alignment	not modelled	11.7	50	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** crystal structure of the mcl-1:bim bh3 complex
23	c3kj2B_	Alignment	not modelled	11.3	50	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** mcl-1 in complex with bim bh3 mutant f4ae
24	c1kmiZ_	Alignment	not modelled	11.2	7	**PDB header:**signaling protein **Chain:** Z: **PDB Molecule:**chemotaxis protein chez; **PDBTitle:** crystal structure of an e.coli chemotaxis protein, chez
25	c1rimA_	Alignment	not modelled	10.9	46	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**e6apc2 peptide; **PDBTitle:** e6-binding zinc finger (e6apc2)
26	c2kdtA_	Alignment	not modelled	10.8	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**neuroendocrine convertase 1; **PDBTitle:** pc1/3 dcsg sorting domain structure in dpc
27	c3d1dC_	Alignment	not modelled	9.3	17	**PDB header:**nuclear protein **Chain:** C: **PDB Molecule:**rna-induced transcriptional silencing complex **PDBTitle:** hexagonal crystal structure of tas3 c-terminal alpha motif
28	d1vlga_	Alignment	not modelled	9.0	9	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
						PDB header:endocytosis/exocytosis

29	c3c98B_	Alignment	not modelled	8.8	14	**Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** revised structure of the munc18a-syntaxin1 complex
30	d1jgca_	Alignment	not modelled	8.8	17	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
31	c3kz0C_	Alignment	not modelled	7.9	42	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**mcl-1 specific peptide mb7; **PDBTitle:** mcl-1 complex with mcl-1-specific selected peptide
32	c3kz0D_	Alignment	not modelled	7.9	42	**PDB header:**apoptosis **Chain:** D: **PDB Molecule:**mcl-1 specific peptide mb7; **PDBTitle:** mcl-1 complex with mcl-1-specific selected peptide
33	c3d7vB_	Alignment	not modelled	7.8	43	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** crystal structure of mcl-1 in complex with an mcl-12 selective bh3 ligand
34	c3iz5w_	Alignment	not modelled	6.1	14	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein l22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
35	d2dmda1	Alignment	not modelled	6.0	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
36	d1a87a_	Alignment	not modelled	6.0	20	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
37	c1a87A_	Alignment	not modelled	6.0	20	**PDB header:**bacteriocin **Chain:** A: **PDB Molecule:**colicin n; **PDBTitle:** colicin n
38	d1j0ta_	Alignment	not modelled	6.0	27	**Fold:**Crustacean CHH/MIH/GIH neurohormone **Superfamily:**Crustacean CHH/MIH/GIH neurohormone **Family:**Crustacean CHH/MIH/GIH neurohormone
39	d1uptb_	Alignment	not modelled	6.0	14	**Fold:**GRIP domain **Superfamily:**GRIP domain **Family:**GRIP domain
40	c3cd0B_	Alignment	not modelled	5.7	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxy-3-methylglutaryl-coenzyme a reductase; **PDBTitle:** thermodynamic and structure guided design of statin hmg-coa2 reductase inhibitors
41	c1vh6A_	Alignment	not modelled	5.5	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flagellar protein flis; **PDBTitle:** crystal structure of a flagellar protein
42	d1vh6a_	Alignment	not modelled	5.5	8	**Fold:**Four-helical up-and-down bundle **Superfamily:**Flagellar export chaperone FliS **Family:**Flagellar export chaperone FliS
43	c3znfA_	Alignment	not modelled	5.4	44	**PDB header:**zinc finger dna binding domain **Chain:** A: **PDB Molecule:**zinc finger; **PDBTitle:** high-resolution three-dimensional structure of a single2 zinc finger from a human enhancer binding protein in3 solution
44	d4znfa_	Alignment	not modelled	5.4	44	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
45	c4znfA_	Alignment	not modelled	5.4	44	**PDB header:**zinc finger dna binding domain **Chain:** A: **PDB Molecule:**zinc finger; **PDBTitle:** high-resolution three-dimensional structure of a single2 zinc finger from a human enhancer binding protein in3 solution
46	d256ba_	Alignment	not modelled	5.3	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome b562
47	d1t6ua_	Alignment	not modelled	5.3	11	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nickel-containing superoxide dismutase, NiSOD **Family:**Nickel-containing superoxide dismutase, NiSOD
48	c1hwjB_	Alignment	not modelled	5.2	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**hmg-coa reductase; **PDBTitle:** complex of the catalytic portion of human hmg-coa reductase2 with cerivastatin
49	d1hw8c2	Alignment	not modelled	5.2	36	**Fold:**Substrate-binding domain of HMG-CoA reductase **Superfamily:**Substrate-binding domain of HMG-CoA reductase **Family:**Substrate-binding domain of HMG-CoA reductase
50	c3qauA_	Alignment	not modelled	5.1	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxy-3-methylglutaryl-coenzyme a reductase; **PDBTitle:** 3-hydroxy-3-methylglutaryl-coenzyme a reductase from streptococcus2 pneumoniae
51	d1o9da_	Alignment	not modelled	5.1	15	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein