Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	Q5SQX6
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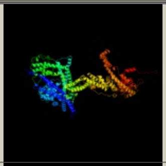
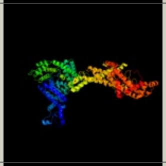
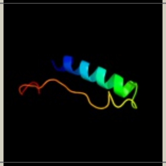
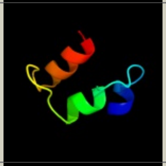
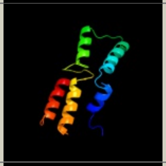
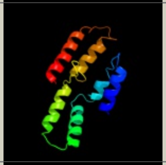
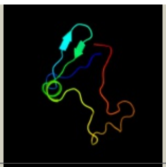
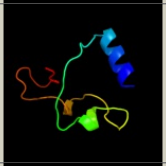
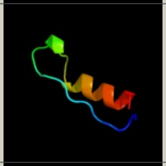
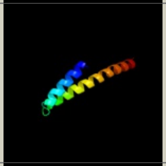
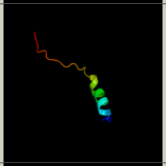
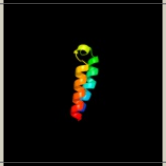
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3p8cA_	Alignment		100.0	89	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**cytoplasmic fmr1-interacting protein 1; **PDBTitle:** structure and control of the actin regulatory wave complex
2	c3p8cB_	Alignment		94.1	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nck-associated protein 1; **PDBTitle:** structure and control of the actin regulatory wave complex
3	d1ug8a_	Alignment		49.6	23	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
4	d1ayia_	Alignment		48.0	27	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
5	d2vlqa1	Alignment		46.7	30	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
6	c2no8A_	Alignment		45.0	24	**PDB header:**immune system **Chain:** A: **PDB Molecule:**colicin-e2 immunity protein; **PDBTitle:** nmr structure analysis of the colicin immuntiy protein im2
7	c1i5pA_	Alignment		43.9	10	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidial crystal protein cry2aa; **PDBTitle:** insecticidal crystal protein cry2aa
8	d1gxha_	Alignment		42.9	22	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
9	c2c9kA_	Alignment		39.4	14	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidal crystal protein cry4aa; **PDBTitle:** structure of the functional form of the mosquito-larvicidal2 cry4aa toxin from bacillus thuringiensis at 2.8 a3 resolution
10	d1g5ma_	Alignment		28.2	44	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
11	c2iv1J_	Alignment		26.8	40	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cyanate hydratase; **PDBTitle:** site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase

12	c1gs0B_	Alignment		24.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**poly (adp-ribose) polymerase-2; **PDBTitle:** crystal structure of the catalytic fragment of murine poly2 (adp-ribose) polymerase-2
13	d1dwka2	Alignment		22.9	40	**Fold:**Cyanase C-terminal domain **Superfamily:**Cyanase C-terminal domain **Family:**Cyanase C-terminal domain
14	c3mhkA_	Alignment		22.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tankyrase-2; **PDBTitle:** human tankyrase 2 - catalytic parp domain in complex with 2-(2-2 pyridyl)-7,8-dihydro-5h-thiino[4,3-d]pyrimidin-4-ol
15	c2wukD_	Alignment		21.1	18	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
16	d2ca5a1	Alignment		20.1	16	**Fold:**Long alpha-hairpin **Superfamily:**MxiH-like **Family:**MxiH-like
17	d1o7xa_	Alignment		19.9	28	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
18	d1niga_	Alignment		19.7	22	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Hypothetical protein Ta1238
19	c2paxA_	Alignment		19.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(adp-ribose) polymerase; **PDBTitle:** the catalytic fragment of poly(adp-ribose) polymerase2 complexed with 4-amino-1,8-naphthalimide
20	d1m6ex_	Alignment		19.4	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Salicylic acid carboxyl methyltransferase (SAMT)
21	c2ketA_	Alignment	not modelled	18.0	50	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**cathelicidin-6; **PDBTitle:** solution structure of bmap-27
22	d1q59a_	Alignment	not modelled	17.9	10	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
23	c4dqyF_	Alignment	not modelled	17.8	26	**PDB header:**transferase/dna **Chain:** F: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** structure of human parp-1 bound to a dna double strand break
24	d1i5pa3	Alignment	not modelled	17.6	11	**Fold:**Toxins' membrane translocation domains **Superfamily:**delta-Endotoxin (insectocide), N-terminal domain **Family:**delta-Endotoxin (insectocide), N-terminal domain
25	c2i3sF_	Alignment	not modelled	17.2	50	**PDB header:**cell cycle **Chain:** F: **PDB Molecule:**checkpoint serine/threonine-protein kinase; **PDBTitle:** bub3 complex with bub1 glebs motif
26	c2i68B_	Alignment	not modelled	15.8	31	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**protein emre; **PDBTitle:** cryo-em based theoretical model structure of transmembrane2 domain of the multidrug-resistance antiporter from e. coli3 emre
27	c4hl5A_	Alignment	not modelled	14.5	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tankyrase-2; **PDBTitle:** complex structure of human tankyrase 2 with 7-hydroxy - 4'-2 methoxyflavone
28	c1dlcA_	Alignment	not modelled	14.5	11	**PDB header:**toxin **Chain:** A: **PDB Molecule:**delta-endotoxin cryiiia; **PDBTitle:** crystal structure of insecticidal delta-endotoxin from2 bacillus thuringiensis at 2.5 angstroms resolution

29	c2p7nA_	Alignment	not modelled	14.3	13	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**pathogenicity island 1 effector protein; **PDBTitle:** crystal structure of the pathogenicity island 1 effector2 protein from chromobacterium violaceum. northeast3 structural genomics consortium (nesgc) target cvr69.
30	c3b5iB_	Alignment	not modelled	13.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosyl-l-methionine:salicylic acid carboxyl **PDBTitle:** crystal structure of indole-3-acetic acid methyltransferase
31	c1rpqW_	Alignment	not modelled	12.0	38	**PDB header:**membrane protein **Chain:** W: **PDB Molecule:**peptide e131; **PDBTitle:** high affinity ige receptor (alpha chain) complexed with tight-binding2 e131 'zeta' peptide from phage display
32	d1zy3a1	Alignment	not modelled	11.8	24	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
33	d1alua_	Alignment	not modelled	11.6	9	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
34	c3c4hA_	Alignment	not modelled	11.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(adp-ribose) polymerase 3; **PDBTitle:** human poly(adp-ribose) polymerase 3, catalytic fragment in complex2 with an inhibitor dr2313
35	d2rd6a2	Alignment	not modelled	11.2	26	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Poly(ADP-ribose) polymerase, C-terminal domain
36	c2lhuA_	Alignment	not modelled	11.2	36	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mybpc3 protein; **PDBTitle:** structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
37	c2xa0A_	Alignment	not modelled	10.7	33	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** crystal structure of bcl-2 in complex with a bax bh32 peptide
38	c2lruA_	Alignment	not modelled	10.2	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase wnk1; **PDBTitle:** solution structure of the wnk1 autoinhibitory domain
39	c2vm6A_	Alignment	not modelled	10.1	35	**PDB header:**immune system **Chain:** A: **PDB Molecule:**bcl-2-related protein a1; **PDBTitle:** human bcl2-a1 in complex with bim-bh3 peptide
40	c1vgmB_	Alignment	not modelled	10.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**378aa long hypothetical citrate synthase; **PDBTitle:** crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaii strain7
41	d1bxla_	Alignment	not modelled	9.6	29	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
42	c2h12C_	Alignment	not modelled	9.4	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**citrate synthase; **PDBTitle:** structure of acetobacter aceti citrate synthase complexed2 with oxaloacetate and carboxymethyldethia coenzyme a (cmx)
43	d1jbob_	Alignment	not modelled	9.4	29	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
44	d1cpca_	Alignment	not modelled	9.1	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
45	c2o2fA_	Alignment	not modelled	9.0	33	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** solution structure of the anti-apoptotic protein bcl-2 in2 complex with an acyl-sulfonamide-based ligand
46	d1f99a_	Alignment	not modelled	8.9	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
47	c2r26C_	Alignment	not modelled	8.9	28	**PDB header:**transferase **Chain:** C: **PDB Molecule:**citrate synthase; **PDBTitle:** the structure of the ternary complex of carboxymethyl2 coenzyme a and oxalateacetate with citrate synthase from3 the thermophilic archaeonthermoplasma acidophilum
48	c3msuA_	Alignment	not modelled	8.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from francisella tularensis
49	d1eyxb_	Alignment	not modelled	8.8	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
50	d1qzga_	Alignment	not modelled	8.3	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
51	c3pmdA_	Alignment	not modelled	8.3	45	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** crystal structure of the sporulation inhibitor pxo1-118 from bacillus2 anthracis
52	d1kzyc2	Alignment	not modelled	8.3	38	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**53BP1
53	c3ongA_	Alignment	not modelled	8.2	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-activating enzyme e1-like; **PDBTitle:** crystal structure of uba2ufd-ubc9: insights into e1-e2 interactions in2 sumo pathways
54	c2dlrA_	Alignment	not modelled	8.2	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulator of g-protein signaling 10; **PDBTitle:** solution structure of the rgs domain of human regulator of2 g-protein signaling 10

55	d1ysga1	Alignment	not modelled	8.1	29	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
56	d1pq1a_	Alignment	not modelled	7.9	29	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
57	c2pfcA_	Alignment	not modelled	7.8	46	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv0098/mt0107; **PDBTitle:** structure of mycobacterium tuberculosis rv0098
58	c2vtgA_	Alignment	not modelled	7.8	14	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**ionized calcium-binding adapter molecule 2; **PDBTitle:** crystal structure of human iba2, trigonal crystal form
59	d1miua1	Alignment	not modelled	7.7	22	**Fold:**BRCA2 helical domain **Superfamily:**BRCA2 helical domain **Family:**BRCA2 helical domain
60	c2dw3A_	Alignment	not modelled	7.5	43	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**intrinsic membrane protein pufx; **PDBTitle:** solution structure of the rhodobacter sphaeroides pufx2 membrane protein
61	d1efya2	Alignment	not modelled	7.5	23	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Poly(ADP-ribose) polymerase, C-terminal domain
62	d1o0la_	Alignment	not modelled	7.4	25	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
63	d1dlca3	Alignment	not modelled	7.4	11	**Fold:**Toxins' membrane translocation domains **Superfamily:**delta-Endotoxin (insectocide), N-terminal domain **Family:**delta-Endotoxin (insectocide), N-terminal domain
64	c1rpqZ_	Alignment	not modelled	7.1	38	**PDB header:**membrane protein **Chain:** Z: **PDB Molecule:**peptide e131; **PDBTitle:** high affinity ige receptor (alpha chain) complexed with tight-binding2 e131 'zeta' peptide from phage display
65	d1jboa_	Alignment	not modelled	6.9	19	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
66	d1e5xa_	Alignment	not modelled	6.8	17	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
67	d1k3pa_	Alignment	not modelled	6.8	22	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
68	c2rf5A_	Alignment	not modelled	6.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tankyrase-1; **PDBTitle:** crystal structure of human tankyrase 1- catalytic parp domain
69	c2y9zB_	Alignment	not modelled	6.8	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**iswi one complex protein 3; **PDBTitle:** chromatin remodeling factor isw1a(del_atpase) in dna complex
70	c3thzA_	Alignment	not modelled	6.8	25	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**dna mismatch repair protein msh2; **PDBTitle:** human mutsbeta complexed with an idl of 6 bases (loop6) and adp
71	d1jc2a_	Alignment	not modelled	6.5	20	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
72	c1jc2A_	Alignment	not modelled	6.5	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c, skeletal muscle; **PDBTitle:** complex of the c-domain of troponin c with residues 1-40 of2 troponin i
73	d1g73a_	Alignment	not modelled	6.5	14	**Fold:**Spectrin repeat-like **Superfamily:**Smac/diablo **Family:**Smac/diablo
74	c3oqhB_	Alignment	not modelled	6.5	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein yvmc; **PDBTitle:** crystal structure of b. licheniformis cdps yvmc-blic
75	c1kcoA_	Alignment	not modelled	6.4	38	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e131 zeta peptide; **PDBTitle:** structure of e131 zeta peptide, a potent antagonist of the2 high-affinity ige receptor
76	d1jlia_	Alignment	not modelled	6.4	18	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
77	c4aj5B_	Alignment	not modelled	6.4	13	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**spindle and kinetochore-associated protein 1; **PDBTitle:** crystal structure of the ska core complex
78	c4d8mA_	Alignment	not modelled	6.4	16	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**pesticidal crystal protein cry5ba; **PDBTitle:** crystal structure of bacillus thuringiensis cry5b nematocidal toxin
79	c2zbkA_	Alignment	not modelled	6.3	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type ii dna topoisomerase vi subunit a; **PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
80	c1ji6A_	Alignment	not modelled	6.3	11	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidial crystal protein cry3bb; **PDBTitle:** crystal structure of the insecticidal bacterial del2 endotoxin cry3bb1 bacillus thuringiensis
						Fold: Ribosomal protein S5 domain 2-like

81	d2hkja2	Alignment	not modelled	6.3	22	**Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
82	d1vp7a_	Alignment	not modelled	6.3	22	**Fold:**Spectrin repeat-like **Superfamily:**XseB-like **Family:**XseB-like
83	c2lsyA_	Alignment	not modelled	6.2	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of the c-terminal domain from human rev1
84	c1iyjB_	Alignment	not modelled	6.2	23	**PDB header:**gene regulation/antitumor protein **Chain:** B: **PDB Molecule:**breast cancer susceptibility; **PDBTitle:** structure of a brca2-dss1 complex
85	c4exmB_	Alignment	not modelled	6.1	23	**PDB header:**toxin, hydrolase **Chain:** B: **PDB Molecule:**pesticin, lysozyme chimera; **PDBTitle:** the crystal structure of an engineered phage lysin containing the2 binding domain of pesticin and the killing domain of t4-lysozyme
86	d1gs0a2	Alignment	not modelled	6.1	18	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Poly(ADP-ribose) polymerase, C-terminal domain
87	c1wpaA_	Alignment	not modelled	6.1	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**occludin; **PDBTitle:** 1.5 angstrom crystal structure of human occludin fragment2 413-522
88	c2jrzA_	Alignment	not modelled	6.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**histone demethylase jarid1c; **PDBTitle:** solution structure of the bright/arid domain from the human2 jarid1c protein.
89	d2ponb1	Alignment	not modelled	6.0	29	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
90	d1fewa_	Alignment	not modelled	6.0	14	**Fold:**Spectrin repeat-like **Superfamily:**Smac/diablo **Family:**Smac/diablo
91	d1vp7b_	Alignment	not modelled	6.0	22	**Fold:**Spectrin repeat-like **Superfamily:**XseB-like **Family:**XseB-like
92	c4i5nE_	Alignment	not modelled	5.9	14	**PDB header:**hydrolase/toxin **Chain:** E: **PDB Molecule:**serine/threonine-protein phosphatase 2a regulatory subunit **PDBTitle:** structural mechanism of trimeric pp2a holoenzyme involving pr70:2 insight for cdc6 dephosphorylation
93	c1rpqX_	Alignment	not modelled	5.9	38	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**peptide e131; **PDBTitle:** high affinity ige receptor (alpha chain) complexed with tight-binding2 e131 'zeta' peptide from phage display
94	d1alla_	Alignment	not modelled	5.8	22	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
95	d1t1va_	Alignment	not modelled	5.8	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
96	c2lsjA_	Alignment	not modelled	5.7	24	**PDB header:**protein binding/protein binding **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** solution structure of the mouse rev1 ctd in complex with the rev1-2 interacting region (rir)of pol kappa
97	c1ykuB_	Alignment	not modelled	5.7	36	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein pxo2-61; **PDBTitle:** crystal structure of a sensor domain homolog
98	c3eb7B_	Alignment	not modelled	5.6	14	**PDB header:**toxin **Chain:** B: **PDB Molecule:**insecticidal delta-endotoxin cry8ea1; **PDBTitle:** crystal structure of insecticidal delta-endotoxin cry8ea1 from2 bacillus thuringiensis at 2.2 angstroms resolution
99	d1ioma_	Alignment	not modelled	5.6	19	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase