Phyre^2

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Description	P0A8I3
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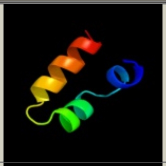
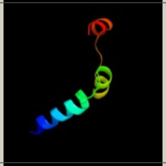
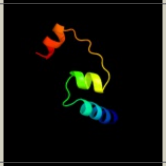
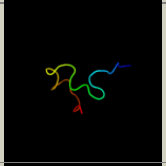
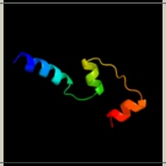
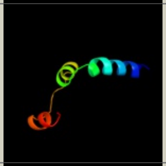
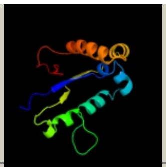
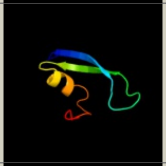
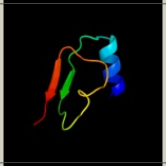
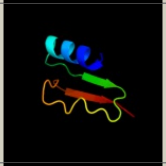
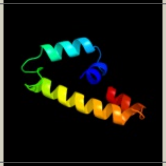
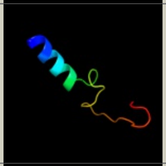
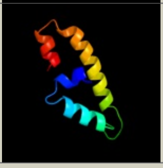
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2aq0a1	Alignment		71.4	16	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
2	d2ovra1	Alignment		35.2	14	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
3	c1kftA_	Alignment		31.6	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc subunit c; **PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli
4	d1kfta_	Alignment		31.6	19	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
5	d1nexa1	Alignment		30.5	18	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
6	c2p1nD_	Alignment		28.9	17	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
7	d1bd0a2	Alignment		27.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
8	c2ovqA_	Alignment		26.9	14	**PDB header:**transcription/cell cycle **Chain:** A: **PDB Molecule:**s-phase kinase-associated protein 1a; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex
9	d1fsea_	Alignment		26.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
10	c1nexC_	Alignment		25.6	17	**PDB header:**ligase, cell cycle **Chain:** C: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** crystal structure of scskp1-scdc4-cpd peptide complex
11	d1x2ia1	Alignment		22.5	9	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like

12	c2rjpC_	Alignment		20.3	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adamts-4; **PDBTitle:** crystal structure of adamts4 with inhibitor bound
13	c2kc2A_	Alignment		19.3	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the f1 domain (residues 86-202) of the2 talin
14	c3ieiD_	Alignment		18.6	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**leucine carboxyl methyltransferase 1; **PDBTitle:** crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine
15	d2bgwa1	Alignment		18.0	16	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
16	c3mntA_	Alignment		17.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucine carboxyl methyltransferase 1; **PDBTitle:** crystal structure of human leucine carboxyl methyltransferase 1
17	d1rjda_	Alignment		17.8	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Leucine carboxy methyltransferase Ppm1
18	d2fm9a1	Alignment		16.3	14	**Fold:**SipA N-terminal domain-like **Superfamily:**SipA N-terminal domain-like **Family:**SipA N-terminal domain-like
19	c2yfvC_	Alignment		15.7	28	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**scm3; **PDBTitle:** the heterotrimeric complex of kluyveromyces lactis scm3, cse4 and h4
20	d2fm8c1	Alignment		15.7	14	**Fold:**SipA N-terminal domain-like **Superfamily:**SipA N-terminal domain-like **Family:**SipA N-terminal domain-like
21	c1wcnA_	Alignment	not modelled	15.3	9	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** nmr structure of the carboxyterminal domains of escherichia2 coli nusa
22	d2a1jb1	Alignment	not modelled	15.2	6	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
23	d1fs2b1	Alignment	not modelled	14.0	17	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
24	d1k78a1	Alignment	not modelled	13.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
25	d1rcqa2	Alignment	not modelled	13.7	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
26	c2bhnD_	Alignment	not modelled	12.3	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xpf endonuclease; **PDBTitle:** xpf from aeropyrum pernix
27	d6paxa1	Alignment	not modelled	12.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
28	c2k9lA_	Alignment	not modelled	11.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
29	c2pfcA_	Alignment	not modelled	10.8	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv0098/mt0107;

						PDBTitle: structure of mycobacterium tuberculosis rv0098
30	d2i1qa1	Alignment	not modelled	10.1	18	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
31	d2cg4a1	Alignment	not modelled	9.6	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
32	c2lfcA_	Alignment	not modelled	9.4	4	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase, flavoprotein subunit; **PDBTitle:** solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
33	d1pzna1	Alignment	not modelled	7.8	12	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
34	d1lb2b_	Alignment	not modelled	7.7	8	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
35	c2o8xA_	Alignment	not modelled	7.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
36	c2g9pA_	Alignment	not modelled	7.2	62	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a; **PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
37	d1lvaa4	Alignment	not modelled	6.7	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
38	d1y0pa3	Alignment	not modelled	6.5	15	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
39	d1szpb1	Alignment	not modelled	6.4	11	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
40	d1y0ua_	Alignment	not modelled	6.3	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
41	c3ijrF_	Alignment	not modelled	6.3	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
42	c2wp0C_	Alignment	not modelled	6.3	13	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** crystal structure of a hoba-dnaa (domain i-ii) complex from2 helicobacter pylori.
43	c1qqp4_	Alignment	not modelled	6.3	56	**PDB header:**virus **Chain:** 4: **PDB Molecule:**protein (genome polyprotein); **PDBTitle:** foot-and-mouth disease virus/ oligosaccharide receptor complex.
44	d1cooa_	Alignment	not modelled	6.2	8	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
45	d2gwfa1	Alignment	not modelled	6.1	8	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Ubiquitin carboxyl-terminal hydrolase 8, USP8
46	c3k0bA_	Alignment	not modelled	6.0	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted n6-adenine-specific dna methylase; **PDBTitle:** crystal structure of a predicted n6-adenine-specific dna methylase2 from listeria monocytogenes str. 4b f2365
47	c3g9kD_	Alignment	not modelled	6.0	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**capsule biosynthesis protein capd; **PDBTitle:** crystal structure of bacillus anthracis transpeptidase enzyme capd
48	d1d4ca3	Alignment	not modelled	6.0	4	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
49	d1bmlc1	Alignment	not modelled	5.9	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
50	d1szpa1	Alignment	not modelled	5.8	11	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
51	c1giqA_	Alignment	not modelled	5.8	11	**PDB header:**toxin **Chain:** A: **PDB Molecule:**iota toxin component ia; **PDBTitle:** crystal structure of the enzymatic componet of iota-toxin2 from clostridium perfringens with nadh
52	c2nrzB_	Alignment	not modelled	5.7	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the c-terminal half of uvrc bound to2 its catalytic divalent cation
53	d1l4db_	Alignment	not modelled	5.7	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase

54	d1z3eb1	Alignment	not modelled	5.6	11	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
55	d1xsva_	Alignment	not modelled	5.6	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
56	c3us8A_	Alignment	not modelled	5.6	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase [nadp]; **PDBTitle:** crystal structure of an isocitrate dehydrogenase from sinorhizobium2 meliloti 1021
57	c3bqsB_	Alignment	not modelled	5.5	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 listeria monocytogenes, trigonal form
58	c2vswB_	Alignment	not modelled	5.5	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 16; **PDBTitle:** the structure of the rhodanese domain of the human dual2 specificity phosphatase 16
59	d1wc9a_	Alignment	not modelled	5.4	16	**Fold:**Ligand-binding domain in the NO signalling and Golgi transport **Superfamily:**Ligand-binding domain in the NO signalling and Golgi transport **Family:**TRAPP components
60	d1vfsa2	Alignment	not modelled	5.4	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
61	d1l4zb_	Alignment	not modelled	5.3	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
62	d2e9xb2	Alignment	not modelled	5.2	16	**Fold:**GINS/PriA/YqbF domain **Superfamily:**PriA/YqbF domain **Family:**PSF2 N-terminal domain-like
63	d1b22a_	Alignment	not modelled	5.2	14	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
64	c1b22A_	Alignment	not modelled	5.2	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
65	d1doqa_	Alignment	not modelled	5.2	5	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
66	d1a04a1	Alignment	not modelled	5.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)