Phyre^2

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Description	O15350
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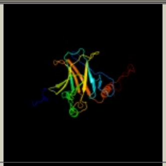
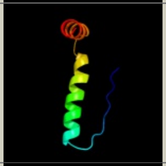
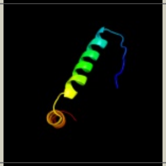
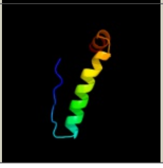
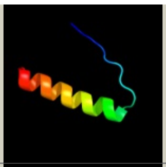
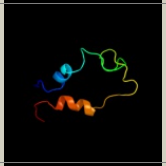
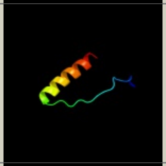
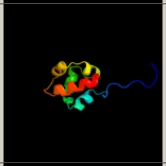
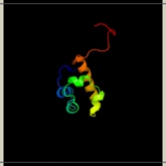
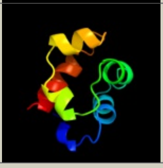
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rmnA_	Alignment		100.0	77	**PDB header:**cell cycle, antitumor protein **Chain:** A: **PDB Molecule:**tumor protein 63; **PDBTitle:** the solution structure of the p63 dna-binding domain
2	c2xipA_	Alignment		100.0	98	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**tumour protein p73; **PDBTitle:** crystal structure of the dna binding domain of human tp732 refined at 1.8 a resolution
3	c2j1xA_	Alignment		100.0	59	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** human p53 core domain mutant m133l-v203a-y220c-n239y-n268d
4	d2ac0a1	Alignment		100.0	59	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
5	d1hu8a_	Alignment		100.0	60	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
6	d1rg6a_	Alignment		99.9	49	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
7	d1dxsa_	Alignment		99.9	100	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
8	c4a9zD_	Alignment		99.6	59	**PDB header:**transcription **Chain:** D: **PDB Molecule:**tumor protein 63; **PDBTitle:** crystal structure of human p63 tetramerization domain
9	c2wttL_	Alignment		99.6	96	**PDB header:**transcription **Chain:** L: **PDB Molecule:**tumor protein p73; **PDBTitle:** structure of the human p73 tetramerization domain (crystal2 form ii)
10	d1coka_	Alignment		99.5	100	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
11	c3zy1A_	Alignment		99.5	55	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tumor protein 63; **PDBTitle:** crystal structure of the human p63 tetramerization domain

12	c2wqjM_	Alignment		98.5	100	**PDB header:**transcription **Chain:** M: **PDB Molecule:**tumor protein p73; **PDBTitle:** crystal structure of a truncated variant of the human p732 tetramerization domain
13	c2l14B_	Alignment		98.3	24	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structure of cbp nuclear coactivator binding domain in complex with2 p53 tad
14	d3saka_	Alignment		98.3	44	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
15	d1b0xa_	Alignment		98.2	17	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
16	c1b0xA_	Alignment		98.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (epha4 receptor tyrosine kinase); **PDBTitle:** the crystal structure of an eph receptor sam domain reveals2 a mechanism for modular dimerization.
17	c2e8nA_	Alignment		98.2	18	**PDB header:**transferase, signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** solution structure of the c-terminal sam-domain of ephaa2:2 ephrin type-a receptor 2 precursor (ec 2.7.10.1)
18	c2eaoA_	Alignment		98.2	17	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**ephrin type-b receptor 1; **PDBTitle:** solution structure of the c-terminal sam-domain of mouse2 ephrin type-b receptor 1 precursor (ec 2.7.1.112)
19	d1t4wa_	Alignment		98.2	23	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
20	c3h8mB_	Alignment		98.2	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 7; **PDBTitle:** sam domain of human ephrin type-a receptor 7 (epha7)
21	d1sgga_	Alignment	not modelled	98.2	17	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
22	c2kg5A_	Alignment	not modelled	98.1	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**arf-gap, rho-gap domain, ank repeat and ph **PDBTitle:** nmr solution structure of arap3-sam
23	d1b4fa_	Alignment	not modelled	98.0	17	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
24	c3kkaD_	Alignment	not modelled	98.0	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** co-crystal structure of the sam domains of epha1 and epha2
25	c3senD_	Alignment	not modelled	98.0	19	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**caskin-1; **PDBTitle:** structure of caskin1 tandem sams
26	d1v38a_	Alignment	not modelled	98.0	17	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
27	c2dl0A_	Alignment	not modelled	98.0	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the sam-domain of the sam and sh32 domain containing protein 1
28	d1x40a1	Alignment	not modelled	98.0	18	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
						PDB header:structural protein

29	c3k1rB_	Alignment	not modelled	97.9	17	**Chain:** B: **PDB Molecule:**usher syndrome type-1g protein; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
30	c3hilB_	Alignment	not modelled	97.9	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** sam domain of human ephrin type-a receptor 1 (epha1)
31	d1ucva_	Alignment	not modelled	97.9	17	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
32	c2eamA_	Alignment	not modelled	97.8	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative 47 kda protein; **PDBTitle:** solution structure of the n-terminal sam-domain of a human2 putative 47 kda protein
33	c2fe9A_	Alignment	not modelled	97.8	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein vts1; **PDBTitle:** solution structure of the vts1 sam domain in the presence2 of rna
34	d1ow5a_	Alignment	not modelled	97.8	24	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
35	c1ow5A_	Alignment	not modelled	97.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase ste11; **PDBTitle:** nmr structure of the saccharomyces cerevisiae sam (sterile2 alpha motif) domain
36	c2k4pA_	Alignment	not modelled	97.8	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**phosphatidylinositol-3,4,5-trisphosphate 5- **PDBTitle:** solution structure of ship2-sam
37	c2lmrA_	Alignment	not modelled	97.8	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ankyrin repeat and sam domain-containing protein 1a; **PDBTitle:** solution structure of the first sam domain of odin
38	c1oxjA_	Alignment	not modelled	97.6	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-binding protein smaug; **PDBTitle:** crystal structure of the smaug rna binding domain
39	c2kivA_	Alignment	not modelled	97.6	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ankyrin repeat and sterile alpha motif domain- **PDBTitle:** aida-1 sam domain tandem
40	c2ke7A_	Alignment	not modelled	97.6	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin repeat and sterile alpha motif domain- **PDBTitle:** nmr structure of the first sam domain from aida1
41	d1hs5a_	Alignment	not modelled	97.6	45	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
42	d1aiea_	Alignment	not modelled	97.6	48	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
43	d1oxja1	Alignment	not modelled	97.6	16	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
44	c2qkqA_	Alignment	not modelled	97.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-b receptor 4; **PDBTitle:** structure of the sam domain of human ephrin type-b receptor2 4
45	d1a1ua_	Alignment	not modelled	97.4	44	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
46	c3bq7A_	Alignment	not modelled	97.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase delta; **PDBTitle:** sam domain of diacylglycerol kinase delta1 (e35g)
47	c2j10A_	Alignment	not modelled	97.4	44	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
48	c2j10D_	Alignment	not modelled	97.4	44	**PDB header:**transcription **Chain:** D: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
49	c2j10B_	Alignment	not modelled	97.4	44	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
50	c2b6gA_	Alignment	not modelled	97.4	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**vts1p; **PDBTitle:** rna recognition by the vts1 sam domain
51	c2j11D_	Alignment	not modelled	97.4	44	**PDB header:**transcription **Chain:** D: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant y327s t329g q331g
52	c3zy0C_	Alignment	not modelled	97.3	62	**PDB header:**transcription **Chain:** C: **PDB Molecule:**tumor protein p63; **PDBTitle:** crystal structure of a truncated variant of the human p632 tetramerization domain lacking the c-terminal helix
53	c2gleA_	Alignment	not modelled	97.2	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**neurabin-1; **PDBTitle:** solution structure of neurabin sam domain
54	c2eseA_	Alignment	not modelled	97.2	12	**PDB header:**protein/rna complex **Chain:** A: **PDB Molecule:**vts1p; **PDBTitle:** structure of the sam domain of vts1p in complex with rna
55	d2f3na1	Alignment	not modelled	97.1	25	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
						PDB header:transferase/transcription

56	c2k8fB_	Alignment	not modelled	96.8	29	**Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structural basis for the regulation of p53 function by p300
57	d1wwva1	Alignment	not modelled	96.3	22	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
58	c3bs5A_	Alignment	not modelled	96.1	15	**PDB header:**signaling protein/membrane protein **Chain:** A: **PDB Molecule:**protein aveugle; **PDBTitle:** crystal structure of hcnk2-sam/dhyp-sam complex
59	c2dkzA_	Alignment	not modelled	96.0	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**hypothetical protein loc64762; **PDBTitle:** solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
60	c3bs7A_	Alignment	not modelled	95.8	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein aveugle; **PDBTitle:** crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
61	c2eanA_	Alignment	not modelled	95.7	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**connector enhancer of kinase suppressor of ras 2; **PDBTitle:** solution structure of the n-terminal sam-domain of human2 kiaa0902 protein (connector enhancer of kinase suppressor3 of ras 2)
62	d1pk1c1	Alignment	not modelled	95.3	18	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
63	c1v85A_	Alignment	not modelled	95.1	26	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**similar to ring finger protein 36; **PDBTitle:** sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator
64	d1pk3a1	Alignment	not modelled	94.9	9	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
65	d1kw4a_	Alignment	not modelled	94.7	19	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
66	c1pk1A_	Alignment	not modelled	94.6	20	**PDB header:**transcription repression **Chain:** A: **PDB Molecule:**polyhomeotic-proximal chromatin protein; **PDBTitle:** hetero sam domain structure of ph and scm.
67	c2e8oA_	Alignment	not modelled	93.7	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam domain and hd domain-containing protein 1; **PDBTitle:** solution structure of the n-terminal sam-domain of the sam2 domain and hd domain containing protein 1 (dendritic cell-3 derived ifng-induced protein) (dcip) (monocyte protein 5)4 (mop-5)
68	c1pk1B_	Alignment	not modelled	92.6	9	**PDB header:**transcription repression **Chain:** B: **PDB Molecule:**sex comb on midleg cg9495-pa; **PDBTitle:** hetero sam domain structure of ph and scm.
69	c1q2iA_	Alignment	not modelled	90.9	43	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**pnc27; **PDBTitle:** nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
70	c2l5yA_	Alignment	not modelled	88.6	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**stromal interaction molecule 2; **PDBTitle:** nmr structure of calcium-loaded stim2 ef-sam.
71	d1uqva_	Alignment	not modelled	87.4	6	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
72	c3dacB_	Alignment	not modelled	80.9	38	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structure of the human mdmx protein bound to the p53 tumor2 suppressor transactivation domain
73	c3if8B_	Alignment		78.1	23	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**protein zwilch homolog; **PDBTitle:** crystal structure of zwilch, a member of the rzz kinetochore complex
74	c3dacP_	Alignment	not modelled	74.2	42	**PDB header:**cell cycle **Chain:** P: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structure of the human mdmx protein bound to the p53 tumor2 suppressor transactivation domain
75	c2k60A_	Alignment	not modelled	68.5	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein (stromal interaction molecule 1); **PDBTitle:** nmr structure of calcium-loaded stim1 ef-sam
76	c2xseA_	Alignment		58.9	56	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thymine dioxygenase jbp1; **PDBTitle:** the structural basis for recognition of j-base containing2 dna by a novel dna-binding domain in jbp1
77	c2rp5A_	Alignment	not modelled	53.5	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative uncharacterized protein cep-1; **PDBTitle:** solution structure of the oligomerization domain in cep-1
78	c3nb2B_	Alignment	not modelled	53.2	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**secreted effector protein; **PDBTitle:** crystal structure of e. coli o157:h7 effector protein nlel
79	d2aq0a1	Alignment	not modelled	48.3	12	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like

						Family: Hef domain-like
80	c2b3gB_	Alignment	not modelled	42.3	25	**PDB header:**replication **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53n (fragment 33-60) bound to rpa70n
81	d1b22a_	Alignment	not modelled	42.1	14	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
82	c1b22A_	Alignment	not modelled	42.1	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
83	c2qzaA_	Alignment	not modelled	39.6	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**secreted effector protein; **PDBTitle:** crystal structure of salmonella effector protein sopa
84	c2xdvA_	Alignment	not modelled	32.7	25	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
85	c4diqA_	Alignment	not modelled	32.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase no66; **PDBTitle:** crystal structure of human no66
86	d1szpa1	Alignment	not modelled	32.5	14	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
87	c3gycB_	Alignment	not modelled	29.1	57	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glycoside hydrolase; **PDBTitle:** crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
88	c3cguB_	Alignment	not modelled	23.2	44	**PDB header:**hormone/signaling protein **Chain:** B: **PDB Molecule:**protein giant-lens; **PDBTitle:** crystal structure of unliganded argos
89	c1v9pB_	Alignment	not modelled	21.6	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
90	d2gsca1	Alignment	not modelled	19.5	22	**Fold:**Bromodomain-like **Superfamily:**IVS-encoded protein-like **Family:**IVS-encoded protein-like
91	d1vrba1	Alignment	not modelled	18.5	13	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
92	c3kf6A_	Alignment	not modelled	17.3	7	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex
93	d1zeta2	Alignment	not modelled	16.9	23	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
94	d2i1qa1	Alignment	not modelled	16.5	21	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
95	c3qwlA_	Alignment	not modelled	16.1	33	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**tbc1 domain family member 7; **PDBTitle:** crystal structure of human tbc1 domain family member 7
96	c3c1zA_	Alignment	not modelled	16.0	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna integrity scanning protein disa; **PDBTitle:** structure of the ligand-free form of a bacterial dna damage2 sensor protein
97	c2p3fN_	Alignment	not modelled	15.4	33	**PDB header:**hydrolase **Chain:** N: **PDB Molecule:**anti-coagulant protein 5; **PDBTitle:** crystal structure of the factor xa/nap5 complex
98	d1lb2b_	Alignment	not modelled	15.0	17	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
99	c3lk2B_	Alignment	not modelled	14.8	25	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**f-actin-capping protein subunit beta isoforms 1 and 2; **PDBTitle:** crystal structure of capz bound to the uncapping motif from carmil