Phyre²

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Description	P02340
Date	Tue Jul 30 12:57:01 BST 2013
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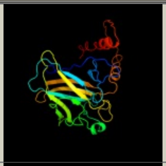
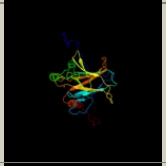
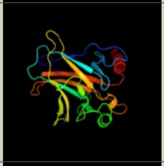
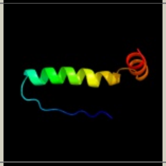
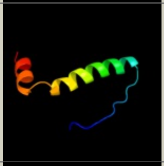
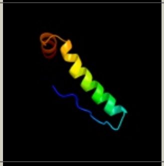
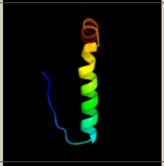
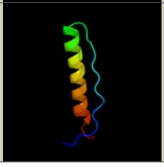
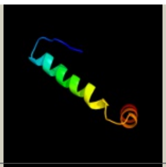
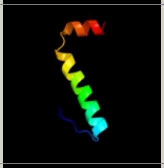
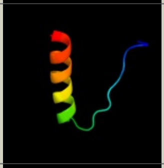
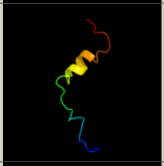
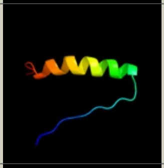
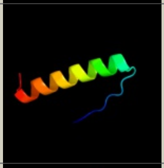
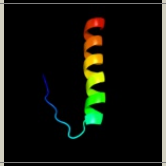
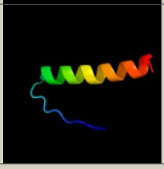
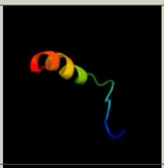
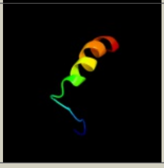
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3q06B_	 Alignment		100.0	86	**PDB header:**cell cycle/dna **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** an induced fit mechanism regulates p53 dna binding kinetics to confer2 sequence specificity
2	c2rmnA_	 Alignment		100.0	51	**PDB header:**cell cycle, antitumor protein **Chain:** A: **PDB Molecule:**tumor protein 63; **PDBTitle:** the solution structure of the p63 dna-binding domain
3	c2j1xA_	 Alignment		100.0	88	**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	89	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
5	c2xipA_	 Alignment		100.0	57	**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
6	d1hu8a_	 Alignment		100.0	99	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
7	c4a9zD_	 Alignment		99.3	31	**PDB header:**transcription **Chain:** D: **PDB Molecule:**tumor protein 63; **PDBTitle:** crystal structure of human p63 tetramerization domain
8	c4a9zC_	 Alignment		99.3	31	**PDB header:**transcription **Chain:** C: **PDB Molecule:**tumor protein 63; **PDBTitle:** crystal structure of human p63 tetramerization domain
9	c3zy1A_	 Alignment		99.3	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tumor protein 63; **PDBTitle:** crystal structure of the human p63 tetramerization domain
10	c2wttL_	 Alignment		99.2	30	**PDB header:**transcription **Chain:** L: **PDB Molecule:**tumor protein p73; **PDBTitle:** structure of the human p73 tetramerization domain (crystal2 form ii)
11	d3saka_	 Alignment		99.2	86	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain

12	c2wttN_	Alignment		99.0	32	**PDB header:**transcription **Chain:** N: **PDB Molecule:**tumor protein p73; **PDBTitle:** structure of the human p73 tetramerization domain (crystal2 form ii)
13	c2wttH_	Alignment		99.0	32	**PDB header:**transcription **Chain:** H: **PDB Molecule:**tumor protein p73; **PDBTitle:** structure of the human p73 tetramerization domain (crystal2 form ii)
14	c2wqjK_	Alignment		98.6	43	**PDB header:**transcription **Chain:** K: **PDB Molecule:**tumor protein p73; **PDBTitle:** crystal structure of a truncated variant of the human p732 tetramerization domain
15	d1t4wa_	Alignment		98.6	21	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
16	c2k8fB_	Alignment		98.6	72	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structural basis for the regulation of p53 function by p300
17	d1hs5a_	Alignment		98.6	79	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
18	d1aiea_	Alignment		98.4	87	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
19	c2j10B_	Alignment		98.3	87	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
20	c2j10A_	Alignment		98.3	87	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
21	c2j10D_	Alignment	not modelled	98.3	87	**PDB header:**transcription **Chain:** D: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
22	c2j11D_	Alignment	not modelled	98.3	81	**PDB header:**transcription **Chain:** D: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant y327s t329g q331g
23	c2wqjM_	Alignment	not modelled	98.3	41	**PDB header:**transcription **Chain:** M: **PDB Molecule:**tumor protein p73; **PDBTitle:** crystal structure of a truncated variant of the human p732 tetramerization domain
24	d1a1ua_	Alignment	not modelled	98.2	79	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
25	c2l14B_	Alignment		97.7	62	**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
26	c3zy0C_	Alignment	not modelled	96.9	41	**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
27	c2ly4B_	Alignment	not modelled	96.9	61	**PDB header:**nuclear protein/antitumour protein **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** hmgb1-facilitated p53 dna binding occurs via hmg-box/p532 transactivation domain interaction and is regulated by the acidic3 tail

28	c1q2iA_	Alignment	not modelled	92.1	87	**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
29	c1dt7Y_	Alignment		91.5	70	**PDB header:**signaling protein **Chain:** Y: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** solution structure of the c-terminal negative regulatory2 domain of p53 in a complex with ca2+-bound s100b(bb)
30	c1dt7X_	Alignment		91.5	70	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** solution structure of the c-terminal negative regulatory2 domain of p53 in a complex with ca2+-bound s100b(bb)
31	c3dacB_	Alignment	not modelled	67.7	77	**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
32	c1jspA_	Alignment	not modelled	63.9	68	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**tumor protein p53; **PDBTitle:** nmr structure of cbp bromodomain in complex with p53 peptide
33	c2xdvA_	Alignment	not modelled	63.1	32	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
34	c3dacP_	Alignment	not modelled	57.6	83	**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
35	c4diqA_	Alignment	not modelled	46.5	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase no66; **PDBTitle:** crystal structure of human no66
36	c3gycB_	Alignment	not modelled	25.3	43	**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
37	d1vrba1	Alignment	not modelled	25.1	20	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
38	c4joiA_	Alignment	not modelled	21.0	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cst complex subunit stn1; **PDBTitle:** crystal structure of the human telomeric stn1-ten1 complex
39	d1iknc_	Alignment	not modelled	19.7	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
40	c3cguB_	Alignment	not modelled	19.2	44	**PDB header:**hormone/signaling protein **Chain:** B: **PDB Molecule:**protein giant-lens; **PDBTitle:** crystal structure of unliganded argos
41	c2b3gB_	Alignment	not modelled	15.6	50	**PDB header:**replication **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53n (fragment 33-60) bound to rpa70n
42	d1ef1c_	Alignment	not modelled	14.8	21	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Moesin tail domain **Family:**Moesin tail domain
43	c4gopB_	Alignment	not modelled	14.7	21	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure and conformational change of a replication protein a2 heterotrimer bound to ssdna
44	c2pi2A_	Alignment	not modelled	11.7	11	**PDB header:**replication, dna binding protein **Chain:** A: **PDB Molecule:**replication protein a 32 kda subunit; **PDBTitle:** full-length replication protein a subunits rpa14 and rpa32
45	d1e7ua3	Alignment	not modelled	11.1	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
46	d1e8ya3	Alignment	not modelled	11.1	36	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
47	d1w5sa1	Alignment	not modelled	10.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
48	d2pi2a1	Alignment	not modelled	10.2	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
49	c3kf6A_	Alignment	not modelled	10.2	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex
50	c3czdA_	Alignment	not modelled	8.6	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaminase kidney isoform; **PDBTitle:** crystal structure of human glutaminase in complex with l-glutamate
51	c3ss4C_	Alignment	not modelled	8.5	42	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glutaminase c; **PDBTitle:** crystal structure of mouse glutaminase c, phosphate-bound form
						PDB header:hydrolase

52	c3ih9A_	Alignment	not modelled	8.4	29	**Chain:** A: **PDB Molecule:**salt-tolerant glutaminase; **PDBTitle:** crystal structure analysis of mglu in its tris form
53	c2dfwA_	Alignment	not modelled	8.2	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**salt-tolerant glutaminase; **PDBTitle:** crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
54	c3lsoA_	Alignment	not modelled	8.1	45	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative membrane anchored protein; **PDBTitle:** crystal structure of putative membrane anchored protein from2 corynebacterium diphtheriae
55	c1pxeA_	Alignment	not modelled	8.0	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**neural zinc finger transcription factor 1; **PDBTitle:** solution structure of a cchhc domain of neural zinc finger2 factor-1
56	d1regx_	Alignment	not modelled	8.0	23	**Fold:**Ferredoxin-like **Superfamily:**Translational regulator protein regA **Family:**Translational regulator protein regA
57	c2pbyB_	Alignment	not modelled	7.9	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaminase; **PDBTitle:** probable glutaminase from geobacillus kaustophilus hta426
58	c1zldA_	Alignment	not modelled	7.9	54	**PDB header:**toxin **Chain:** A: **PDB Molecule:**ptr necrosis toxin; **PDBTitle:** crystal structure of a rgd-containing host-selective toxin:2 pyrenophora tritici-repentis ptr toxa
59	d1o5wa2	Alignment	not modelled	7.9	33	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**L-aminoacid/polyamine oxidase
60	d2je8a3	Alignment	not modelled	7.9	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
61	c3uo9B_	Alignment	not modelled	7.6	42	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**glutaminase kidney isoform, mitochondrial; **PDBTitle:** crystal structure of human gac in complex with glutamate and bptes
62	d1ko7a2	Alignment	not modelled	7.4	19	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**HPr kinase HprK C-terminal domain
63	d1ydua1	Alignment	not modelled	7.2	19	**Fold:**At5g01610-like **Superfamily:**At5g01610-like **Family:**At5g01610-like
64	c1t0pB_	Alignment	not modelled	6.9	19	**PDB header:**immune system **Chain:** B: **PDB Molecule:**intercellular adhesion molecule-3; **PDBTitle:** structural basis of icam recognition by integrin alpahlbeta2 revealed2 in the complex structure of binding domains of icam-3 and alphalbeta23 at 1.65 a
65	d1u60a_	Alignment	not modelled	6.8	29	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Glutaminase
66	c2q37A_	Alignment	not modelled	6.6	30	**PDB header:**plant protein, lyase **Chain:** A: **PDB Molecule:**ohcu decarboxylase; **PDBTitle:** crystal structure of ohcu decarboxylase in the presence of2 (s)-allantoin
67	d2q37a1	Alignment	not modelled	6.6	30	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
68	c1svcP_	Alignment	not modelled	6.4	15	**PDB header:**transcription/dna **Chain:** P: **PDB Molecule:**protein (nuclear factor kappa-b (nf-kb)); **PDBTitle:** nfkb p50 homodimer bound to dna
69	d1e6vc_	Alignment	not modelled	6.2	58	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase gamma chain
70	c1ixtA_	Alignment	not modelled	6.0	80	**PDB header:**toxin **Chain:** A: **PDB Molecule:**spasmodic protein tx9a-like protein; **PDBTitle:** structure of a novel p-superfamily spasmodic conotoxin2 reveals an inhibitory cystine knot motif
71	d1ixta_	Alignment	not modelled	6.0	80	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Conotoxin
72	d2o8ia1	Alignment	not modelled	6.0	13	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
73	d1fx0b1	Alignment	not modelled	5.7	28	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
74	d3c7ba1	Alignment	not modelled	5.5	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
75	d2bosa_	Alignment	not modelled	5.4	38	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
76	c2wxoA_	Alignment	not modelled	5.1	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** the crystal structure of the murine class ia pi 3-kinase2 p110delta in complex with as5.
77	c3kbyB_	Alignment	not modelled	5.1	22	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of hypothetical protein from staphylococcus aureus