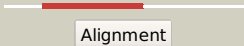

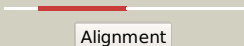

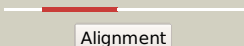







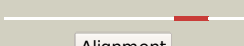











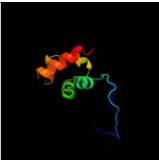
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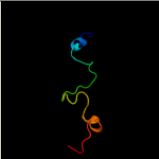
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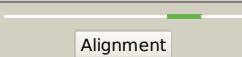
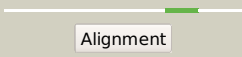
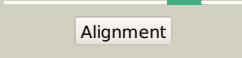
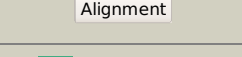
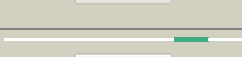

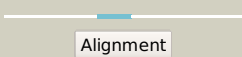
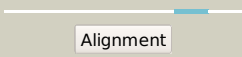
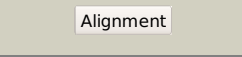
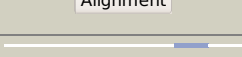
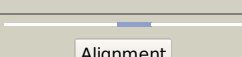
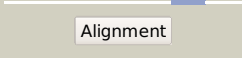
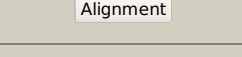
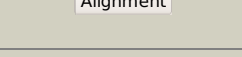
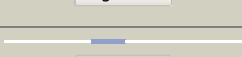
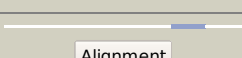
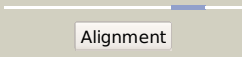
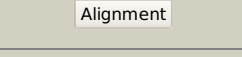
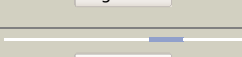
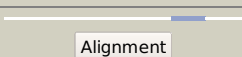


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3q06B	 Alignment		100.0	55	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	77	PDB header: cell cycle, antitumor protein Chain: A: PDB Molecule: tumor protein p63; PDBTitle: the solution structure of the p63 dna-binding domain
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	c2xipA	 Alignment		100.0	96	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
5	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
6	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
7	d1rg6a	 Alignment		99.9	45	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
8	d1dxsa	 Alignment		99.8	95	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
9	c4a9zC	 Alignment		99.7	54	PDB header: transcription Chain: C: PDB Molecule: tumor protein p63; PDBTitle: crystal structure of human p63 tetramerization domain
10	c4a9zD	 Alignment		99.6	57	PDB header: transcription Chain: D: PDB Molecule: tumor protein p63; PDBTitle: crystal structure of human p63 tetramerization domain
11	c2wttL	 Alignment		99.6	83	PDB header: transcription Chain: L: PDB Molecule: tumor protein p73; PDBTitle: structure of the human p73 tetramerization domain (crystal2 form ii)

12	c2wttH_	Alignment		99.5	85	PDB header: transcription Chain: H: PDB Molecule: tumor protein p73; PDBTitle: structure of the human p73 tetramerization domain (crystal2 form ii)
13	c2wttN_	Alignment		99.5	85	PDB header: transcription Chain: N: PDB Molecule: tumor protein p73; PDBTitle: structure of the human p73 tetramerization domain (crystal2 form ii)
14	c3zy1A_	Alignment		99.5	53	PDB header: transcription Chain: A: PDB Molecule: tumor protein 63; PDBTitle: crystal structure of the human p63 tetramerization domain
15	d1coka_	Alignment		99.4	93	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
16	c2wqjK_	Alignment		98.8	83	PDB header: transcription Chain: K: PDB Molecule: tumor protein p73; PDBTitle: crystal structure of a truncated variant of the human p732 tetramerization domain
17	c2wqjM_	Alignment		98.5	82	PDB header: transcription Chain: M: PDB Molecule: tumor protein p73; PDBTitle: crystal structure of a truncated variant of the human p732 tetramerization domain
18	d3saka_	Alignment		98.4	38	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
19	d1t4wa_	Alignment		98.1	23	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: p53 DNA-binding domain-like
20	c2e8nA_	Alignment		98.1	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)
21	c2eaoA_	Alignment	not modelled	98.0	16	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)
22	c1b0xA_	Alignment	not modelled	98.0	15	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.
23	d1b0xa_	Alignment	not modelled	98.0	15	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
24	d1sgga_	Alignment	not modelled	98.0	18	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
25	c3h8mB_	Alignment	not modelled	97.9	21	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 7; PDBTitle: sam domain of human ephrin type-a receptor 7 (epha7)
26	d1x40a1	Alignment	not modelled	97.8	15	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
27	c3senD_	Alignment	not modelled	97.8	17	PDB header: signaling protein Chain: D: PDB Molecule: caskin-1; PDBTitle: structure of caskin1 tandem sams

28	c2dl0A_	Alignment		97.8	18	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
29	c2kg5A_	Alignment	not modelled	97.8	20	PDB header: signaling protein Chain: A: PDB Molecule: arf-gap, rho-gap domain, ank repeat and ph PDBTitle: nmr solution structure of arap3-sam
30	c3kkaD_	Alignment	not modelled	97.8	20	PDB header: transferase Chain: D: PDB Molecule: ephrin type-a receptor 2; PDBTitle: co-crystal structure of the sam domains of epha1 and epha2
31	c3k1rB_	Alignment	not modelled	97.8	19	PDB header: structural protein Chain: B: PDB Molecule: usher syndrome type-1g protein; PDBTitle: structure of harmonin npd21 in complex with the sam-pbm of2 sans
32	d1b4fa_	Alignment	not modelled	97.8	18	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
33	d1v38a_	Alignment	not modelled	97.7	14	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
34	c2k4pA_	Alignment	not modelled	97.6	20	PDB header: signaling protein Chain: A: PDB Molecule: phosphatidylinositol-3,4,5-trisphosphate 5- PDBTitle: solution structure of ship2-sam
35	d1aiea_	Alignment	not modelled	97.6	41	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
36	d1ucva_	Alignment	not modelled	97.6	14	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
37	c3hilB_	Alignment	not modelled	97.6	23	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: sam domain of human ephrin type-a receptor 1 (epha1)
38	d1hs5a_	Alignment	not modelled	97.5	41	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
39	c2eamA_	Alignment	not modelled	97.5	16	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
40	c1oxjA_	Alignment	not modelled	97.5	14	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein smaug; PDBTitle: crystal structure of the smaug rna binding domain
41	d1a1ua_	Alignment	not modelled	97.5	41	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
42	c2lmrA_	Alignment	not modelled	97.5	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
43	c2j10D_	Alignment	not modelled	97.4	41	PDB header: transcription Chain: D: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k
44	c2j10A_	Alignment	not modelled	97.4	41	PDB header: transcription Chain: A: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k
45	c2j10B_	Alignment	not modelled	97.4	41	PDB header: transcription Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k
46	c3zy0C_	Alignment	not modelled	97.4	58	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
47	c2fe9A_	Alignment	not modelled	97.4	17	PDB header: rna binding protein Chain: A: PDB Molecule: protein vts1; PDBTitle: solution structure of the vts1 sam domain in the presence2 of rna
48	c1ow5A_	Alignment	not modelled	97.4	25	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase ste11; PDBTitle: nmr structure of the saccharomyces cerevisiae sam (sterile2 alpha motif) domain
49	d1ow5a_	Alignment	not modelled	97.4	25	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
50	c2j11D_	Alignment	not modelled	97.4	41	PDB header: transcription Chain: D: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant y327s t329g q331g
51	c2ke7A_	Alignment	not modelled	97.3	17	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
52	c2kivA_	Alignment	not modelled	97.3	20	PDB header: signaling protein Chain: A: PDB Molecule: ankyrin repeat and sterile alpha motif domain- PDBTitle: aida-1 sam domain tandem
53	d1oxja1	Alignment	not modelled	97.3	18	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain

54	c2qkqA	Alignment	not modelled	97.2	21	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
55	c3bq7A	Alignment	not modelled	96.9	23	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase delta; PDBTitle: sam domain of diacylglycerol kinase delta1 (e35g)
56	c2b6gA	Alignment	not modelled	96.8	14	PDB header: rna binding protein Chain: A: PDB Molecule: vts1p; PDBTitle: rna recognition by the vts1 sam domain
57	c2eseA	Alignment	not modelled	96.8	14	PDB header: protein/rna complex Chain: A: PDB Molecule: vts1p; PDBTitle: structure of the sam domain of vts1p in complex with rna
58	c2gleA	Alignment	not modelled	96.7	27	PDB header: protein binding Chain: A: PDB Molecule: neurabin-1; PDBTitle: solution structure of neurabin sam domain
59	d2f3na1	Alignment	not modelled	96.5	27	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
60	c2l14B	Alignment		96.4	32	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
61	c3tadB	Alignment	not modelled	96.4	26	PDB header: protein binding Chain: B: PDB Molecule: liprin-alpha-2; PDBTitle: crystal structure of the liprin-alpha/liprin-beta complex
62	c2ly4B	Alignment		95.7	33	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
63	c3bs5A	Alignment	not modelled	95.5	18	PDB header: signaling protein/membrane protein Chain: A: PDB Molecule: protein aveugle; PDBTitle: crystal structure of the hcnk2-sam/dhyp-sam complex
64	d1wwva1	Alignment	not modelled	95.5	24	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
65	c2dkzA	Alignment	not modelled	95.4	26	PDB header: signaling protein Chain: A: PDB Molecule: hypothetical protein loc64762; PDBTitle: solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
66	c2eanA	Alignment	not modelled	95.2	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)
67	c3bs7A	Alignment	not modelled	94.6	18	PDB header: signaling protein Chain: A: PDB Molecule: protein aveugle; PDBTitle: crystal structure of the sterile alpha motif (sam) domain2 of hypphen/aveugle
68	d1pk1c1	Alignment	not modelled	93.3	18	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
69	d1kw4a	Alignment	not modelled	93.3	19	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
70	d1pk3a1	Alignment	not modelled	92.6	9	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
71	c1pk1A	Alignment	not modelled	92.1	20	PDB header: transcription repression Chain: A: PDB Molecule: polyhomeotic-proximal chromatin protein; PDBTitle: hetero sam domain structure of ph and scm.
72	c2k8fB	Alignment	not modelled	90.5	32	PDB header: transferase/transcription Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: structural basis for the regulation of p53 function by p300
73	c2e8oA	Alignment	not modelled	88.9	22	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)
74	c1pk1B	Alignment	not modelled	88.8	9	PDB header: transcription repression Chain: B: PDB Molecule: sex comb on midleg cg9495-pa; PDBTitle: hetero sam domain structure of ph and scm.
75	c1v85A	Alignment	not modelled	88.2	23	PDB header: apoptosis Chain: A: PDB Molecule: similar to ring finger protein 36; PDBTitle: sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator
76	c2l5yA	Alignment	not modelled	80.9	15	PDB header: signaling protein Chain: A: PDB Molecule: stromal interaction molecule 2; PDBTitle: nmr structure of calcium-loaded stim2 ef-sam.
77	d1uqva	Alignment	not modelled	80.4	10	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain

78	c1q2iA	 Alignment	not modelled	59.8	50	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
79	c3if8B	 Alignment	not modelled	51.7	22	PDB header: cell cycle Chain: B: PDB Molecule: protein zwilch homolog; PDBTitle: crystal structure of zwilch, a member of the rzz kinetochore complex
80	c3no4A	 Alignment	not modelled	51.2	13	PDB header: hydrolase Chain: A: PDB Molecule: creatinine amidohydrolase; PDBTitle: crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
81	c2rp5A	 Alignment	not modelled	48.5	19	PDB header: transcription Chain: A: PDB Molecule: putative uncharacterized protein cep-1; PDBTitle: solution structure of the oligomerization domain in cep-1
82	c2k60A	 Alignment	not modelled	45.6	19	PDB header: signaling protein Chain: A: PDB Molecule: protein (stromal interaction molecule 1); PDBTitle: nmr structure of calcium-loaded stim1 ef-sam
83	c3dacB	 Alignment	not modelled	45.5	36	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
84	d2a1ja1	 Alignment	not modelled	41.7	15	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
85	c3dacP	 Alignment	not modelled	37.7	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
86	c3gycB	 Alignment	not modelled	33.5	57	PDB header: hydrolase Chain: B: PDB Molecule: putative glycoside hydrolase; PDBTitle: crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distazonis atcc 8503 at 1.85 a resolution
87	c2xseA	 Alignment	not modelled	31.5	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
88	d2aq0a1	 Alignment	not modelled	30.6	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
89	d1b22a	 Alignment	not modelled	29.6	10	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
90	c1b22A	 Alignment	not modelled	29.6	10	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
91	c2xdvA	 Alignment	not modelled	28.8	17	PDB header: nuclear protein Chain: A: PDB Molecule: myc-induced nuclear antigen; PDBTitle: crystal structure of the catalytic domain of flj14393
92	c1v9pB	 Alignment	not modelled	27.6	19	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
93	c3cguB	 Alignment	not modelled	27.4	44	PDB header: hormone/signaling protein Chain: B: PDB Molecule: protein giant-lens; PDBTitle: crystal structure of unliganded argos
94	c3lubE	 Alignment	not modelled	27.2	19	PDB header: hydrolase Chain: E: PDB Molecule: putative creatinine amidohydrolase; PDBTitle: crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
95	c3nb2B	 Alignment	not modelled	26.7	17	PDB header: ligase Chain: B: PDB Molecule: secreted effector protein; PDBTitle: crystal structure of e. coli o157:h7 effector protein nlel
96	c4joiA	 Alignment	not modelled	25.4	11	PDB header: dna binding protein Chain: A: PDB Molecule: cst complex subunit stn1; PDBTitle: crystal structure of the human telomeric stn1-ten1 complex
97	c2owoA	 Alignment	not modelled	24.7	19	PDB header: ligase/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
98	d1lb2b	 Alignment	not modelled	23.9	19	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
99	d1doqa	 Alignment	not modelled	23.7	22	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
100	c4akaA	 Alignment	not modelled	23.3	42	PDB header: immune system Chain: A: PDB Molecule: il-4-inducing protein; PDBTitle: ipse alpha-1, an ige-binding crystallin
101	d1v7za	Alignment	not modelled	23.2	44	Fold: Creatininase Superfamily: Creatininase Family: Creatininase
102	d1coaA	Alignment	not modelled	22.3	19	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
103	d1jx4a2	Alignment	not modelled	22.1	8	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain

104	c4diqA_	Alignment	not modelled	22.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase no66; PDBTitle: crystal structure of human no66
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