



























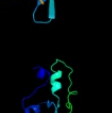





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kzyD_	 Alignment		100.0	100	PDB header: dna binding protein, protein binding Chain: D: PDB Molecule: tumor suppressor p53-binding protein 1; PDBTitle: crystal structure of the 53bp1 brct region complexed to 2 tumor suppressor p53
2	d1kzyc2	 Alignment		100.0	100	Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1
3	c2vxcA_	 Alignment		100.0	24	PDB header: cell cycle Chain: A: PDB Molecule: dna repair protein rhp9; PDBTitle: structure of the crb2-brct2 domain complex with 2 phosphopeptide.
4	d1kzyc1	 Alignment		100.0	100	Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1
5	c1xniI_	 Alignment		99.9	100	PDB header: cell cycle Chain: I: PDB Molecule: tumor suppressor p53-binding protein 1; PDBTitle: tandem tudor domain of 53bp1
6	c3l40A_	 Alignment		99.9	17	PDB header: cell cycle Chain: A: PDB Molecule: brct-containing protein 1; PDBTitle: crystal structure of s. pombe brct1 brct5-brct6 domains
7	c2azmB_	 Alignment		99.9	20	PDB header: cell cycle Chain: B: PDB Molecule: mediator of dna damage checkpoint protein 1; PDBTitle: crystal structure of the mdc1 brct repeat in complex with 2 the histone tail of gamma-h2ax
8	c1ssfA_	 Alignment		99.9	100	PDB header: cell cycle Chain: A: PDB Molecule: transformation related protein 53 binding PDBTitle: solution structure of the mouse 53bp1 fragment (residues 2 1463-1617)
9	c3al3A_	 Alignment		99.9	19	PDB header: dna binding protein/protein binding Chain: A: PDB Molecule: dna topoisomerase 2-binding protein 1; PDBTitle: crystal structure of topbp1 brct7/8-bach1 peptide complex
10	c3tlnA_	 Alignment		99.9	16	PDB header: cell cycle/peptide Chain: A: PDB Molecule: microcephalin; PDBTitle: structure of human microcephalin (mcph1) tandem brct domains in 2 complex with a cdc27 phosphopeptide
11	c2rlzB_	 Alignment		99.8	13	PDB header: antitumor protein Chain: B: PDB Molecule: brca1-associated ring domain protein 1; PDBTitle: crystal structure of the bard1 brct repeat

12	c1z56C_	Alignment		99.8	16	PDB header: ligase Chain: C: PDB Molecule: dna ligase iv; PDBTitle: co-crystal structure of lif1p-lig4p
13	c1y98A_	Alignment		99.8	17	PDB header: antitumor protein Chain: A: PDB Molecule: breast cancer type 1 susceptibility protein; PDBTitle: structure of the brct repeats of brca1 bound to a ctip2 phosphopeptide.
14	c1i0bA_	Alignment		99.8	19	PDB header: unknown function Chain: A: PDB Molecule: brca1; PDBTitle: crystal structure of rat brca1 tandem-brct region
15	c2xnkA_	Alignment		99.8	12	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 2-binding protein 1; PDBTitle: structure and function of the rad9-binding region of the dna damage2 checkpoint adaptor topbp1
16	c3ii6Y_	Alignment		99.8	18	PDB header: ligase/dna binding protein Chain: Y: PDB Molecule: dna ligase 4; PDBTitle: structure of human xrcc4 in complex with the tandem brct2 domains of dna ligaseiv.
17	d2g3ra2	Alignment		99.6	100	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
18	c3t7kB_	Alignment		99.6	13	PDB header: protein binding Chain: B: PDB Molecule: regulator of ty1 transposition protein 107; PDBTitle: complex structure of rtt107p and phosphorylated histone h2a
19	d2g3ra1	Alignment		99.6	100	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
20	c2d8mA_	Alignment		99.3	21	PDB header: dna binding protein Chain: A: PDB Molecule: dna-repair protein xrcc1; PDBTitle: solution structure of the first brct domain of dna-repair2 protein xrcc1
21	d1t15a2	Alignment	not modelled	99.2	19	Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
22	d1wf6a_	Alignment	not modelled	99.1	16	Fold: BRCT domain Superfamily: BRCT domain Family: DNA topoisomerase II binding protein 1, TopBP1
23	c2qqSB_	Alignment	not modelled	99.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: jmjC domain-containing histone demethylation PDBTitle: jmjd2a tandem tudor domains in complex with a trimethylated2 histone h4-k20 peptide
24	c2e2wA_	Alignment	not modelled	99.0	19	PDB header: ligase Chain: A: PDB Molecule: dna ligase 4; PDBTitle: solution structure of the first brct domain of human dna2 ligase iv
25	d1i0ba1	Alignment	not modelled	99.0	28	Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
26	c2xdpA_	Alignment	not modelled	98.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 4c; PDBTitle: crystal structure of the tudor domain of human jmjd2c
27	d1t15a1	Alignment	not modelled	98.9	24	Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
28	c3dlmA_	Alignment	not modelled	98.9	21	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setdb1; PDBTitle: crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1

29	c2couA	Alignment	not modelled	98.8	19	PDB header: cell cycle Chain: A: PDB Molecule: ect2 protein; PDBTitle: solution structure of the second brct domain of epithelial2 cell transforming 2
30	c2ebwA	Alignment	not modelled	98.8	18	PDB header: transferase Chain: A: PDB Molecule: dna repair protein rev1; PDBTitle: solution structure of the brct domain from human dna repair2 protein rev1
31	c3l3eA	Alignment	not modelled	98.8	18	PDB header: cell cycle Chain: A: PDB Molecule: dna topoisomerase 2-binding protein 1; PDBTitle: crystal structure of the sixth brct domain of human topbp1
32	d1cdza	Alignment	not modelled	98.8	19	Fold: BRCT domain Superfamily: BRCT domain Family: DNA-repair protein XRCC1
33	c3ktfB	Alignment	not modelled	98.8	15	PDB header: cell cycle Chain: B: PDB Molecule: microcephalin; PDBTitle: structure of the n-terminal brct domain of human2 microcephalin (mcph1).
34	c2ep8A	Alignment	not modelled	98.7	29	PDB header: cell cycle Chain: A: PDB Molecule: pescadillo homolog 1; PDBTitle: solution structure of the brct domain from human pescadillo2 homolog 1
35	c3ef1A	Alignment	not modelled	98.6	21	PDB header: hydrolase Chain: A: PDB Molecule: rna polymerase ii subunit a c-terminal domain PDBTitle: the structure of fcp1, an essential rna polymerase ii ctd2 phosphatase
36	c2cokA	Alignment	not modelled	98.6	16	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase-1; PDBTitle: solution structure of brct domain of poly(adp-ribose)2 polymerase-1
37	c3ef0A	Alignment	not modelled	98.6	22	PDB header: hydrolase Chain: A: PDB Molecule: rna polymerase ii subunit a c-terminal domain PDBTitle: the structure of fcp1, an essential rna polymerase ii ctd2 phosphatase
38	c2fhdA	Alignment		98.6	20	PDB header: cell cycle Chain: A: PDB Molecule: dna repair protein rhp9/crb2; PDBTitle: crystal structure of crb2 tandem tudor domains
39	c2jw5A	Alignment	not modelled	98.5	11	PDB header: protein binding Chain: A: PDB Molecule: dna polymerase lambda; PDBTitle: polymerase lambda brct domain
40	c3qiiA	Alignment	not modelled	98.4	31	PDB header: transcription regulator Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 2 of human phd finger protein 20
41	c2equA	Alignment	not modelled	98.4	27	PDB header: protein binding Chain: A: PDB Molecule: phd finger protein 20-like 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 20-like 1
42	d1l0ba2	Alignment	not modelled	98.2	26	Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
43	c3p8dB	Alignment	not modelled	98.1	29	PDB header: protein binding Chain: B: PDB Molecule: medulloblastoma antigen mu-mb-50.72; PDBTitle: crystal structure of the second tudor domain of human phf20 (homodimer2 form)
44	c2ebuA	Alignment	not modelled	98.1	16	PDB header: replication Chain: A: PDB Molecule: replication factor c subunit 1; PDBTitle: solution structure of the brct domain from human2 replication factor c large subunit 1
45	c2dunA	Alignment	not modelled	98.0	17	PDB header: transferase Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: solution structure of brct domain of dna polymerase mu
46	d1l7ba	Alignment	not modelled	97.7	16	Fold: BRCT domain Superfamily: BRCT domain Family: DNA ligase
47	dlin1a	Alignment	not modelled	97.7	18	Fold: BRCT domain Superfamily: BRCT domain Family: DNA ligase
48	c2coeA	Alignment	not modelled	97.4	17	PDB header: transferase Chain: A: PDB Molecule: deoxynucleotidyltransferase, terminal variant; PDBTitle: solution structure of brct domain of terminal2 deoxynucleotidyltransferase
49	c2l42A	Alignment	not modelled	97.2	22	PDB header: protein binding Chain: A: PDB Molecule: dna-binding protein rap1; PDBTitle: the solution structure of rap1 brct domain from saccharomyces2 cerevisiae
50	c2e5qA	Alignment	not modelled	97.1	31	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 19; PDBTitle: solution structure of the tudor domain of phd finger2 protein 19, isoform b [homo sapiens]
51	c2e5pA	Alignment	not modelled	97.1	34	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 1 (phf1 protein)
52	c2eqjA	Alignment	not modelled	97.0	36	PDB header: transcription Chain: A: PDB Molecule: metal-response element-binding transcription PDBTitle: solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
						PDB header: transcription

53	c2xk0A_	Alignment	not modelled	96.3	22	Chain: A: PDB Molecule: polycomb protein pcl; PDBTitle: solution structure of the tudor domain from drosophila2 polycomblike (pcl)
54	c4a4fA_	Alignment	not modelled	95.7	25	PDB header: rna binding protein Chain: A: PDB Molecule: survival of motor neuron-related-splicing factor 30; PDBTitle: solution structure of spf30 tudor domain in complex with2 symmetrically dimethylated arginine
55	d1mhna_	Alignment	not modelled	95.1	26	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
56	c1g5vA_	Alignment	not modelled	94.8	26	PDB header: translation Chain: A: PDB Molecule: survival motor neuron protein 1; PDBTitle: solution structure of the tudor domain of the human smn2 protein
57	d2diga1	Alignment	not modelled	94.7	27	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
58	d1qo0d_	Alignment	not modelled	94.6	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: Positive regulator of the amidase operon AmiR
59	c3mmnA_	Alignment	not modelled	94.0	22	PDB header: transferase Chain: A: PDB Molecule: histidine kinase homolog; PDBTitle: crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
60	c2d9tA_	Alignment	not modelled	93.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tudor domain-containing protein 3; PDBTitle: solution structure of the tudor domain of tudor domain2 containing protein 3 from mouse
61	d2d9ta1	Alignment	not modelled	93.5	21	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
62	c3pnwX_	Alignment	not modelled	93.2	21	PDB header: protein binding/immune system Chain: X: PDB Molecule: tudor domain-containing protein 3; PDBTitle: crystal structure of the tudor domain of human tdrd3 in complex with2 an anti-tdrd3 fab
63	c3metB_	Alignment	not modelled	93.0	22	PDB header: transcription Chain: B: PDB Molecule: saga-associated factor 29 homolog; PDBTitle: crystal structure of sgf29 in complex with h3k4me2
64	c2rjnA_	Alignment	not modelled	92.8	20	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
65	c4dadA_	Alignment	not modelled	92.5	17	PDB header: signaling protein, signal transduction Chain: A: PDB Molecule: putative pilus assembly-related protein; PDBTitle: crystal structure of a putative pilus assembly-related protein2 (bpss2195) from burkholderia pseudomallei k96243 at 2.50 a resolution
66	c3snkA_	Alignment	not modelled	92.1	19	PDB header: signaling protein Chain: A: PDB Molecule: response regulator chey-like protein; PDBTitle: crystal structure of a response regulator chey-like protein (ml16475)2 from mesorhizobium loti at 2.02 a resolution
67	c1a2oB_	Alignment	not modelled	91.7	22	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
68	c2ayxA_	Alignment	not modelled	90.8	17	PDB header: transferase Chain: A: PDB Molecule: sensor kinase protein rcsc; PDBTitle: solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
69	c3izbA_	Alignment	not modelled	90.1	23	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein rps0 (s2p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
70	d2qqra1	Alignment	not modelled	89.4	36	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
71	c1ny5A_	Alignment	not modelled	89.2	24	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
72	c3r0jA_	Alignment	not modelled	88.8	26	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
73	c2hqrA_	Alignment	not modelled	88.7	15	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
74	c2zwmA_	Alignment	not modelled	88.7	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
75	d2diga1	Alignment	not modelled	88.3	29	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
76	d2hqa1	Alignment	not modelled	88.2	17	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
77	c2hqxB_	Alignment	not modelled	88.2	17	PDB header: transcription Chain: B: PDB Molecule: p100 co-activator tudor domain; PDBTitle: crystal structure of human p100 tudor domain conserved2 region

78	c3cz5B_	Alignment	not modelled	87.6	15	PDB header: transcription regulator Chain: B: PDB Molecule: two-component response regulator, luxr family; PDBTitle: crystal structure of two-component response regulator, luxr family, 2 from aurantiomonas sp. si85-9a1
79	d2qgra2	Alignment	not modelled	87.2	27	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
80	c3f6cB_	Alignment	not modelled	86.8	13	PDB header: dna binding protein Chain: B: PDB Molecule: positive transcription regulator evga; PDBTitle: crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
81	c3eodA_	Alignment	not modelled	86.5	22	PDB header: signaling protein Chain: A: PDB Molecule: protein hnr; PDBTitle: crystal structure of n-terminal domain of e. coli rssb
82	d2qqa2	Alignment	not modelled	86.3	26	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
83	d1jbea_	Alignment	not modelled	86.3	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
84	c3hv2B_	Alignment	not modelled	85.7	18	PDB header: signaling protein Chain: B: PDB Molecule: response regulator/hd domain protein; PDBTitle: crystal structure of signal receiver domain of hd domain-2 containing protein from pseudomonas fluorescens pf-5
85	d1kgsa2	Alignment	not modelled	85.5	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
86	c3pdiB_	Alignment	not modelled	85.3	18	PDB header: protein binding Chain: B: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nifn; PDBTitle: precursor bound nifen
87	d1qkka_	Alignment	not modelled	84.8	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
88	d2b4aa1	Alignment	not modelled	84.7	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
89	c3nhzA_	Alignment	not modelled	84.2	20	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
90	c3mp6A_	Alignment	not modelled	84.0	24	PDB header: histone binding protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, linker, saga- PDBTitle: complex structure of sgf29 and dimethylated h3k4
91	c1s1hB_	Alignment	not modelled	83.9	23	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein s0-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
92	d1dcfa_	Alignment	not modelled	83.6	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: Receiver domain of the ethylene receptor
93	c2hqoA_	Alignment	not modelled	81.9	15	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
94	d1vmda_	Alignment	not modelled	81.7	21	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
95	c2rdmB_	Alignment	not modelled	81.6	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
96	d1heya_	Alignment	not modelled	81.5	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
97	c3t8yA_	Alignment	not modelled	81.4	20	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of the response regulator domain of thermotoga2 maritima cheb
98	c1w25B_	Alignment	not modelled	81.3	23	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
99	d1xhfa1	Alignment	not modelled	81.3	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
100	c3hn7A_	Alignment	not modelled	81.0	14	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
101	c3h1gA_	Alignment	not modelled	80.6	22	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis protein chey homolog; PDBTitle: crystal structure of chey mutant t84a of helicobacter pylori
102	d1s8na_	Alignment	not modelled	80.6	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
						PDB header: signaling protein

103	c3n0rA_	Alignment	not modelled	80.3	12	Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution
104	c2ef0A_	Alignment	not modelled	80.2	17	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
105	c1zn2A_	Alignment	not modelled	80.0	19	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
106	d1ny5a1	Alignment	not modelled	79.2	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
107	d1wgsa_	Alignment	not modelled	79.2	11	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
108	d2ayxa1	Alignment	not modelled	79.1	18	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
109	c3dzdA_	Alignment	not modelled	79.1	21	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
110	c2j48A_	Alignment	not modelled	78.7	16	PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika2 protein.
111	c2xznB_	Alignment	not modelled	78.3	17	PDB header: ribosome Chain: B: PDB Molecule: rps0e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
112	c1kgsA_	Alignment	not modelled	78.1	25	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
113	c3grcD_	Alignment	not modelled	77.4	20	PDB header: transferase Chain: D: PDB Molecule: sensor protein, kinase; PDBTitle: crystal structure of a sensor protein from polaromonas sp.2 js666
114	d1a2oa1	Alignment	not modelled	76.3	20	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
115	d1zgza1	Alignment	not modelled	76.1	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
116	c2wacA_	Alignment	not modelled	76.0	22	PDB header: splicing Chain: A: PDB Molecule: cg7008-pa; PDBTitle: extended tudor domain of drosophila melanogaster tudor-sn (2 p100)
117	c3c3wB_	Alignment	not modelled	75.1	25	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
118	d1dbwa_	Alignment	not modelled	73.9	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
119	c3a0rB_	Alignment	not modelled	73.8	28	PDB header: transferase Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
120	c2eqkA_	Alignment	not modelled	73.7	21	PDB header: transcription Chain: A: PDB Molecule: tudor domain-containing protein 4; PDBTitle: solution structure of the tudor domain of tudor domain-2 containing protein 4