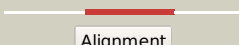


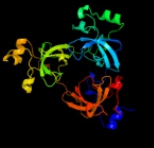
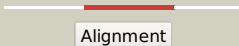

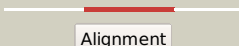



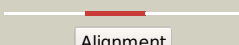

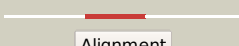








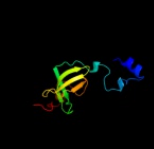

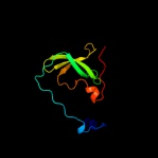

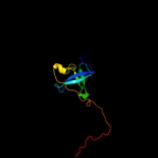

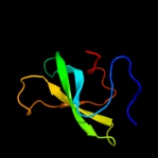





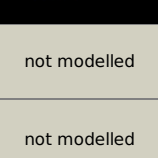


Phyre2

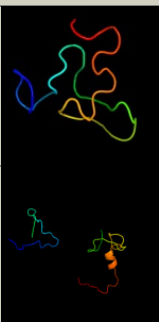
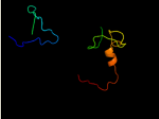

Email	l.a.kelley@imperial.ac.uk
Description	A2A5N8
Date	Wed Jul 10 14:39:59 BST 2013
Unique Job ID	ea015dd284e7c5af


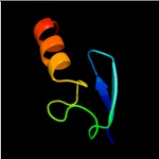
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1oz3C_	 Alignment		100.0	94	PDB header: transcription Chain: C; PDB Molecule: lethal(3)malignant brain tumor-like protein; PDBTitle: crystal structure of 3-mbt repeats of lethal (3) malignant brain tumor2 (native-i) at 1.85 angstrom
2	c3ut1A_	 Alignment		100.0	65	PDB header: transcription Chain: A; PDB Molecule: lethal(3)malignant brain tumor-like protein 3; PDBTitle: crystal structure of the 3-mbt repeat domain of l3mbt13
3	c3h6zA_	 Alignment		100.0	36	PDB header: transcription Chain: A; PDB Molecule: polycomb protein sfmbt; PDBTitle: crystal structure of the four mbt repeats of drosophila melanogaster2 sfmbt in complex with peptide rhr (me)k vlr
4	c3ceyA_	 Alignment		100.0	38	PDB header: transcription regulator Chain: A; PDB Molecule: lethal(3)malignant brain tumor-like 2 protein; PDBTitle: crystal structure of l3mbt12
5	c3feoB_	 Alignment		100.0	36	PDB header: metal binding protein Chain: B; PDB Molecule: mbt domain-containing protein 1; PDBTitle: the crystal structure of mbtd1
6	c2r58A_	 Alignment		100.0	41	PDB header: transcription Chain: A; PDB Molecule: polycomb protein scm; PDBTitle: crystal structure of the two mbt repeats from sex-comb on midleg (scm)2 in complex with di-methyl lysine
7	c2vytA_	 Alignment		100.0	42	PDB header: transcription Chain: A; PDB Molecule: sex comb on midleg-like protein 2; PDBTitle: the mbt repeats of human scm12 bind to peptides containing2 mono methylated lysine.
8	d1wjsa_	 Alignment		100.0	69	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
9	d1oz2a1	 Alignment		100.0	96	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
10	d1oz2a2	 Alignment		100.0	37	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
11	d1oi1a1	 Alignment		100.0	46	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat

12	d1oz2a3	Alignment		100.0	43	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
13	d1oi1a2	Alignment		100.0	39	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
14	d1wjra_	Alignment		100.0	27	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
15	d1wjqa_	Alignment		100.0	46	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
16	c2eqmA_	Alignment		99.9	24	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 20-like 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 20-like 1 [homo sapiens]
17	c3q1jA_	Alignment		99.8	31	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 1 of human phd finger protein 20
18	c1pk1B_	Alignment		99.8	38	PDB header: transcription repression Chain: B: PDB Molecule: sex comb on midleg cg9495-pa; PDBTitle: hetero sam domain structure of ph and scm.
19	d1pk3a1	Alignment		99.7	40	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
20	c1pk1A_	Alignment		99.7	36	PDB header: transcription repression Chain: A: PDB Molecule: polyhomeotic-proximal chromatin protein; PDBTitle: hetero sam domain structure of ph and scm.
21	d1pk1c1	Alignment		99.7	35	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
22	d1kw4a_	Alignment		99.6	34	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
23	d1uqva_	Alignment	not modelled	99.6	15	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
24	c2dkzA_	Alignment	not modelled	99.5	23	PDB header: signaling protein Chain: A: PDB Molecule: hypothetical protein loc64762; PDBTitle: solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
25	c2e8oA_	Alignment		99.4	14	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)
PDB header: signaling protein						

26	c2eanA	Alignment	not modelled	99.1	21	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)
27	c3bs5A	Alignment	not modelled	99.1	21	PDB header: signaling protein/membrane protein Chain: A: PDB Molecule: protein aveugle; PDBTitle: crystal structure of hcnk2-sam/dhyp-sam complex
28	c3bq7A	Alignment	not modelled	99.1	27	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase delta; PDBTitle: sam domain of diacylglycerol kinase delta1 (e35g)
29	d1wwva1	Alignment	not modelled	99.1	18	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
30	c2gleA	Alignment	not modelled	99.0	15	PDB header: protein binding Chain: A: PDB Molecule: neurabin-1; PDBTitle: solution structure of neurabin sam domain
31	c1v85A	Alignment	not modelled	99.0	17	PDB header: apoptosis Chain: A: PDB Molecule: similar to ring finger protein 36; PDBTitle: sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator
32	c2k60A	Alignment	not modelled	99.0	21	PDB header: signaling protein Chain: A: PDB Molecule: protein (stromal interaction molecule 1); PDBTitle: nmr structure of calcium-loaded stim1 ef-sam
33	d2f3na1	Alignment	not modelled	98.9	20	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
34	c3k1rB	Alignment	not modelled	98.9	34	PDB header: structural protein Chain: B: PDB Molecule: usher syndrome type-1g protein; PDBTitle: structure of harmonin npd21 in complex with the sam-pbm of 2 sans
35	c3bs7A	Alignment	not modelled	98.9	23	PDB header: signaling protein Chain: A: PDB Molecule: protein aveugle; PDBTitle: crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
36	c2l5yA	Alignment	not modelled	98.8	18	PDB header: signaling protein Chain: A: PDB Molecule: stromal interaction molecule 2; PDBTitle: nmr structure of calcium-loaded stim2 ef-sam.
37	c2eaoA	Alignment	not modelled	98.6	13	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)
38	c3tadB	Alignment	not modelled	98.6	14	PDB header: protein binding Chain: B: PDB Molecule: liprin-alpha-2; PDBTitle: crystal structure of the liprin-alpha/liprin-beta complex
39	c3h8mB	Alignment	not modelled	98.3	19	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 7; PDBTitle: sam domain of human ephrin type-a receptor 7 (epha7)
40	c2fe9A	Alignment	not modelled	98.2	13	PDB header: rna binding protein Chain: A: PDB Molecule: protein vts1; PDBTitle: solution structure of the vts1 sam domain in the presence2 of rna
41	d1b4fa	Alignment	not modelled	98.2	12	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
42	c1ow5A	Alignment	not modelled	98.2	21	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase ste11; PDBTitle: nmr structure of the saccharomyces cerevisiae sam (sterile2 alpha motif) domain
43	d1ow5a	Alignment	not modelled	98.2	21	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
44	d1oxja1	Alignment	not modelled	98.1	20	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
45	d1x40a1	Alignment	not modelled	98.1	13	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
46	d1sxea	Alignment	not modelled	98.0	15	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain
47	c2eseA	Alignment	not modelled	98.0	11	PDB header: protein/rna complex Chain: A: PDB Molecule: vts1p; PDBTitle: structure of the sam domain of vts1p in complex with rna
48	c2b6gA	Alignment	not modelled	98.0	11	PDB header: rna binding protein Chain: A: PDB Molecule: vts1p; PDBTitle: rna recognition by the vts1 sam domain
49	c2eamA	Alignment	not modelled	98.0	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
50	c1oxjA	Alignment	not modelled	98.0	20	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein smaug; PDBTitle: crystal structure of the smaug rna binding domain
51	c2e8nA	Alignment	not modelled	97.9	21	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)
52	d1lucva	Alignment	not modelled	97.8	13	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain

53	d1v38a_	Alignment	not modelled	97.8	8	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
54	d1b0xa_	Alignment	not modelled	97.7	15	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
55	c1b0xA_	Alignment	not modelled	97.7	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.
56	c2d10A_	Alignment	not modelled	97.7	16	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
57	c2kivA_	Alignment	not modelled	97.7	8	PDB header: signaling protein Chain: A: PDB Molecule: ankyrin repeat and sterile alpha motif domain- PDBTitle: aida-1 sam domain tandem
58	c3senD_	Alignment	not modelled	97.7	12	PDB header: signaling protein Chain: D: PDB Molecule: caskin-1; PDBTitle: structure of caskin1 tandem sams
59	c3kkaD_	Alignment	not modelled	97.7	15	PDB header: transferase Chain: D: PDB Molecule: ephrin type-a receptor 2; PDBTitle: co-crystal structure of the sam domains of epha1 and epha2
60	c2k4pA_	Alignment	not modelled	97.6	13	PDB header: signaling protein Chain: A: PDB Molecule: phosphatidylinositol-3,4,5-trisphosphate 5- PDBTitle: solution structure of ship2-sam
61	c2jydA_	Alignment		97.6	52	PDB header: metal binding protein Chain: A: PDB Molecule: zf5 domain of myelin transcription factor 1; PDBTitle: structure of the fifth zinc finger of myelin transcription2 factor 1
62	c2cs8A_	Alignment		97.6	38	PDB header: transcription Chain: A: PDB Molecule: kiaa0535 protein; PDBTitle: solution structure of tandem repeat of the fifth and sixth2 zinc-finger c2hc domains from human st18
63	c2kg5A_	Alignment	not modelled	97.6	13	PDB header: signaling protein Chain: A: PDB Molecule: arf-gap, rho-gap domain, ank repeat and ph PDBTitle: nmr solution structure of arap3-sam
64	c1pxeA_	Alignment		97.6	45	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
65	d1sgga_	Alignment	not modelled	97.5	13	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
66	d1z1va1	Alignment	not modelled	97.4	17	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
67	c3dlmA_	Alignment	not modelled	97.4	22	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
68	c2lmrA_	Alignment	not modelled	97.3	10	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
69	c2bkdN_	Alignment	not modelled	97.1	8	PDB header: nuclear protein Chain: N: PDB Molecule: fragile x mental retardation 1 protein; PDBTitle: structure of the n-terminal domain of fragile x mental2 retardation protein
70	c2qkqA_	Alignment	not modelled	97.1	12	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
71	d1sv0a_	Alignment	not modelled	97.0	22	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain
72	c2ke7A_	Alignment	not modelled	97.0	12	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
73	c2dkxA_	Alignment	not modelled	96.9	10	PDB header: signaling protein Chain: A: PDB Molecule: sam pointed domain-containing ets transcription PDBTitle: solution structure of the sam_pnt-domain of ets2 transcription factor pdef (prostate ets)
74	d1sxda_	Alignment	not modelled	96.9	17	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain
75	c2e8pA_	Alignment	not modelled	96.7	9	PDB header: signaling protein Chain: A: PDB Molecule: elf3 protein; PDBTitle: solution structure of the n-terminal sam-domain of e74-like2 factor 3

76	d1ji7a_	Alignment	not modelled	96.7	15	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain
77	c3hiIB_	Alignment	not modelled	96.7	18	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: sam domain of human ephrin type-a receptor 1 (epha1)
78	c2ytuA_	Alignment	not modelled	96.6	11	PDB header: signaling protein Chain: A: PDB Molecule: friend leukemia integration 1 transcription PDBTitle: solution structure of the sam_pnt-domain of the human2 friend leukemiaintegration 1 transcription factor
79	d1bqva_	Alignment	not modelled	96.5	17	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain
80	d1sv0c_	Alignment	not modelled	96.1	17	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain
81	d1wgsa_	Alignment	not modelled	95.9	14	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
82	c2ekoA_	Alignment	not modelled	95.8	14	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase htatip; PDBTitle: solution structure of ruh-073, a pseudo chromo domain from2 human cDNA
83	c2qb0D_	Alignment	not modelled	95.6	15	PDB header: hydrolase regulator Chain: D: PDB Molecule: telsam domain - lysozyme chimera; PDBTitle: structure of the 2tel crystallization module fused to t4 lysozyme with2 an ala-gly-pro linker.
84	c2ro0A_	Alignment	not modelled	95.5	13	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase esa1; PDBTitle: solution structure of the knotted tudor domain of the yeast2 histone acetyltransferase, esa1
85	c2eapA_	Alignment	not modelled	95.5	25	PDB header: signaling protein Chain: A: PDB Molecule: lymphocyte cytosolic protein 2; PDBTitle: solution structure of the n-terminal sam-domain of human2 lymphocyte cytosolic protein 2
86	c2lrqA_	Alignment	not modelled	95.5	17	PDB header: transcription Chain: A: PDB Molecule: nua4 complex subunit eaf3 homolog; PDBTitle: chemical shift assignment and solution structure of fr822a from2 drosophila melanogaster. northeast structural genomics consortium3 target fr822a
87	d1coka_	Alignment	not modelled	95.2	12	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
88	c2l8eA_	Alignment		95.1	20	PDB header: dna binding protein Chain: A: PDB Molecule: polyhomeotic-like protein 1; PDBTitle: solution nmr structure of fcs domain of human polyhomeotic homolog 12 (hph1)
89	d2f5ka1	Alignment	not modelled	94.9	24	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
90	c2w0tA_	Alignment		94.0	13	PDB header: transcription Chain: A: PDB Molecule: lethal(3)malignant brain tumor-like 2 protein; PDBTitle: solution structure of the fcs zinc finger domain of human2 lmb12
91	c2lccA_	Alignment	not modelled	92.2	26	PDB header: transcription Chain: A: PDB Molecule: at-rich interactive domain-containing protein 4a; PDBTitle: solution structure of rbbp1 chromobarrel domain
92	c3m9qA_	Alignment	not modelled	91.8	24	PDB header: dna binding protein Chain: A: PDB Molecule: protein male-specific lethal-3; PDBTitle: drosophila msl3 chromodomain
93	c3m9pA_	Alignment	not modelled	91.8	26	PDB header: dna binding protein/dna Chain: A: PDB Molecule: male-specific lethal 3 homolog; PDBTitle: human msl3 chromodomain bound to dna and h4k20me1 peptide
94	c2rnzA_	Alignment	not modelled	90.1	17	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase esa1; PDBTitle: solution structure of the presumed chromodomain of the2 yeast histone acetyltransferase, esa1
95	c2qqsB_	Alignment	not modelled	90.0	20	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
96	c3idwA_	Alignment	not modelled	83.5	7	PDB header: endocytosis Chain: A: PDB Molecule: actin cytoskeleton-regulatory complex protein sla1; PDBTitle: crystal structure of sla1 homology domain 2
97	c4iutB_	Alignment	not modelled	77.2	23	PDB header: gene regulation Chain: B: PDB Molecule: sawadee homeodomain homolog 1; PDBTitle: crystal structure of shh1 sawadee domain in complex with h3k9me22 peptide
98	c2e8mA_	Alignment	not modelled	76.9	17	PDB header: signaling protein Chain: A: PDB Molecule: epidermal growth factor receptor kinase PDBTitle: solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
99	c1wwuA_	Alignment	not modelled	76.4	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein flj21935; PDBTitle: solution structure of the sam_pnt domain of human protein2 flj21935

100	c2xdpA_	Alignment	not modelled	69.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 4c; PDBTitle: crystal structure of the tudor domain of human jmj2c
101	c1ssfA_	Alignment	not modelled	67.1	28	PDB header: cell cycle Chain: A: PDB Molecule: transformation related protein 53 binding PDBTitle: solution structure of the mouse 53bp1 fragment (residues2 1463-1617)
102	d2buda1	Alignment	not modelled	62.6	18	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
103	c3qiiA_	Alignment	not modelled	60.0	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
104	c2ldmA_	Alignment	not modelled	58.4	32	PDB header: transcription/protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of human phf20 tudor2 domain bound to a p53 segment2 containing a dimethyllysine analog p53k370me2
105	d2d8ca1	Alignment	not modelled	55.5	18	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
106	c2eefA_	Alignment	not modelled	55.1	19	PDB header: sugar binding protein Chain: A: PDB Molecule: protein phosphatase 1, regulatory (inhibitor) PDBTitle: solution structure of the cbm_21 domain from human protein2 phosphatase 1, regulatory (inhibitor) subunit 3b
107	c2jz2A_	Alignment	not modelled	50.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ssl0352 protein; PDBTitle: solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
108	c2e5qA_	Alignment	not modelled	49.6	28	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]
109	c3p8dB_	Alignment	not modelled	49.3	30	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)
110	c2k3yA_	Alignment	not modelled	49.1	21	PDB header: transcription regulator Chain: A: PDB Molecule: chromatin modification-related protein eaf3; PDBTitle: solution structure of eaf3 chromo barrel domain bound to2 histone h3 with a dimethyllysine analog h3k36me2
111	c4he5A_	Alignment	not modelled	48.7	20	PDB header: unknown function Chain: A: PDB Molecule: peptidase family u32; PDBTitle: crystal structure of the selenomethionine variant of the c-terminal2 domain of geobacillus thermoleovorans putative u32 peptidase
112	c2lycA_	Alignment	not modelled	48.7	14	PDB header: protein binding Chain: A: PDB Molecule: spindle and kinetochore-associated protein 1 homolog; PDBTitle: structure of c-terminal domain of ska1
113	c2equA_	Alignment	not modelled	45.2	23	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
114	c3metB_	Alignment	not modelled	44.5	9	PDB header: transcription Chain: B: PDB Molecule: isaga-associated factor 29 homolog; PDBTitle: crystal structure of sgf29 in complex with h3k4me2
115	c2xk0A_	Alignment	not modelled	41.2	23	PDB header: transcription Chain: A: PDB Molecule: polycomb protein pcl; PDBTitle: solution structure of the tudor domain from drosophila2 polycomblike (pcl)
116	c1miyB_	Alignment	not modelled	39.6	19	PDB header: translation, transferase Chain: B: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of bacillus stearotherophilus cca-adding enzyme in2 complex with ctp
117	c3p9aI_	Alignment	not modelled	39.4	29	PDB header: dna binding protein Chain: I: PDB Molecule: dna-packaging protein gp3; PDBTitle: an atomic view of the nonameric small terminase subunit of2 bacteriophage p22
118	c2innA_	Alignment	not modelled	38.8	10	PDB header: oxidoreductase Chain: A: PDB Molecule: phenol hydroxylase component phn; PDBTitle: structure of the phenol hydroxylase-regulatory protein2 complex
119	c3m6wA_	Alignment	not modelled	37.2	14	PDB header: transferase Chain: A: PDB Molecule: rrna methylase; PDBTitle: multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
120	c1xnI_	Alignment	not modelled	35.5	20	PDB header: cell cycle Chain: I: PDB Molecule: tumor suppressor p53-binding protein 1; PDBTitle: tandem tudor domain of 53bp1