




















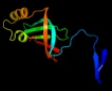

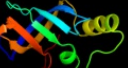

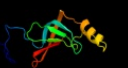




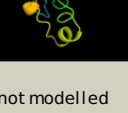


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P21513
Date	Thu Jan 5 11:38:24 GMT 2012
Unique Job ID	45260adf866effd8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2c4rL_	 Alignment		100.0	100	PDB header: hydrolase Chain: L: PDB Molecule: ribonuclease e; PDBTitle: catalytic domain of e. coli rnase e
2	d1smxa_	 Alignment		99.9	100	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
3	d2z0sa1	 Alignment		98.3	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
4	c2cqoA_	 Alignment		98.2	16	PDB header: ribosome Chain: A: PDB Molecule: nucleolar protein of 40 kda; PDBTitle: solution structure of the s1 rna binding domain of human2 hypothetical protein flj11067
5	d2ba0a1	 Alignment		98.2	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
6	c1yz6A_	 Alignment		98.1	24	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor 2 alpha PDBTitle: crystal structure of intact alpha subunit of aif2 from2 pyrococcus abyssi
7	d1q46a2	 Alignment		98.1	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
8	c2z0sA_	 Alignment		98.1	14	PDB header: rna binding protein Chain: A: PDB Molecule: probable exosome complex rna-binding protein 1; PDBTitle: crystal structure of putative exosome complex rna-binding2 protein
9	c2k4kA_	 Alignment		98.1	23	PDB header: rna binding protein Chain: A: PDB Molecule: general stress protein 13; PDBTitle: solution structure of gsp13 from bacillus subtilis
10	d3bzka4	 Alignment		98.1	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
11	c2je6l_	 Alignment		98.0	19	PDB header: hydrolase Chain: I: PDB Molecule: exosome complex rna-binding protein 1; PDBTitle: structure of a 9-subunit archaeal exosome

12	c2khjA_	Alignment		98.0	25	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
13	d2je6i1	Alignment		98.0	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
14	c2khiA_	Alignment		98.0	14	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 4 of the e. coli ribosomal2 protein s1
15	c2ba0A_	Alignment		97.9	16	PDB header: rna binding protein Chain: A: PDB Molecule: archeal exosome rna binding protein rrp4; PDBTitle: archaeal exosome core
16	d2nn6h1	Alignment		97.9	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
17	c1q8kA_	Alignment		97.9	19	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2 PDBTitle: solution structure of alpha subunit of human eif2
18	c2eqsA_	Alignment		97.9	38	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dhx8; PDBTitle: solution structure of the s1 rna binding domain of human2 atp-dependent rna helicase dhx8
19	d1wi5a_	Alignment		97.9	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
20	d1sroa_	Alignment		97.9	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
21	d1go3e1	Alignment	not modelled	97.8	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
22	c1q46A_	Alignment	not modelled	97.8	19	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
23	d1hh2p1	Alignment	not modelled	97.7	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
24	c3go5A_	Alignment	not modelled	97.6	12	PDB header: gene regulation Chain: A: PDB Molecule: multidomain protein with s1 rna-binding domains; PDBTitle: crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
25	c2oceA_	Alignment	not modelled	97.6	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
26	c1hh2P_	Alignment	not modelled	97.6	26	PDB header: transcription regulation Chain: P: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima
27	c2ba1B_	Alignment	not modelled	97.5	16	PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core
						PDB header: translation Chain: B: PDB Molecule: translation initiation factor 2 alpha

28	c2ahoB_	Alignment	not modelled	97.4	27	subunit; PDBTitle: structure of the archaeal initiation factor eif2 alpha-2 gamma heterodimer from sulfolobus solfataricus complexed3 with gdpnp
29	d2ahob2	Alignment	not modelled	97.4	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
30	c1l2fA_	Alignment	not modelled	97.4	27	PDB header: transcription Chain: A: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain
31	d2nn6i1	Alignment	not modelled	97.4	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
32	d1kl9a2	Alignment	not modelled	97.3	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
33	c2k52A_	Alignment	not modelled	97.3	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mj1198; PDBTitle: structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b
34	c1go3E_	Alignment	not modelled	97.1	20	PDB header: transferase Chain: E: PDB Molecule: dna-directed rna polymerase subunit e; PDBTitle: structure of an archeal homolog of the eukaryotic rna2 polymerase ii rpb4/rpb7 complex
35	c3psiA_	Alignment	not modelled	97.1	13	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
36	c2nn6l_	Alignment	not modelled	97.0	19	PDB header: hydrolase/transferase Chain: I: PDB Molecule: 3'-5' exoribonuclease csl4 homolog; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
37	d1y14b1	Alignment	not modelled	97.0	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
38	c2c35F_	Alignment	not modelled	96.5	15	PDB header: polymerase Chain: F: PDB Molecule: dna-directed rna polymerase ii 19 kda PDBTitle: subunits rpb4 and rpb7 of human rna polymerase ii
39	c3h0gS_	Alignment	not modelled	96.5	12	PDB header: transcription Chain: S: PDB Molecule: dna-directed rna polymerase ii subunit rpb7; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
40	c1kl9A_	Alignment	not modelled	96.4	21	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2 subunit 1; PDBTitle: crystal structure of the n-terminal segment of human eukaryotic2 initiation factor 2alpha
41	d2nn6g1	Alignment	not modelled	96.3	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
42	c2b8kG_	Alignment	not modelled	96.2	14	PDB header: transferase Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kda PDBTitle: 12-subunit rna polymerase ii
43	d2c35b1	Alignment	not modelled	95.6	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
44	c2pmzE_	Alignment	not modelled	95.4	16	PDB header: translation, transferase Chain: E: PDB Molecule: dna-directed rna polymerase subunit e; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
45	c2bh8B_	Alignment	not modelled	95.4	20	PDB header: transcription Chain: B: PDB Molecule: 1b11; PDBTitle: combinatorial protein 1b11
46	c1nt9G_	Alignment	not modelled	95.3	14	PDB header: transcription, transferase Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kd polypeptide; PDBTitle: complete 12-subunit rna polymerase ii
47	c3aaqD_	Alignment	not modelled	95.1	25	PDB header: dna binding protein Chain: D: PDB Molecule: calcium-regulated heat stable protein 1; PDBTitle: crystal structure of human crhsp-24
48	c2nn6H_	Alignment	not modelled	94.7	15	PDB header: hydrolase/transferase Chain: H: PDB Molecule: exosome complex exonuclease rrp4; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
49	c2ckzB_	Alignment	not modelled	94.6	13	PDB header: transferase Chain: B: PDB Molecule: dna-directed rna polymerase iii 25 kd PDBTitle: x-ray structure of rna polymerase iii subcomplex c17-c25.
50	d2asba1	Alignment	not modelled	94.4	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
51	c2nn6G_	Alignment	not modelled	94.2	19	PDB header: hydrolase/transferase Chain: G: PDB Molecule: exosome complex exonuclease rrp40; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
52	c1k0rB_	Alignment	not modelled	94.0	20	PDB header: transcription Chain: B: PDB Molecule: nusa; PDBTitle: crystal structure of mycobacterium tuberculosis nusa
53	c2asbA_	Alignment	not modelled	94.0	23	PDB header: transcription/rna Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: structure of a mycobacterium tuberculosis nusa-rna complex
						Fold: OB-fold

54	d2ja9a1	Alignment	not modelled	92.9	22	Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
55	d1c9oa	Alignment	not modelled	92.5	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
56	d1h95a	Alignment	not modelled	91.3	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
57	c2ljpa	Alignment	not modelled	90.8	10	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease p protein component; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for e.coli2 ribonuclease p protein
58	d1mjca	Alignment	not modelled	90.5	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
59	d2es2a1	Alignment	not modelled	90.5	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
60	c2kcmA	Alignment	not modelled	88.7	19	PDB header: nucleic acid binding protein Chain: A: PDB Molecule: cold shock domain family protein; PDBTitle: solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a.
61	d1g6pa	Alignment	not modelled	88.3	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
62	d1d6ta	Alignment	not modelled	87.7	21	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: RNase P protein
63	d1nz0a	Alignment	not modelled	87.6	21	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: RNase P protein
64	c2eqjA	Alignment	not modelled	86.9	19	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
65	c2ja9A	Alignment	not modelled	86.2	14	PDB header: rna-binding protein Chain: A: PDB Molecule: exosome complex exonuclease rrp40; PDBTitle: structure of the n-terminal deletion of yeast exosome2 component rrp40
66	d1k3ra1	Alignment	not modelled	85.8	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Hypothetical protein MTH1 (MT0001), insert domain
67	c2hncC	Alignment	not modelled	85.6	20	PDB header: transferase Chain: C: PDB Molecule: sam-dependent o-methyltransferase; PDBTitle: crystal structure of sam-dependent o-methyltransferase from2 pathogenic bacterium leptospira interrogans
68	c2wp8j	Alignment	not modelled	85.3	11	PDB header: hydrolase Chain: J: PDB Molecule: exosome complex exonuclease dis3; PDBTitle: yeast rrp44 nuclease
69	c2e5pA	Alignment	not modelled	84.0	20	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)
70	c3d0fA	Alignment	not modelled	83.6	10	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
71	c2k5nA	Alignment	not modelled	83.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cold-shock protein; PDBTitle: solution nmr structure of the n-terminal domain of protein2 eca1580 from erwinia carotovora, northeast structural3 genomics consortium target ewr156a
72	c2pe4A	Alignment	not modelled	83.4	20	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase-1; PDBTitle: structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
73	d1a6fa	Alignment	not modelled	82.7	16	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: RNase P protein
74	c3trzE	Alignment	not modelled	81.5	25	PDB header: rna binding protein/rna Chain: E: PDB Molecule: protein lin-28 homolog a; PDBTitle: mouse lin28a in complex with let-7d microRNA pre-element
75	c3pihA	Alignment	not modelled	81.5	20	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
76	c3pnwX	Alignment	not modelled	81.0	23	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
77	c2bx9j	Alignment	not modelled	79.8	36	PDB header: transcription regulation Chain: J: PDB Molecule: tryptophan rna-binding attenuator protein-inhibitory PDBTitle: crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
78	c3a0jB	Alignment	not modelled	78.1	17	PDB header: transcription Chain: B: PDB Molecule: cold shock protein; PDBTitle: crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
79	c2vtrA	Alignment	not modelled	77.2	20	PDB header: rna binding protein Chain: A: PDB Molecule: cold shock domain-containing protein e1;

79	c2ytwA	Alignment	not modelled	77.2	20	PDBTitle: solution structure of the fifth cold-shock domain of the human2 kiaa0885 protein (unr protein) PDB header: transcription
80	c2e5qA	Alignment	not modelled	76.0	24	Chain: A: PDB Molecule: phd finger protein 19; PDBTitle: solution structure of the tudor domain of phd finger2 protein 19, isoform b [homo sapiens]
81	c3ld0Q	Alignment	not modelled	75.1	30	PDB header: gene regulation Chain: Q: PDB Molecule: inhibitor of trap, regulated by t-box (trp) sequence rtpa; PDBTitle: crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions
82	c2d9tA	Alignment	not modelled	73.8	23	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
83	c2atmA	Alignment	not modelled	73.6	23	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: crystal structure of the recombinant allergen ves v 2
84	d1fcqa	Alignment	not modelled	72.4	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Bee venom hyaluronidase
85	c1g5vA	Alignment	not modelled	70.2	19	PDB header: translation Chain: A: PDB Molecule: survival motor neuron protein 1; PDBTitle: solution structure of the tudor domain of the human smn2 protein
86	d1mhna	Alignment	not modelled	70.0	19	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
87	c1fcuA	Alignment	not modelled	69.6	26	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: crystal structure (trigonal) of bee venom hyaluronidase
88	c3cbgA	Alignment	not modelled	68.7	28	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: functional and structural characterization of a2 cationdependent o-methyltransferase from the3 cyanobacterium synechocystis sp. strain pcc 6803
89	d1nltA	Alignment	not modelled	67.9	28	Fold: DnaJ/Hsp40 cysteine-rich domain Superfamily: DnaJ/Hsp40 cysteine-rich domain Family: DnaJ/Hsp40 cysteine-rich domain
90	c3camB	Alignment	not modelled	67.4	21	PDB header: gene regulation Chain: B: PDB Molecule: cold-shock domain family protein; PDBTitle: crystal structure of the cold shock domain protein from neisseria2 meningitidis
91	c3ayhB	Alignment	not modelled	66.8	15	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase iii subunit rpc8; PDBTitle: crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii
92	c3tr6A	Alignment	not modelled	65.4	30	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: structure of a o-methyltransferase from coxiella burnetii
93	d3d3ra1	Alignment	not modelled	63.8	20	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
94	d1bi9a	Alignment	not modelled	63.2	19	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
95	d2ix0a2	Alignment	not modelled	62.6	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
96	c3nthA	Alignment	not modelled	62.6	25	PDB header: transcription Chain: A: PDB Molecule: maternal protein tudor; PDBTitle: crystal structure of tudor and aubergine [r13(me2s)] complex
97	c2hl7A	Alignment	not modelled	61.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccmh; PDBTitle: crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
98	d1wfga	Alignment	not modelled	58.1	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
99	c1nltA	Alignment	not modelled	57.8	21	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial protein import protein mas5; PDBTitle: the crystal structure of hsp40 ydj1
100	c1x65A	Alignment	not modelled	56.9	15	PDB header: rna binding protein Chain: A: PDB Molecule: unr protein; PDBTitle: solution structure of the third cold-shock domain of the human2 kiaa0885 protein (unr protein)
101	c1t9B	Alignment	not modelled	56.5	38	PDB header: transferase, lyase Chain: B: PDB Molecule: formimidoyltransferase-cyclodeaminase PDBTitle: structure of the bifunctional and golgi associated2 formiminotransferase cyclodeaminase octamer
102	c2hqxB	Alignment	not modelled	56.2	21	PDB header: transcription Chain: B: PDB Molecule: p100 co-activator tudor domain; PDBTitle: crystal structure of human p100 tudor domain conserved2 region
103	d2hqxa1	Alignment	not modelled	56.2	21	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
104	c3d3rA	Alignment	not modelled	55.4	20	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase assembly chaperone hupc/hupf; PDBTitle: crystal structure of the hydrogenase assembly chaperone

					hypr/hupf2 family protein from shewanella oneidensis mr-1
105	c2ix1A	Alignment	not modelled	55.4	16 PDB header: hydrolase Chain: A: PDB Molecule: exoribonuclease 2; PDBTitle: rnase ii d209n mutant
106	d1h9ma1	Alignment	not modelled	54.5	19 Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
107	d1vlua	Alignment	not modelled	54.4	18 Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
108	d1a62a2	Alignment	not modelled	53.4	16 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
109	d1h9ra1	Alignment	not modelled	52.8	26 Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
110	c2cttA	Alignment	not modelled	52.7	31 PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily a member 3; PDBTitle: solution structure of zinc finger domain from human dnaj2 subfamily a member 3
111	c3bdlA	Alignment	not modelled	52.6	21 PDB header: hydrolase Chain: A: PDB Molecule: staphylococcal nuclease domain-containing PDBTitle: crystal structure of a truncated human tudor-sn
112	d2d9ta1	Alignment	not modelled	52.1	26 Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
113	d1exka	Alignment	not modelled	50.9	38 Fold: Dnaj/Hsp40 cysteine-rich domain Superfamily: Dnaj/Hsp40 cysteine-rich domain Family: Dnaj/Hsp40 cysteine-rich domain
114	d1p6oa	Alignment	not modelled	50.1	14 Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
115	c3lz8A	Alignment	not modelled	49.8	20 PDB header: chaperone Chain: A: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone dnaj from klebsiella pneumoniae2 subsp. pneumoniae mgh 78578 at 2.9 a resolution.
116	c4a4fA	Alignment	not modelled	49.5	26 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
117	c2ytxA	Alignment	not modelled	49.3	15 PDB header: rna binding protein Chain: A: PDB Molecule: cold shock domain-containing protein e1; PDBTitle: solution structure of the second cold-shock domain of the human2 kiaa0885 protein (unr protein)
118	d1guta	Alignment	not modelled	49.2	17 Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
119	c2eqkA	Alignment	not modelled	49.2	25 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
120	d2diqa1	Alignment	not modelled	46.8	25 Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain