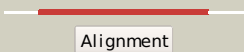
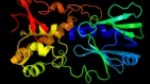
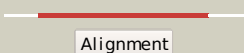
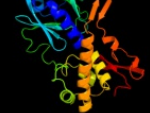
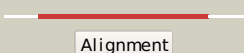



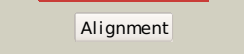


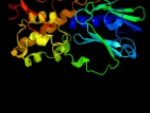


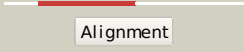

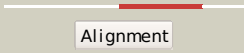








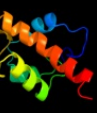







#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2f5qA_	 Alignment		100.0	40	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
2	c1k82D_	 Alignment		100.0	100	PDB header: hydrolase/dna Chain: D: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
3	c1nnjA_	 Alignment		100.0	37	PDB header: hydrolase Chain: A: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
4	c1ee8A_	 Alignment		100.0	41	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
5	c2opfA_	 Alignment		100.0	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: endonuclease viii; PDBTitle: crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
6	c3a46B_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of mvnei1/thf complex
7	c1tdhA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: nei endonuclease viii-like 1; PDBTitle: crystal structure of human endonuclease viii-like 1 (nei1)
8	d1k82a2	 Alignment		100.0	100	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
9	d1r2za1	 Alignment		100.0	41	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
10	d1r2za2	 Alignment		100.0	34	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
11	d1k82a1	 Alignment		100.0	100	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins

12	dlee8a1	Alignment		100.0	42	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
13	d1tdza1	Alignment		100.0	38	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
14	d1tdza2	Alignment		99.9	33	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
15	d1k3xa1	Alignment		99.9	22	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
16	dlee8a2	Alignment		99.9	39	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
17	d1k3xa2	Alignment		99.9	22	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
18	d1tdha2	Alignment		99.9	27	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
19	d1tdha1	Alignment		99.8	29	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
20	dlee8a3	Alignment		99.6	42	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
21	d2hkja1	Alignment	not modelled	99.6	19	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Topoisomerase VI-B subunit middle domain
22	d1tdza3	Alignment	not modelled	99.6	46	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
23	d1r2za3	Alignment	not modelled	99.6	52	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
24	d1k82a3	Alignment	not modelled	99.5	100	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
25	d1l1ta3	Alignment	not modelled	99.5	55	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
26	d1k3xa3	Alignment	not modelled	99.3	39	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
27	c3doaA	Alignment	not modelled	97.3	13	PDB header: protein binding Chain: A: PDB Molecule: fibrinogen binding protein; PDBTitle: the crystal structure of the fibrinogen binding protein from2 staphylococcus aureus
28	d2uubm1	Alignment	not modelled	96.8	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
						Fold: S13-like H2TH domain

29	d2gy9m1	Alignment	not modelled	96.6	27	Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
30	c3iz6M_	Alignment	not modelled	96.5	27	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18 (s13p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
31	c2zkqm_	Alignment	not modelled	96.4	25	PDB header: ribosomal protein/rna Chain: M: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
32	c2xznM_	Alignment	not modelled	96.4	22	PDB header: ribosome Chain: M: PDB Molecule: rps18e; 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
33	d1i94m_	Alignment	not modelled	96.3	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
34	c1mx0D_	Alignment	not modelled	95.3	23	PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
35	d2i0za2	Alignment	not modelled	92.4	26	Fold: HI0933 insert domain-like Superfamily: HI0933 insert domain-like Family: HI0933 insert domain-like
36	c3fuxB_	Alignment	not modelled	92.0	21	PDB header: transferase Chain: B: PDB Molecule: dimethyladenosine transferase; PDBTitle: t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksga) in2 complex with 5'-methylthioadenosine in space group p212121
37	c3fteA_	Alignment	not modelled	89.3	31	PDB header: transferase/rna Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of a. aeolicus ksga in complex with rna
38	d1qyra_	Alignment	not modelled	89.2	25	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
39	c2gb5B_	Alignment	not modelled	86.1	21	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
40	c2zbkB_	Alignment	not modelled	85.5	22	PDB header: isomerase Chain: B: PDB Molecule: type 2 dna topoisomerase 6 subunit b; PDBTitle: crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
41	c3uzuA_	Alignment	not modelled	84.6	15	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei
42	c3tqsB_	Alignment	not modelled	78.9	6	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii
43	c2h1rA_	Alignment	not modelled	78.8	11	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase, putative; PDBTitle: crystal structure of a dimethyladenosine transferase from2 plasmodium falciparum
44	c3bbnM_	Alignment	not modelled	76.4	17	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein s13; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
45	d2jneal	Alignment	not modelled	71.9	21	Fold: Rubredoxin-like Superfamily: Yfgj-like Family: Yfgj-like
46	c2jneA_	Alignment	not modelled	71.9	21	PDB header: metal binding protein Chain: A: PDB Molecule: hypothetical protein yfgj; PDBTitle: nmr structure of e.coli yfgj modelled with two zn+2 bound.2 northeast structural genomics consortium target er317.
47	c2jrpA_	Alignment	not modelled	71.2	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
48	d2fiya1	Alignment	not modelled	70.5	20	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
49	d2gqfa2	Alignment	not modelled	67.2	17	Fold: HI0933 insert domain-like Superfamily: HI0933 insert domain-like Family: HI0933 insert domain-like
50	c3u50C_	Alignment	not modelled	65.2	26	PDB header: dna binding protein Chain: C: PDB Molecule: telomerase-associated protein 82; PDBTitle: crystal structure of the tetrahymena telomerase processivity factor2 teb1 ob-c
51	c1dvbA_	Alignment	not modelled	63.4	21	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
52	c3grrA_	Alignment	not modelled	59.2	12	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.
53	d1qf8a_	Alignment	not modelled	59.2	27	Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit
						PDB header: metal binding protein

54	c2lcqA_	Alignment	not modelled	58.9	20	Chain: A: PDB Molecule: putative toxin vappc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
55	d1lloc_	Alignment	not modelled	57.9	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
56	c2q2eB_	Alignment	not modelled	57.9	16	PDB header: isomerase Chain: B: PDB Molecule: type 2 dna topoisomerase 6 subunit b; PDBTitle: crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazel
57	d1pfta_	Alignment	not modelled	57.4	20	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
58	c1dgsB_	Alignment	not modelled	56.1	30	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
59	c2owoA_	Alignment	not modelled	55.5	29	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
60	c2kpiA_	Alignment	not modelled	55.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein sco3027; PDBTitle: solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
61	d1vd4a_	Alignment	not modelled	54.6	42	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
62	d2f4ma1	Alignment	not modelled	51.8	31	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
63	c3fydA_	Alignment	not modelled	51.6	12	PDB header: transferase Chain: A: PDB Molecule: probable dimethyladenosine transferase; PDBTitle: crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi
64	d1odha_	Alignment	not modelled	51.1	17	Fold: GCM domain Superfamily: GCM domain Family: GCM domain
65	d2akla2	Alignment	not modelled	51.0	26	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
66	c2js4A_	Alignment	not modelled	49.8	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0434 protein bb2007; PDBTitle: solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
67	c3na7A_	Alignment	not modelled	49.4	14	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
68	d2avue1	Alignment	not modelled	49.2	28	Fold: FlhC-like Superfamily: FlhC-like Family: FlhC-like
69	c1yuzB_	Alignment	not modelled	48.8	30	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
70	c2hr5B_	Alignment	not modelled	48.3	40	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
71	c3kp9A_	Alignment	not modelled	47.4	30	PDB header: blood coagulation,oxidoreductase Chain: A: PDB Molecule: vkorc1/thioredoxin domain protein; PDBTitle: structure of a bacterial homolog of vitamin k epoxide reductase
72	c2jr6A_	Alignment	not modelled	46.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0434 protein nma0874; PDBTitle: solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
73	d1jwhc_	Alignment	not modelled	46.3	27	Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit
74	c2avuF_	Alignment	not modelled	45.4	28	PDB header: transcription activator Chain: F: PDB Molecule: flagellar transcriptional activator flhc; PDBTitle: structure of the escherichia coli flhdc complex, a2 prokaryotic heteromeric regulator of transcription
75	c3eswA_	Alignment	not modelled	41.7	19	PDB header: hydrolase Chain: A: PDB Molecule: peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine PDBTitle: complex of yeast pngase with glcnac2-iac.
76	d1ctla1	Alignment	not modelled	41.5	25	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
77	c2ba1B_	Alignment	not modelled	41.4	23	PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core
78	d1twfi2	Alignment	not modelled	40.8	31	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
79	d2jnya1	Alignment	not modelled	40.7	9	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
						PDB header: signaling protein, cell cycle

80	c2qkdA_	Alignment	not modelled	39.9	24	Chain: A: PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains
81	c2riqA_	Alignment	not modelled	39.3	24	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: crystal structure of the third zinc-binding domain of human parp-1
82	d1liba1	Alignment	not modelled	38.8	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
83	c1nypA_	Alignment	not modelled	38.6	23	PDB header: cell adhesion Chain: A: PDB Molecule: pinch protein; PDBTitle: 4th lim domain of pinch protein
84	d1i4wa_	Alignment	not modelled	38.6	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
85	c1i4wA_	Alignment	not modelled	38.6	14	PDB header: transcription Chain: A: PDB Molecule: mitochondrial replication protein mtf1; PDBTitle: the crystal structure of the transcription factor sc-mtffb2 offers intriguing insights into mitochondrial transcription
86	c3eg9B_	Alignment	not modelled	38.0	15	PDB header: protein transport Chain: B: PDB Molecule: sec24 related gene family, member d; PDBTitle: crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
87	d1x3za1	Alignment	not modelled	37.6	19	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
88	d2k4xa1	Alignment	not modelled	37.2	36	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
89	d1dl6a_	Alignment	not modelled	36.6	17	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
90	c3egxB_	Alignment	not modelled	36.1	42	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24a; PDBTitle: crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22b and3 bound to the transport signal sequence of the snare protein4 bet1
91	d2pk7a1	Alignment	not modelled	36.1	17	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
92	c2jvnA_	Alignment	not modelled	35.4	35	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: domain c of human parp-1
93	d2hf1a1	Alignment	not modelled	35.2	22	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
94	c1pd0A_	Alignment	not modelled	35.1	27	PDB header: transport protein Chain: A: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
95	c1mpgB_	Alignment	not modelled	35.1	19	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli
96	d1qypa_	Alignment	not modelled	35.0	25	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
97	d2ct7a1	Alignment	not modelled	34.1	21	Fold: RING/U-box Superfamily: RING/U-box Family: IBR domain
98	c1m2vB_	Alignment	not modelled	33.6	27	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the yeast sec23/24 heterodimer
99	d2cu8a1	Alignment	not modelled	33.2	30	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
100	c2yg8B_	Alignment	not modelled	33.2	26	PDB header: hydrolase Chain: B: PDB Molecule: dna-3-methyladenine glycosidase ii, putative; PDBTitle: structure of an unusual 3-methyladenine dna glycosylase ii (2 alka) from deinococcus radiodurans
101	c3a44D_	Alignment	not modelled	33.1	23	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
102	c2jr7A_	Alignment	not modelled	32.4	33	PDB header: metal binding protein Chain: A: PDB Molecule: dph3 homolog; PDBTitle: solution structure of human desr1
103	c3eh2B_	Alignment	not modelled	30.9	19	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24c; PDBTitle: crystal structure of the human copii-coat protein sec24c
104	d2b9da1	Alignment	not modelled	30.4	26	Fold: E7 C-terminal domain-like Superfamily: E7 C-terminal domain-like Family: E7 C-terminal domain-like
105	d1woua_	Alignment	not modelled	30.4	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Txn15-like
106	d1e29a_	Alignment	not modelled	29.2	13	Fold: Cytochrome c Superfamily: Cytochrome c

					Family: monodomain cytochrome c
107	c2h56C	Alignment	not modelled	28.7	11 PDB header: hydrolase Chain: C: PDB Molecule: dna-3-methyladenine glycosidase; PDBTitle: crystal structure of dna-3-methyladenine glycosidase (10174367) from2 bacillus halodurans at 2.55 a resolution
108	d1x3ha1	Alignment	not modelled	28.3	16 Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
109	c2jhnB	Alignment	not modelled	27.8	26 PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
110	d1pcfa	Alignment	not modelled	27.7	26 Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: Transcriptional coactivator PC4 C-terminal domain
111	d1ywsa1	Alignment	not modelled	27.6	25 Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
112	c1m2oA	Alignment	not modelled	27.6	12 PDB header: protein transport/signaling protein Chain: A: PDB Molecule: protein transport protein sec23; PDBTitle: crystal structure of the sec23-sar1 complex
113	c2nn6l	Alignment	not modelled	26.5	8 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
114	c1x3ha	Alignment	not modelled	26.2	16 PDB header: metal binding protein Chain: A: PDB Molecule: leupaxin; PDBTitle: solution structure of the lim domain of human leupaxin
115	d1wd2a	Alignment	not modelled	26.1	21 Fold: RING/U-box Superfamily: RING/U-box Family: RING finger domain, C3HC4
116	c3f6qB	Alignment	not modelled	26.0	19 PDB header: signaling protein/signaling protein Chain: B: PDB Molecule: lim and senescent cell antigen-like-containing PDBTitle: crystal structure of integrin-linked kinase ankyrin repeat2 domain in complex with pinch1 lim1 domain
117	d1wgea1	Alignment	not modelled	25.9	33 Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
118	d2ct1a1	Alignment	not modelled	25.7	40 Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
119	c2eloA	Alignment	not modelled	25.6	30 PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 12th c2h2 zinc finger of human2 zinc finger protein 406
120	d1u5ka2	Alignment	not modelled	25.4	21 Fold: ArfGap/RecO-like zinc finger Superfamily: ArfGap/RecO-like zinc finger Family: RecO C-terminal domain-like