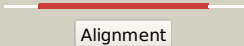

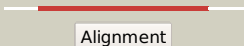

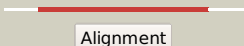







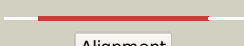












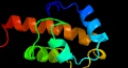



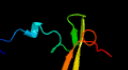



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0944 (-) _1053769_1054245
Date	Fri Jul 26 01:50:54 BST 2019
Unique Job ID	d0b96bc227dc0f05

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nnjA_			100.0	28	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
2	c2f5qA_			100.0	33	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
3	c1k82D_			100.0	31	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
4	c1ee8A_			100.0	33	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_			100.0	27	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	c3twkB_			100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
7	c3a46B_			100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of mvnei1/thf complex
8	c3w0fA_			100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like 3; PDBTitle: crystal structure of mouse endonuclease viii-like 3 (mnei3)
9	c4mb7A_			100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like l720; PDBTitle: crystal structure of a viral dna glycosylase
10	c1tdhA_			100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: nei endonuclease viii-like 1; PDBTitle: crystal structure of human endonuclease viii-like 1 (nei1)
11	c5ituB_			100.0	28	PDB header: dna binding protein/dna Chain: B: PDB Molecule: endonuclease 8-like 1; PDBTitle: crystal structure of human nei1(242k) bound to duplex dna containing2 thf

12	d1r2za1	Alignment		100.0	33	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
13	d1ee8a1	Alignment		100.0	31	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
14	d1k82a1	Alignment		100.0	31	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
15	d1tdza1	Alignment		100.0	29	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
16	d1k3xa1	Alignment		100.0	27	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
17	d1tdha1	Alignment		99.8	33	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
18	d2hkja1	Alignment		99.8	19	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Topoisomerase VI-B subunit middle domain
19	d1ee8a3	Alignment		99.6	37	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
20	d1tdza3	Alignment		99.6	30	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	d1r2za3	Alignment	not modelled	99.5	35	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
22	d1k82a3	Alignment	not modelled	99.5	35	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	d1l1ta3	Alignment	not modelled	99.5	35	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	d1k3xa3	Alignment	not modelled	99.4	32	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	c1mx0D_	Alignment	not modelled	97.5	22	PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
26	d2uubm1	Alignment	not modelled	97.2	28	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
27	c2zqmq_	Alignment	not modelled	97.1	27	PDB header: ribosomal protein/rna Chain: M: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
28	c3iz6M_	Alignment	not modelled	97.1	25	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

29	d2gy9m1	Alignment	not modelled	97.0	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
30	c5o5jM_	Alignment	not modelled	97.0	28	PDB header: ribosome Chain: M: PDB Molecule: 30s ribosomal protein s13; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
31	d1i94m_	Alignment	not modelled	97.0	29	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
32	c3j200_	Alignment	not modelled	96.9	27	PDB header: ribosome Chain: O: PDB Molecule: 30s ribosomal protein s13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
33	c2xznM_	Alignment	not modelled	96.9	29	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
34	c5xyiS_	Alignment	not modelled	96.7	20	PDB header: ribosome Chain: S: PDB Molecule: ribosomal protein s13p/s18e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
35	c2zkbB_	Alignment	not modelled	96.6	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
36	c3zeyM_	Alignment	not modelled	96.4	20	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
37	c3doaA_	Alignment	not modelled	96.2	21	PDB header: protein binding Chain: A: PDB Molecule: fibrinogen binding protein; PDBTitle: the crystal structure of the fibrinogen binding protein from2 staphylococcus aureus
38	c5mmjm_	Alignment	not modelled	95.9	22	PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
39	c4gc5A_	Alignment	not modelled	95.4	10	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase 1, mitochondrial; PDBTitle: crystal structure of murine tfb1m
40	c6ifsB_	Alignment	not modelled	95.1	11	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: ksga from bacillus subtilis 168
41	c5h3xA_	Alignment	not modelled	94.0	18	PDB header: cell adhesion Chain: A: PDB Molecule: fibronectin/fibrinogen binding protein; PDBTitle: the structure of the n-terminal of the fibronectin/fibrinogen-binding2 protein from streptococcus suis (fbps)
42	c4itqA_	Alignment	not modelled	93.7	24	PDB header: gene regulation, structural protein/dna Chain: A: PDB Molecule: putative uncharacterized protein sco1480; PDBTitle: crystal structure of hypothetical protein sco1480 bound to dna
43	c3fuxB_	Alignment	not modelled	93.7	17	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
44	c6erpJ_	Alignment	not modelled	93.2	9	PDB header: transcription Chain: J: PDB Molecule: dimethyladenosine transferase 2, mitochondrial; PDBTitle: structure of the human mitochondrial transcription initiation complex2 at the lsp promoter
45	c2q2eB_	Alignment	not modelled	92.9	17	PDB header: isomerase Chain: B: PDB Molecule: type 2 dna topoisomerase 6 subunit b; PDBTitle: crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
46	d1qyra_	Alignment	not modelled	91.5	25	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
47	d2i0za2	Alignment	not modelled	90.6	12	Fold: HI0933 insert domain-like Superfamily: HI0933 insert domain-like Family: HI0933 insert domain-like
48	c3fteA_	Alignment	not modelled	89.3	26	PDB header: transferase/rna Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of a. aeolicus ksga in complex with rna
49	c4jxiA_	Alignment	not modelled	88.0	23	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: crystal structure of ribosomal rna small subunit methyltransferase a2 from rickettsia bellii determined by iodide sad phasing
50	c2h1rA_	Alignment	not modelled	86.4	9	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase, putative; PDBTitle: crystal structure of a dimethyladenosine transferase from2 plasmodium falciparum
51	c2gb5B_	Alignment	not modelled	85.1	25	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
52	c3uzuA_	Alignment	not modelled	83.8	9	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 PDB header: transferase

53	c3tqsB_	Alignment	not modelled	82.7	7	Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii
54	c3bbnM_	Alignment	not modelled	81.1	26	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein s13; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
55	c2m6nA_	Alignment	not modelled	77.4	19	PDB header: cell cycle Chain: A: PDB Molecule: f-box only protein 5; PDBTitle: 3d solution structure of emi1 (early mitotic inhibitor 1)
56	c1dvbA_	Alignment	not modelled	73.4	15	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
57	c4ui9S_	Alignment	not modelled	72.5	11	PDB header: cell cycle Chain: S: PDB Molecule: f-box only protein 5; PDBTitle: atomic structure of the human anaphase-promoting complex
58	c3grrA_	Alignment	not modelled	71.3	16	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.
59	d2fiya1	Alignment	not modelled	71.2	22	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
60	c1yuzB_	Alignment	not modelled	68.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
61	c3fydA_	Alignment	not modelled	66.0	16	PDB header: transferase Chain: A: PDB Molecule: probable dimethyladenosine transferase; PDBTitle: crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi
62	c2jneA_	Alignment	not modelled	63.5	17	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. northeast2 structural genomics consortium target er317.
63	d2jneA1	Alignment	not modelled	63.5	17	Fold: Rubredoxin-like Superfamily: Yfgj-like Family: Yfgj-like
64	d2f4ma1	Alignment	not modelled	63.3	21	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
65	c6o3pA_	Alignment	not modelled	62.4	16	PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
66	c4rula_	Alignment	not modelled	61.4	18	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of full-length e.coli topoisomerase i in complex2 with ssdna
67	c1i3qI_	Alignment	not modelled	61.1	21	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii 14.2kd PDBTitle: rna polymerase ii crystal form i at 3.1 a resolution
68	c2mvwA_	Alignment	not modelled	59.3	20	PDB header: metal binding protein Chain: A: PDB Molecule: protein pml; PDBTitle: solution structure of the trim19 b-box1 (b1) of human promyelocytic2 leukemia (pml)
69	c2jrpA_	Alignment	not modelled	59.0	17	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
70	c2pziA_	Alignment	not modelled	58.3	29	PDB header: transferase Chain: A: PDB Molecule: probable serine/threonine-protein kinase pkng; PDBTitle: crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
71	d2gqfa2	Alignment	not modelled	58.1	7	Fold: HI0933 insert domain-like Superfamily: HI0933 insert domain-like Family: HI0933 insert domain-like
72	c2lcqA_	Alignment	not modelled	57.6	35	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
73	c5ijlA_	Alignment	not modelled	55.7	47	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
74	c3u50C_	Alignment	not modelled	55.5	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
75	d1tdha3	Alignment	not modelled	54.0	20	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
76	c2hr5B_	Alignment	not modelled	53.8	50	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
77	c2aklA_	Alignment	not modelled	53.0	39	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phna-like protein pa0128; PDBTitle: solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
						PDB header: dna binding protein

78	c6i52C_	Alignment	not modelled	51.6	27	Chain: C: PDB Molecule: replication factor a protein 1; PDBTitle: yeast rpa bound to ssdna
79	d2akla2	Alignment	not modelled	50.4	39	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
80	c6hmsB_	Alignment	not modelled	49.9	47	PDB header: replication Chain: B: PDB Molecule: dna polymerase ii large subunit,dna polymerase ii large PDBTitle: cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna
81	c5fywW_	Alignment	not modelled	49.4	23	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
82	c2kpiA_	Alignment	not modelled	47.9	22	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
83	c4gopC_	Alignment	not modelled	47.4	23	PDB header: dna binding protein/dna Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and conformational change of a replication protein a2 heterotrimer bound to ssdna
84	c2js4A_	Alignment	not modelled	47.2	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
85	c3wwnB_	Alignment	not modelled	46.8	29	PDB header: metal binding protein/transferase Chain: B: PDB Molecule: orff; PDBTitle: crystal structure of lysz from thermus thermophilus complex with lysw
86	c2owoA_	Alignment	not modelled	45.7	35	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
87	c6f5zC_	Alignment	not modelled	45.6	4	PDB header: transferase Chain: C: PDB Molecule: upf0434 family protein; PDBTitle: complex between the haloferax volcanii trm112 methyltransferase2 activator and the hvo_0019 putative methyltransferase
88	c5fjaI_	Alignment	not modelled	44.9	24	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase iii subunit rpc10; PDBTitle: cryo-em structure of yeast rna polymerase iii at 4.7 a
89	d1pfta_	Alignment	not modelled	44.4	19	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
90	d1lbia1	Alignment	not modelled	44.3	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
91	c2jr6A_	Alignment	not modelled	43.0	22	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
92	d2avue1	Alignment	not modelled	42.9	20	Fold: FlhC-like Superfamily: FlhC-like Family: FlhC-like
93	c4c2mX_	Alignment	not modelled	42.3	29	PDB header: transcription Chain: X: PDB Molecule: dna-directed rna polymerase i subunit rpa12; PDBTitle: structure of rna polymerase i at 2.8 a resolution
94	c3na7A_	Alignment	not modelled	41.8	17	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
95	d1twfi2	Alignment	not modelled	41.7	28	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
96	c5fmfR_	Alignment	not modelled	41.6	24	PDB header: transcription Chain: R: PDB Molecule: transcription initiation factor iie subunit alpha, tfa1; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex
97	c4esjA_	Alignment	not modelled	41.0	36	PDB header: hydrolase/dna Chain: A: PDB Molecule: type-2 restriction enzyme dpni; PDBTitle: restriction endonuclease dpni in complex with target dna
98	c1dgsB_	Alignment	not modelled	40.8	29	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
99	c5flmI_	Alignment	not modelled	40.6	17	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
100	c2l6IA_	Alignment	not modelled	40.2	15	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 24; PDBTitle: solution structure of human j-protein co-chaperone, dph4
101	d1qf8a_	Alignment	not modelled	39.9	28	Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit
102	c5oqjW_	Alignment	not modelled	39.2	24	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih PDB header: transcription

103	c5oqmW_	Alignment	not modelled	38.9	24	Chain: W: PDB Molecule: transcription factor tfiie subunit; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
104	d1cta1	Alignment	not modelled	38.6	45	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
105	c3a44D_	Alignment	not modelled	38.5	26	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
106	d1zq9a1	Alignment	not modelled	38.5	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
107	c2avuF_	Alignment	not modelled	38.2	20	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
108	d1loc_	Alignment	not modelled	38.0	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
109	c5ah5B_	Alignment	not modelled	37.7	29	PDB header: ligase/rna Chain: B: PDB Molecule: leucine--trna ligase; PDBTitle: crystal structure of the ternary complex of agrobacterium2 radiobacter k84 agnb2 leurs-trna-leuams
110	d1odha_	Alignment	not modelled	37.5	13	Fold: GCM domain Superfamily: GCM domain Family: GCM domain
111	d1x3za1	Alignment	not modelled	37.5	26	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
112	c1wz2B_	Alignment	not modelled	37.4	20	PDB header: ligase/rna Chain: B: PDB Molecule: leucyl-trna synthetase; PDBTitle: the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex
113	c2jhnB_	Alignment	not modelled	36.7	26	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
114	d2b9da1	Alignment	not modelled	35.4	36	Fold: E7 C-terminal domain-like Superfamily: E7 C-terminal domain-like Family: E7 C-terminal domain-like
115	d2jnya1	Alignment	not modelled	35.4	13	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
116	c3s6iA_	Alignment	not modelled	35.2	30	PDB header: hydrolase/dna Chain: A: PDB Molecule: dna-3-methyladenine glycosylase 1; PDBTitle: schizosaccharomyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
117	c3eg9B_	Alignment	not modelled	34.2	16	PDB header: protein transport Chain: B: PDB Molecule: sec24 related gene family, member d; PDBTitle: crystal structure of the mammalian copii-coat protein sec23/24 bound2 to the transport signal sequence of membrin
118	c2riqA_	Alignment	not modelled	34.1	29	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
119	c4glxA_	Alignment	not modelled	34.1	35	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
120	c4lw2C_	Alignment	not modelled	33.9	13	PDB header: lyase Chain: C: PDB Molecule: cysteine sulfinate desulfinate; PDBTitle: structural changes during cysteine desulfurase csda and sulfur-2 acceptor csde interactions provide insight into the trans-3 persulfuration