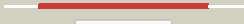



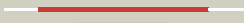






































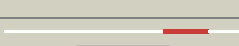
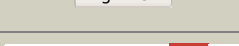
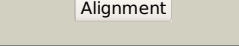

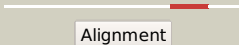
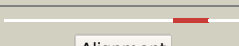


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3297_(nei)_3681317_3682084
Date	Thu Aug 8 16:20:50 BST 2019
Unique Job ID	c9e82c7131eff0cc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1k82D_	Alignment 		100.0	25	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
2	c2f5qA_	Alignment 		100.0	27	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
3	c1nnjA_	Alignment 		100.0	24	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	c3twkB_	Alignment 		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
5	c1ee8A_	Alignment 		100.0	28	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
6	c2opfA_	Alignment 		100.0	25	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
7	c3a46B_	Alignment 		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of mvnei1/thf complex
8	c3w0fA_	Alignment 		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like 3; PDBTitle: crystal structure of mouse endonuclease viii-like 3 (mnei3)
9	c4mb7A_	Alignment 		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like l720; PDBTitle: crystal structure of a viral dna glycosylase
10	c1tdhA_	Alignment 		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: nei endonuclease viii-like 1; PDBTitle: crystal structure of human endonuclease viii-like 1 (nei1)
11	c5ituB_	Alignment 		100.0	20	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	d1k82a2	 Alignment		100.0	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
13	d1r2za2	 Alignment		100.0	20	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
14	d1k3xa1	 Alignment		99.9	24	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
15	d1tdza2	 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
16	d1ee8a2	 Alignment		99.9	25	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	d1k82a1	 Alignment		99.9	22	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
18	d1r2za1	 Alignment		99.9	28	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
19	d1ee8a1	 Alignment		99.9	29	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
20	d1tdza1	 Alignment		99.9	21	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
21	d1k3xa2	 Alignment	not modelled	99.9	23	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
22	d1tdha2	 Alignment	not modelled	99.8	14	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
23	d1tdha1	 Alignment	not modelled	99.8	28	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
24	d1ee8a3	 Alignment	not modelled	99.6	27	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	d1tdza3	 Alignment	not modelled	99.6	33	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	d1r2za3	 Alignment	not modelled	99.6	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	d1k82a3	 Alignment	not modelled	99.6	36	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
28	d1l1ta3	 Alignment	not modelled	99.6	45	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
		 Alignment				Fold: S13-like H2TH domain

29	d2hkja1	Alignment	not modelled	99.5	18	Superfamily: S13-like H2TH domain Family: Topoisomerase VI-B subunit middle domain
30	d1k3xa3	Alignment	not modelled	99.5	47	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
31	d2uubm1	Alignment	not modelled	95.7	24	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
32	c3doaA	Alignment	not modelled	95.4	14	PDB header: protein binding Chain: A: PDB Molecule: fibrinogen binding protein; PDBTitle: the crystal structure of the fibrinogen binding protein from2 staphylococcus aureus
33	d2gy9m1	Alignment	not modelled	95.2	18	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
34	c3iz6M	Alignment	not modelled	95.0	16	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
35	c2zkqm	Alignment	not modelled	94.9	20	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
36	c5o5jM	Alignment	not modelled	94.7	29	PDB header: ribosome Chain: M: PDB Molecule: 30s ribosomal protein s13; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
37	c2xznM	Alignment	not modelled	94.6	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
38	c3j20O	Alignment	not modelled	94.3	24	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)
39	d1i94m	Alignment	not modelled	94.2	24	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
40	c5xyiS	Alignment	not modelled	93.8	18	PDB header: ribosome Chain: S: PDB Molecule: ribosomal protein s13p/s18e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
41	c3zeyM	Alignment	not modelled	91.8	18	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
42	c5mmjm	Alignment	not modelled	90.9	13	PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
43	c5h3xA	Alignment	not modelled	90.7	17	PDB header: cell adhesion Chain: A: PDB Molecule: fibrinectin/fibrinogen binding protein; PDBTitle: the structure of the n-terminal of the fibrinectin/fibrinogen-binding2 protein from streptococcus suis (fbps)
44	c2gb5B	Alignment	not modelled	89.5	20	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
45	c4rulA	Alignment	not modelled	86.3	29	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
46	c2m6nA	Alignment	not modelled	83.0	30	PDB header: cell cycle Chain: A: PDB Molecule: f-box only protein 5; PDBTitle: 3d solution structure of emi1 (early mitotic inhibitor 1)
47	c6i52C	Alignment	not modelled	81.2	17	PDB header: dna binding protein Chain: C: PDB Molecule: replication factor a protein 1; PDBTitle: yeast rpa bound to ssdna
48	c2jneA	Alignment	not modelled	78.8	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. northeast2 structural genomics consortium target er317.
49	d2jneA1	Alignment	not modelled	78.8	21	Fold: Rubredoxin-like Superfamily: Yfgj-like Family: Yfgj-like
50	c2jrpA	Alignment	not modelled	77.8	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
51	c4gopC	Alignment	not modelled	77.7	26	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
52	c4ui9S	Alignment	not modelled	77.6	26	PDB header: cell cycle Chain: S: PDB Molecule: f-box only protein 5; PDBTitle: atomic structure of the human anaphase-promoting complex
53	c5f4tA	Alignment	not modelled	76.5	32	PDB header: cell adhesion Chain: A: PDB Molecule: izumo sperm-egg fusion protein 1; PDBTitle: crystal structure of the human sperm izumo1 residues 22-254
						PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase

54	c6o3pA_	Alignment	not modelled	75.5	9	nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
55	c3u50C_	Alignment	not modelled	75.0	24	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
56	c6ifsB_	Alignment	not modelled	73.7	5	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: ksga from bacillus subtilis 168
57	c4gc5A_	Alignment	not modelled	72.7	11	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase 1, mitochondrial; PDBTitle: crystal structure of murine tfb1m
58	d2fiya1	Alignment	not modelled	72.0	20	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
59	d1lloc_	Alignment	not modelled	71.4	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
60	c5b5kA_	Alignment	not modelled	71.2	32	PDB header: cell adhesion Chain: A: PDB Molecule: izumo sperm-egg fusion protein 1; PDBTitle: crystal structure of izumo1, the mammalian sperm ligand for egg jun0
61	c2lcqA_	Alignment	not modelled	70.5	19	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
62	d1qyra_	Alignment	not modelled	67.4	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
63	d1pfta_	Alignment	not modelled	65.6	24	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
64	c6f5zC_	Alignment	not modelled	65.3	8	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
65	c5fywW_	Alignment	not modelled	65.3	24	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
66	c2kpiA_	Alignment	not modelled	63.4	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
67	c5ijlA_	Alignment	not modelled	62.5	41	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
68	c2owoA_	Alignment	not modelled	62.2	21	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
69	d1qf8a_	Alignment	not modelled	62.0	31	Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit
70	c3wnnB_	Alignment	not modelled	61.8	21	PDB header: metal binding protein/transferase Chain: B: PDB Molecule: orff; PDBTitle: crystal structure of lysz from thermus thermophilus complex with lysw
71	c1dgsB_	Alignment	not modelled	61.7	30	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
72	d1vd4a_	Alignment	not modelled	61.5	33	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
73	c2js4A_	Alignment	not modelled	60.4	17	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
74	c3bbnM_	Alignment	not modelled	60.0	10	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.
75	c3na7A_	Alignment	not modelled	59.2	23	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
76	c2jr6A_	Alignment	not modelled	57.6	13	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
77	c3kp9A_	Alignment	not modelled	56.5	60	PDB header: blood coagulation,oxidoreductase Chain: A: PDB Molecule: vkorc1/thioredoxin domain protein; PDBTitle: structure of a bacterial homolog of vitamin k epoxide reductase
78	c5oqmW_	Alignment	not modelled	55.8	24	PDB header: transcription Chain: W: PDB Molecule: transcription factor tfiie subunit; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
						PDB header: transferase/rna

79	c3fteA_	Alignment	not modelled	55.4	13	Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of a. aeolicus ksga in complex with rna
80	c5oqiW_	Alignment	not modelled	55.2	24	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
81	c5d5hA_	Alignment	not modelled	55.1	17	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of mycobacterium tuberculosis topoisomerase i
82	d2f4ma1	Alignment	not modelled	55.1	27	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
83	c2riqA_	Alignment	not modelled	54.6	19	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
84	c2hr5B_	Alignment	not modelled	54.4	30	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
85	d2avue1	Alignment	not modelled	54.1	20	Fold: FhC-like Superfamily: FhC-like Family: FhC-like
86	d1odha_	Alignment	not modelled	53.8	13	Fold: GCM domain Superfamily: GCM domain Family: GCM domain
87	c3fuxB_	Alignment	not modelled	53.6	18	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
88	c4opxD_	Alignment	not modelled	53.5	19	PDB header: transferase/dna/transferase inhibitor Chain: D: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: structure of human parp-1 bound to a dna double strand break in2 complex with (2r)-5-fluoro-2-methyl-2,3-dihydro-1-benzofuran-7-3 carboxamide
89	c5fmfR_	Alignment	not modelled	53.4	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
90	c4itqA_	Alignment	not modelled	52.9	19	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
91	c1dvbA_	Alignment	not modelled	52.6	38	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
92	c4kblA_	Alignment	not modelled	52.5	23	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase arih1; PDBTitle: structure of hhari, a ring-ibr-ring ubiquitin ligase: autoinhibition2 of an ariadne-family e3 and insights into ligation mechanism
93	d1jwhc_	Alignment	not modelled	52.0	31	Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit
94	c6hmsB_	Alignment	not modelled	51.8	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
95	d2akla2	Alignment	not modelled	51.7	26	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
96	c4u3eA_	Alignment	not modelled	51.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase
97	c4kisA_	Alignment	not modelled	50.9	17	PDB header: recombination/dna Chain: A: PDB Molecule: putative integrase [bacteriophage a118]; PDBTitle: crystal structure of a lsr-dna complex
98	c4qlxA_	Alignment	not modelled	50.5	17	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
99	c1yuzB_	Alignment	not modelled	50.5	30	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
100	c2avuF_	Alignment	not modelled	50.4	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
101	d2jnva1	Alignment	not modelled	50.0	9	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
102	d2i0za2	Alignment	not modelled	49.4	17	Fold: HI0933 insert domain-like Superfamily: HI0933 insert domain-like Family: HI0933 insert domain-like
103	c2jvnA_	Alignment	not modelled	48.9	19	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: domain c of human parp-1
104	d2k4xa1	Alignment	not modelled	48.3	36	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a

105	c6gymW_	 Alignment	not modelled	48.2	24	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha, PDBTitle: structure of a yeast closed complex with distorted dna (ccdist)
106	c3eg9B_	 Alignment	not modelled	48.0	27	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
107	c6erpj_	 Alignment	not modelled	47.7	8	PDB header: transcription Chain: J: PDB Molecule: dimethyladenosine transferase 2, mitochondrial; PDBTitle: structure of the human mitochondrial transcription initiation complex2 at the lsp promoter
108	d2pk7a1	 Alignment	not modelled	46.3	8	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
109	c2mvwA_	 Alignment	not modelled	45.3	35	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)
110	c1pd0A_	 Alignment	not modelled	45.1	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)
111	d1twfi2	 Alignment	not modelled	44.9	21	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
112	d1dl6a_	 Alignment	not modelled	44.2	22	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
113	d1qypa_	 Alignment	not modelled	44.1	26	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
114	d1cta1	 Alignment	not modelled	43.9	45	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
115	d2hf1a1	 Alignment	not modelled	43.7	17	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
116	c6g5iy_	 Alignment	not modelled	43.3	13	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
117	d2ct7a1	 Alignment	not modelled	43.1	29	Fold: RING/U-box Superfamily: RING/U-box Family: IBR domain
118	d2b9da1	 Alignment	not modelled	43.0	30	Fold: E7 C-terminal domain-like Superfamily: E7 C-terminal domain-like Family: E7 C-terminal domain-like
119	c2m48A_	 Alignment	not modelled	42.4	23	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase parkin; PDBTitle: solution structure of ibr-ring2 tandem domain from parkin
120	c3uzuA_	 Alignment	not modelled	42.2	11	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