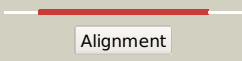
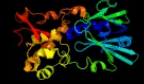


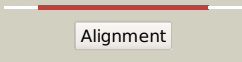





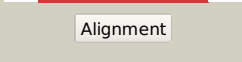

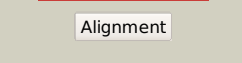

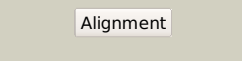
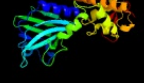
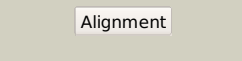

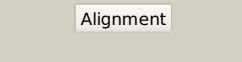

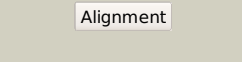












Phyre2

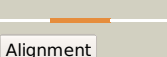
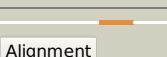
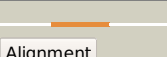
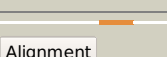
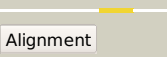
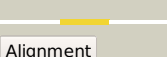
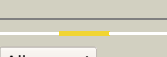
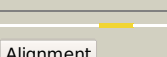
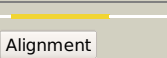
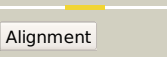
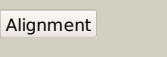
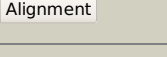
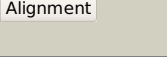
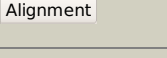
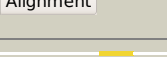
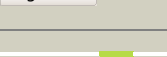

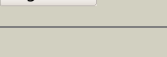
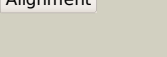
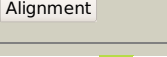
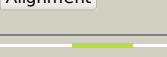
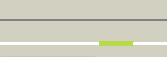


Email	mdejesus@rockefeller.edu
Description	RVBD2924c_(fpg)_3238611_3239480
Date	Thu Aug 8 16:20:08 BST 2019
Unique Job ID	045b2dec93df59ba

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2f5qA_	 Alignment		100.0	36	PDB header: hydrolase/dna Chain: A; PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
2	c1nnjA_	 Alignment		100.0	35	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
3	c1k82D_	 Alignment		100.0	34	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_	 Alignment		100.0	37	PDB header: dna binding protein Chain: A; PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
5	c3twkB_	 Alignment		100.0	30	PDB header: hydrolase Chain: B; PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
6	c3a46B_	 Alignment		100.0	20	PDB header: hydrolase Chain: B; PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of mvnei1/thf complex
7	c2opfA_	 Alignment		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
8	c3w0fA_	 Alignment		100.0	23	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	18	PDB header: hydrolase Chain: A; PDB Molecule: endonuclease 8-like l720; PDBTitle: crystal structure of a viral dna glycosylase
10	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)
11	c5ituB_	 Alignment		100.0	23	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	34	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
13	d1k82a1	Alignment		100.0	26	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
14	d1ee8a1	Alignment		100.0	35	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
15	d1tdza1	Alignment		100.0	30	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
16	d1r2za2	Alignment		100.0	35	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	d1k3xa1	Alignment		100.0	34	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
18	d1k82a2	Alignment		100.0	37	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	d1tdza2	Alignment		100.0	37	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
20	d1ee8a2	Alignment		100.0	40	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
21	d1k3xa2	Alignment	not modelled	99.9	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
22	d1tdha2	Alignment	not modelled	99.9	24	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	99.9	24	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
24	d2hkja1	Alignment	not modelled	99.7	12	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Topoisomerase VI-B subunit middle domain
25	d1ee8a3	Alignment	not modelled	99.7	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
26	d1tdza3	Alignment	not modelled	99.7	38	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	d1r2za3	Alignment	not modelled	99.7	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
28	d1k82a3	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
						Fold: Glucocorticoid receptor-like (DNA-binding domain)

29	d1l1ta3	Alignment	not modelled	99.6	45	Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
30	d1k3xa3	Alignment	not modelled	99.5	34	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	c3doA	Alignment	not modelled	97.4	18	PDB header: protein binding Chain: A: PDB Molecule: fibrinogen binding protein; PDBTitle: the crystal structure of the fibrinogen binding protein from2 staphylococcus aureus
32	c5h3xA	Alignment	not modelled	97.0	19	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)
33	d2uubm1	Alignment	not modelled	96.9	22	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
34	d2gy9m1	Alignment	not modelled	96.8	16	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
35	c3iz6M	Alignment	not modelled	96.6	12	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
36	c2zkqm	Alignment	not modelled	96.6	18	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
37	c5o5jM	Alignment	not modelled	96.5	14	PDB header: ribosome Chain: M: PDB Molecule: 30s ribosomal protein s13; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
38	c2xznM	Alignment	not modelled	96.4	16	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
39	c3j20O	Alignment	not modelled	96.4	18	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)
40	d1i94m	Alignment	not modelled	96.3	22	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
41	c5xyiS	Alignment	not modelled	96.2	24	PDB header: ribosome Chain: S: PDB Molecule: ribosomal protein s13p/s18e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
42	c1mx0D	Alignment	not modelled	96.0	15	PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
43	c3zeyM	Alignment	not modelled	95.5	24	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
44	c5mmjm	Alignment	not modelled	94.8	18	PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
45	c6ifsB	Alignment	not modelled	94.5	9	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: ksga from bacillus subtilis 168
46	c4gc5A	Alignment	not modelled	94.1	13	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase 1, mitochondrial; PDBTitle: crystal structure of murine tfb1m
47	c4itqA	Alignment	not modelled	92.3	18	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
48	c3fuxB	Alignment	not modelled	92.0	16	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
49	c6erpj	Alignment	not modelled	91.7	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
50	d2i0za2	Alignment	not modelled	91.3	10	Fold: HI0933 insert domain-like Superfamily: HI0933 insert domain-like Family: HI0933 insert domain-like
51	d1qyra	Alignment	not modelled	89.5	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
52	c3fteA	Alignment	not modelled	89.4	18	PDB header: transferase/rna Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of a. aeolicus ksga in complex with rna
53	c2gb5B	Alignment	not modelled	87.5	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

54	c3uzuA	 Alignment	not modelled	87.4	20	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
55	c4rulA	 Alignment	not modelled	85.7	26	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
56	c3tqsB	 Alignment	not modelled	81.9	6	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii
57	c2m6nA	 Alignment	not modelled	80.0	30	PDB header: cell cycle Chain: A: PDB Molecule: f-box only protein 5; PDBTitle: 3d solution structure of emi1 (early mitotic inhibitor 1)
58	c4ui9S	 Alignment	not modelled	79.7	19	PDB header: cell cycle Chain: S: PDB Molecule: f-box only protein 5; PDBTitle: atomic structure of the human anaphase-promoting complex
59	c4jxA	 Alignment	not modelled	79.6	13	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
60	c2h1rA	 Alignment	not modelled	79.3	13	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase, putative; PDBTitle: crystal structure of a dimethyladenosine transferase from2 plasmodium falciparum
61	c3u50C	 Alignment	not modelled	79.2	28	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
62	c2zkbB	 Alignment	not modelled	77.5	15	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
63	c3bbnM	 Alignment	not modelled	77.2	17	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.
64	c6i52C	 Alignment	not modelled	76.1	17	PDB header: dna binding protein Chain: C: PDB Molecule: replication factor a protein 1; PDBTitle: yeast rpa bound to ssdna
65	d2fiya1	 Alignment	not modelled	75.0	24	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
66	c6o3pA	 Alignment	not modelled	73.3	21	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
67	c2q2eB	 Alignment	not modelled	73.2	18	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
68	c4gopC	 Alignment	not modelled	70.4	22	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
69	c5f4tA	 Alignment	not modelled	70.1	26	PDB header: cell adhesion Chain: A: PDB Molecule: sizumo sperm-egg fusion protein 1; PDBTitle: crystal structure of the human sperm izumo1 residues 22-254
70	c5fywW	 Alignment	not modelled	68.7	24	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
71	c5jilA	 Alignment	not modelled	68.5	41	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
72	c2pziA	 Alignment	not modelled	66.9	27	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
73	d2jneA1	 Alignment	not modelled	66.7	13	Fold: Rubredoxin-like Superfamily: Yfgj-like Family: Yfgj-like
74	c2jneA	 Alignment	not modelled	66.7	13	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.
75	c1dvbA	 Alignment	not modelled	66.1	21	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
76	c2jrpA	 Alignment	not modelled	65.0	13	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
77	d1qf8a	 Alignment	not modelled	64.4	28	Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit

78	c2kpiA	Alignment	not modelled	63.9	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
79	d1l1oc	Alignment	not modelled	63.1	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
80	c5b5kA	Alignment	not modelled	62.6	26	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 juno
81	c2lcqA	Alignment	not modelled	62.5	20	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
82	c5oqmW	Alignment	not modelled	62.5	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
83	c5fmfR	Alignment	not modelled	62.1	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
84	c5oqiW	Alignment	not modelled	62.0	24	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
85	c6hmsB	Alignment	not modelled	61.9	41	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
86	c4esjA	Alignment	not modelled	61.1	36	PDB header: hydrolase/dna Chain: A: PDB Molecule: type-2 restriction enzyme dpni; PDBTitle: restriction endonuclease dpni in complex with target dna
87	c2js4A	Alignment	not modelled	61.0	13	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
88	c4kblA	Alignment	not modelled	59.5	19	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
89	c6f5zC	Alignment	not modelled	59.1	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
90	d2f4ma1	Alignment	not modelled	59.0	35	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
91	c2jr6A	Alignment	not modelled	58.9	4	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	c3wwnB	Alignment	not modelled	57.9	33	PDB header: metal binding protein/transferase Chain: B: PDB Molecule: orff; PDBTitle: crystal structure of lysz from thermus thermophilus complex with lysw
93	c2mvvA	Alignment	not modelled	57.7	30	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)
94	d1pfta	Alignment	not modelled	57.5	19	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
95	c2owoA	Alignment	not modelled	57.4	25	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
96	c5fjal	Alignment	not modelled	56.5	15	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
97	d2gqfa2	Alignment	not modelled	56.2	14	Fold: HI0933 insert domain-like Superfamily: HI0933 insert domain-like Family: HI0933 insert domain-like
98	c4kisA	Alignment	not modelled	56.1	13	PDB header: recombination/dna Chain: A: PDB Molecule: putative integrase [bacteriophage a118]; PDBTitle: crystal structure of a lsr-dna complex
99	c1dgsB	Alignment	not modelled	56.0	35	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
100	c6gymW	Alignment	not modelled	55.7	24	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha, PDBTitle: structure of a yeast closed complex with distorted dna (ccd1st)
101	d1vd4a	Alignment	not modelled	55.4	54	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
102	d2avue1	Alignment	not modelled	54.6	28	Fold: FlhC-like Superfamily: FlhC-like

					Family:FlhC-like
103	c5iy9Q_	Alignment	not modelled	54.0	25 PDB header: transcription, transferase/dna/rna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the initial transcribing state (no iis)
104	c2ba1B_	Alignment	not modelled	53.4	23 PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein cs14; PDBTitle: archaeal exosome core
105	c5d5hA_	Alignment	not modelled	52.7	17 PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of mycobacterium tuberculosis topoisomerase i
106	d2jnya1	Alignment	not modelled	52.5	13 Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
107	d1odha_	Alignment	not modelled	52.3	9 Fold: GCM domain Superfamily: GCM domain Family: GCM domain
108	c3grrA_	Alignment	not modelled	51.8	8 PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of the complex between s-adenosyl homocysteine and 2 methanocaldococcus jannaschi dim1.
109	d2akla2	Alignment	not modelled	51.3	22 Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
110	c2avuF_	Alignment	not modelled	51.0	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
111	d1jwhc_	Alignment	not modelled	50.9	28 Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit
112	c3na7A_	Alignment	not modelled	48.9	21 PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
113	d2pk7a1	Alignment	not modelled	48.4	8 Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
114	d2hf1a1	Alignment	not modelled	48.4	13 Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
115	c3fydA_	Alignment	not modelled	48.2	8 PDB header: transferase Chain: A: PDB Molecule: probable dimethyladenosine transferase; PDBTitle: crystal structure of dim1 from the thermophilic archeon, 2 methanocaldococcus jannaschi
116	d2k4xa1	Alignment	not modelled	47.6	32 Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
117	c3eg9B_	Alignment	not modelled	47.3	24 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 bound to the transport signal sequence of membrin
118	c2xzn9_	Alignment	not modelled	44.8	29 PDB header: ribosome Chain: 9: PDB Molecule: rps31e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal 2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for 4 molecule 2
119	c1pd0A_	Alignment	not modelled	44.5	24 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)
120	d1libia1	Alignment	not modelled	44.4	50 Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain