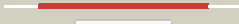
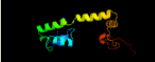


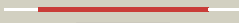


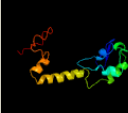



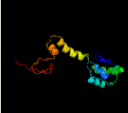









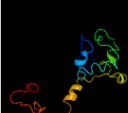


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3460c_(rpsM)_3879875_3880249
Date	Fri Aug 9 18:20:13 BST 2019
Unique Job ID	2e241605c5ec7b3c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2uubm1	 Alignment		100.0	62	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
2	c3j200_	 Alignment		100.0	38	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)
3	c3iz6M_	 Alignment		100.0	34	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
4	c3zeyM_	 Alignment		100.0	27	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
5	c2xznM_	 Alignment		100.0	35	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
6	c2zqkm_	 Alignment		100.0	31	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
7	c5o5jM_	 Alignment		100.0	89	PDB header: ribosome Chain: M: PDB Molecule: 30s ribosomal protein s13; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
8	d2gy9m1	 Alignment		100.0	56	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
9	c5xyiS_	 Alignment		100.0	32	PDB header: ribosome Chain: S: PDB Molecule: ribosomal protein s13p/s18e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
10	c5mmjm_	 Alignment		100.0	46	PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
11	c3bbnM_	 Alignment		100.0	52	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.

12	d1i94m_	Alignment		100.0	56	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
13	d2hkja1	Alignment		97.2	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Topoisomerase VI-B subunit middle domain
14	c3a46B_	Alignment		96.7	31	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of mvnei1/thf complex
15	c1ee8A_	Alignment		96.7	26	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
16	d1ee8a1	Alignment		96.7	26	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
17	d1tdza1	Alignment		96.7	28	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
18	d1k82a1	Alignment		96.5	28	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
19	d1r2za1	Alignment		96.4	21	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
20	c2f5qA_	Alignment		96.3	21	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
21	c3w0fA_	Alignment	not modelled	96.3	26	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like 3; PDBTitle: crystal structure of mouse endonuclease viii-like 3 (mnei3)
22	d1k3xa1	Alignment	not modelled	96.2	28	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
23	c1k82D_	Alignment	not modelled	96.2	28	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
24	c1nnjA_	Alignment	not modelled	96.2	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
25	c3twkB_	Alignment	not modelled	96.1	31	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
26	c4mb7A_	Alignment	not modelled	96.0	21	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like I720; PDBTitle: crystal structure of a viral dna glycosylase
27	c2opfA_	Alignment	not modelled	95.9	28	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
28	c4itqA_	Alignment	not modelled	95.7	29	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

29	c5ituB	Alignment	not modelled	93.0	26	PDB header: dna binding protein/dna Chain: B: PDB Molecule: endonuclease 8-like 1; PDBTitle: crystal structure of human neil1(242k) bound to duplex dna containing2 thf
30	d2i0za2	Alignment	not modelled	92.8	14	Fold: HI0933 insert domain-like Superfamily: HI0933 insert domain-like Family: HI0933 insert domain-like
31	d1tdha1	Alignment	not modelled	91.9	22	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
32	c6ifsB	Alignment	not modelled	90.6	20	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: ksga from bacillus subtilis 168
33	c3fuxB	Alignment	not modelled	90.2	31	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
34	c4gc5A	Alignment	not modelled	89.2	22	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase 1, mitochondrial; PDBTitle: crystal structure of murine tfb1m
35	c1tdhA	Alignment	not modelled	88.0	32	PDB header: hydrolase Chain: A: PDB Molecule: nei endonuclease viii-like 1; PDBTitle: crystal structure of human endonuclease viii-like 1 (neil1)
36	c1mx0D	Alignment	not modelled	86.6	25	PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
37	c6erpJ	Alignment	not modelled	86.5	17	PDB header: transcription Chain: J: PDB Molecule: dimethyladenosine transferase 2, mitochondrial; PDBTitle: structure of the human mitochondrial transcription initiation complex2 at the lsp promoter
38	c2mutA	Alignment	not modelled	86.3	20	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
39	d2i1qa1	Alignment	not modelled	85.2	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
40	c1s5lu	Alignment	not modelled	84.3	24	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
41	d1x2ia1	Alignment	not modelled	83.9	14	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
42	c4jxA	Alignment	not modelled	83.3	26	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
43	d2gqfa2	Alignment	not modelled	83.2	10	Fold: HI0933 insert domain-like Superfamily: HI0933 insert domain-like Family: HI0933 insert domain-like
44	d1pzna1	Alignment	not modelled	82.9	13	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
45	d2bgwa1	Alignment	not modelled	81.7	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
46	d2axtu1	Alignment	not modelled	81.7	24	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
47	c2zkbB	Alignment	not modelled	80.8	26	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
48	d2a1jb1	Alignment	not modelled	80.6	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
49	d1qyra	Alignment	not modelled	80.3	28	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
50	c1vddC	Alignment	not modelled	77.4	25	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
51	c3tqsB	Alignment	not modelled	76.7	22	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii
52	c3fteA	Alignment	not modelled	74.7	28	PDB header: transferase/rna Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of a. aeolicus ksga in complex with rna
53	d1kfta	Alignment	not modelled	74.1	24	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
54	c1kftA	Alignment	not modelled	74.1	24	PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc subunit c; PDBTitle: solution structure of the c-terminal domain of uvrC from

					e-2 coli
55	d1vdda	Alignment	not modelled	73.5	25 Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
56	d1bvsa2	Alignment	not modelled	71.7	35 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
57	d1ixra1	Alignment	not modelled	71.0	30 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
58	c4p4oA	Alignment	not modelled	70.6	27 PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
59	c3kntC	Alignment	not modelled	69.9	18 PDB header: hydrolase, lyase/dna Chain: C: PDB Molecule: n-glycosylase/dna lyase; PDBTitle: crystal structure of methanocaldococcus jannaschii 8-oxoguanine2 glycosylase/lyase in complex with 15mer dna containing 8-oxoguanine
60	d1cuka2	Alignment	not modelled	69.6	23 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
61	c1d8IA	Alignment	not modelled	69.1	25 PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
62	c1nomA	Alignment	not modelled	68.5	32 PDB header: nucleotidyltransferase Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mncI2 (5 millimolar)
63	c3fhgA	Alignment	not modelled	67.7	26 PDB header: dna repair, hydrolase, lyase Chain: A: PDB Molecule: n-glycosylase/dna lyase; PDBTitle: crystal structure of sulfolobus solfataricus 8-oxoguanine dna2 glycosylase (ssogg)
64	d2duya1	Alignment	not modelled	67.5	24 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
65	c5z2vB	Alignment	not modelled	65.7	15 PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
66	d1jmsa3	Alignment	not modelled	65.6	21 Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
67	c2h5xA	Alignment	not modelled	65.1	30 PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
68	d2fmpa2	Alignment	not modelled	65.0	35 Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
69	c1ixrB	Alignment	not modelled	64.6	30 PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
70	c3uzuA	Alignment	not modelled	63.8	17 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
71	c3mr2A	Alignment	not modelled	63.7	21 PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
72	c1ixrA	Alignment	not modelled	62.6	23 PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
73	d2vana1	Alignment	not modelled	59.9	35 Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
74	c2lyhA	Alignment	not modelled	58.9	12 PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
75	d2bcqa2	Alignment	not modelled	58.5	20 Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
76	c5zvqA	Alignment	not modelled	56.9	26 PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
77	c1hjpA	Alignment	not modelled	55.8	25 PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
78	d2aq0a1	Alignment	not modelled	54.6	11 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
79	d1gm5a2	Alignment	not modelled	53.5	37 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain
80	c2nrzB	Alignment	not modelled	50.9	22 PDB header: hydrolase Chain: B: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrC bound to

						its2 catalytic divalent cation PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase beta family (x family); PDBTitle: dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
81	c3auoB_	Alignment	not modelled	50.8	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
82	d2noha1	Alignment	not modelled	50.4	25	PDB header: hydrolase/dna Chain: A: PDB Molecule: 3-methyladenine dna glycosylase; PDBTitle: structure of mboggl1 in complex with high affinity dna ligand
83	c4ejyA_	Alignment	not modelled	50.3	24	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
84	c3ve5D_	Alignment	not modelled	49.1	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
85	d2edu1	Alignment	not modelled	48.8	20	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: polymerase mu in ternary complex with gapped 11mer dna duplex and2 bound incoming nucleotide
86	c2ihmA_	Alignment	not modelled	48.6	27	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
87	c2jhnB_	Alignment	not modelled	47.2	28	PDB header: hydrolase Chain: A: PDB Molecule: 8-oxoguanine dna glycosylase; PDBTitle: native structure of the human 8-oxoguanine dna glycosylase2 hogg1
88	c1ko9A_	Alignment	not modelled	47.0	29	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
89	c2w9mB_	Alignment	not modelled	46.0	27	PDB header: hydrolase, lyase Chain: B: PDB Molecule: probable n-glycosylase/dna lyase; PDBTitle: crystal structure of tm1821, the 8-oxoguanine dna glycosylase of2 thermotoga maritima
90	c3n0uB_	Alignment	not modelled	45.9	22	PDB header: transferase/dna Chain: A: PDB Molecule: terminal deoxynucleotidyltransferase short PDBTitle: binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
91	c1kdhA_	Alignment	not modelled	44.3	23	PDB header: hydrolase, lyase Chain: A: PDB Molecule: 8-oxoguanine-dna-glycosylase; PDBTitle: crystal structure of clostridium acetobutylicum 8-oxoguanine dna2 glycosylase in complex with 8-oxoguanosine
92	c3f10A_	Alignment	not modelled	44.0	25	PDB header: hydrolase/dna Chain: A: PDB Molecule: n-glycosylase/dna lyase; PDBTitle: catalytically inactive human 8-oxoguanine glycosylase2 crosslinked to 7-deazaguanine containing dna
93	c1yqmA_	Alignment	not modelled	44.0	25	PDB header: hydrolase/dna Chain: A: PDB Molecule: dna-3-methyladenine glycosylase 1; PDBTitle: schizosaccaromyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
94	c3s6iA_	Alignment	not modelled	43.9	35	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase beta (e.c.2.7.7.7)); PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
95	c8iczA_	Alignment	not modelled	42.5	19	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
96	d2abka_	Alignment	not modelled	42.1	32	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
97	d1a77a1	Alignment	not modelled	41.2	29	PDB header: hydrolase Chain: B: PDB Molecule: dna-3-methyladenine glycosidase ii, putative; PDBTitle: structure of an unusual 3-methyladenine dna glycosylase ii (alka) from2 deinococcus radiodurans
98	c2yg8B_	Alignment	not modelled	41.0	28	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
99	c2bhnD_	Alignment	not modelled	40.5	20	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
100	d1kq2a_	Alignment	not modelled	40.5	26	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
101	d1mpga1	Alignment	not modelled	40.5	38	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii alpha subunit; PDBTitle: crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
102	c2hnhA_	Alignment	not modelled	40.5	16	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
103	c5fkvA_	Alignment	not modelled	39.7	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 mazei
104	c2q2eB_	Alignment	not modelled	39.6	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: fanconi anemia group m protein; PDBTitle: architecture and dna recognition elements of the fanconi
105	c4bxoA_	Alignment	not modelled	38.6	10	

						anemia fancm-2 faap24 complex
106	d1pu6a_	Alignment	not modelled	38.6	38	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
107	d1zq9a1	Alignment	not modelled	38.4	26	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
108	d1szpa1	Alignment	not modelled	38.0	26	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
109	d1orna_	Alignment	not modelled	37.6	26	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
110	d1mc8a1	Alignment	not modelled	37.1	16	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
111	c2bcuA_	Alignment	not modelled	37.0	12	PDB header: transferase, lyase/dna Chain: A: PDB Molecule: dna polymerase lambda; PDBTitle: dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
112	d1keaa_	Alignment	not modelled	36.8	11	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
113	d1b43a1	Alignment	not modelled	36.7	18	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
114	d1rxwa1	Alignment	not modelled	35.3	18	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
115	d1jha2	Alignment	not modelled	35.3	12	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
116	c1rrqA_	Alignment	not modelled	34.9	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
117	c4b24A_	Alignment	not modelled	34.9	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: probable dna-3-methyladenine glycosylase 2; PDBTitle: unprecedented sculpting of dna at abasic sites by dna glycosylase2 homolog mag2
118	c4uobA_	Alignment	not modelled	34.6	25	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3
119	c4unfA_	Alignment	not modelled	33.4	25	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-1; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-1
120	d1rrqa1	Alignment	not modelled	33.2	16	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase