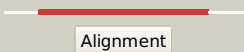

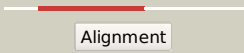

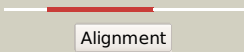

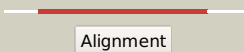

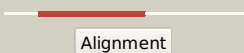

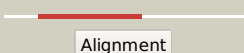

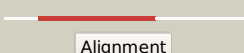





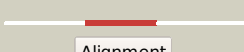

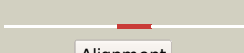
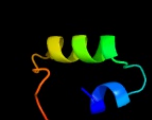


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2424c (-) _2720786_2721787
Date	Wed Aug 7 12:50:04 BST 2019
Unique Job ID	0c2ca2d6f440a329

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o9zH_	 Alignment		97.7	15	PDB header: splicing Chain: H: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp31; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
2	d2ozbb1	 Alignment		97.4	11	Fold: Nop domain Superfamily: Nop domain Family: Nop domain
3	c3fhgA_	 Alignment		96.7	10	PDB header: dna repair, hydrolase, lyase Chain: A: PDB Molecule: n-glycosylase/dna lyase; PDBTitle: crystal structure of sulfobolus solfataricus 8-oxoguanine dna2 glycosylase (ssogg)
4	c5ganF_	 Alignment		96.6	9	PDB header: transcription Chain: F: PDB Molecule: pre-mrna-processing factor 31; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
5	c2nnwC_	 Alignment		96.6	13	PDB header: transferase Chain: C: PDB Molecule: nop5/nop56 related protein; PDBTitle: alternative conformations of nop56/58-fibrillar complex and2 implication for induced-fit assenly of box c/d rnps
6	c3icxB_	 Alignment		96.3	11	PDB header: rna binding protein Chain: B: PDB Molecule: pre mrna splicing protein; PDBTitle: crystal structure of sulfobolus solfataricus nop5 (135-380)
7	c3n0uB_	 Alignment		96.2	14	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
8	c3id5E_	 Alignment		95.8	11	PDB header: transferase/ribosomal protein/rna Chain: E: PDB Molecule: pre mrna splicing protein; PDBTitle: crystal structure of sulfobolus solfataricus c/d rnp assembled with2 nop5, fibrillar, l7ae and a split half c/d rna
9	c6nd4b_	 Alignment		95.3	10	PDB header: ribosome Chain: B: PDB Molecule: PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
10	d1pu6a_	 Alignment		94.2	10	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
11	c4itqA_	 Alignment		94.0	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

12	c1rrqA_	Alignment		93.7	14	PDB header: hydrolase/dna Chain: A; PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
13	c6nd4a_	Alignment		93.7	15	PDB header: ribosome Chain: A; PDB Molecule: mpp10; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
14	d2bgwa1	Alignment		93.5	17	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
15	c3kntC_	Alignment		93.4	11	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
16	d1x2ia1	Alignment		92.9	9	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
17	c4b24A_	Alignment		92.9	15	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
18	d2aq0a1	Alignment		92.9	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
19	d1kfta_	Alignment		92.8	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
20	c1kftA_	Alignment		92.8	20	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
21	c2h5xA_	Alignment	not modelled	92.5	17	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
22	c2nrzB_	Alignment	not modelled	92.4	17	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
23	d1rrqa1	Alignment	not modelled	92.4	12	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
24	d3bzka1	Alignment	not modelled	91.9	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HHH-containing domain-like
25	c2mutA_	Alignment	not modelled	91.7	22	PDB header: hydrolase Chain: A; PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
26	c1ixrA_	Alignment	not modelled	91.6	26	PDB header: hydrolase Chain: A; PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
27	d1keaa_	Alignment	not modelled	91.1	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
28	d1bvsa2	Alignment	not modelled	90.9	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
						Fold: SAM domain-like

29	d1cuka2	Alignment	not modelled	90.8	16	Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
30	d1ixra1	Alignment	not modelled	90.8	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
31	c1d8A_	Alignment	not modelled	90.7	21	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
32	d2axtu1	Alignment	not modelled	90.4	18	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
33	d1kg2a_	Alignment	not modelled	90.3	15	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
34	c4unfA_	Alignment	not modelled	90.1	10	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-1; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-1
35	d2abka_	Alignment	not modelled	90.1	10	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
36	d1rxwa1	Alignment	not modelled	89.8	22	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
37	c2lyhA_	Alignment	not modelled	89.6	17	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
38	d1ul1x1	Alignment	not modelled	89.5	26	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
39	d2duya1	Alignment	not modelled	89.1	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
40	d1a77a1	Alignment	not modelled	88.8	17	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
41	d1orna_	Alignment	not modelled	88.7	16	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
42	c4q0rB_	Alignment	not modelled	88.6	29	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna repair protein rad2; PDBTitle: the catalytic core of rad2 (complex i)
43	d2a1jb1	Alignment	not modelled	88.5	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
44	d1pzna1	Alignment	not modelled	88.5	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
45	c8icza_	Alignment	not modelled	88.4	12	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), mnc12 (5 millimolar), and lithium sulfate4 (75 millimolar)
46	c1ixrB_	Alignment	not modelled	88.3	20	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
47	d2ilqa1	Alignment	not modelled	88.0	10	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
48	d1mc8a1	Alignment	not modelled	87.5	14	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
49	c4bxoA_	Alignment	not modelled	87.5	12	PDB header: hydrolase/dna Chain: A: PDB Molecule: fanconi anemia group m protein; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
50	c1kdhA_	Alignment	not modelled	87.3	18	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
51	c1hjpA_	Alignment	not modelled	87.2	12	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
52	c2w9mB_	Alignment	not modelled	87.2	15	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
53	c3auoB_	Alignment	not modelled	87.1	17	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
54	d1b43a1	Alignment	not modelled	86.9	19	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
						Fold: SAM domain-like

55	d2eduA1	Alignment	not modelled	86.8	17	Superfamily: RuvA domain 2-like Family: ComEA-like
56	d1xo1A1	Alignment	not modelled	86.8	28	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
57	c3s6iA	Alignment	not modelled	86.6	19	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.
58	c2ihmA	Alignment	not modelled	86.3	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
59	c3n5nX	Alignment	not modelled	86.1	13	PDB header: hydrolase Chain: X: PDB Molecule: a/g-specific adenine dna glycosylase; PDBTitle: crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
60	c2oceA	Alignment	not modelled	85.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
61	d1ngna	Alignment	not modelled	85.5	11	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
62	c1s5lu	Alignment	not modelled	85.4	18	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
63	c4p4oA	Alignment	not modelled	84.7	17	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
64	d2noha1	Alignment	not modelled	84.4	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
65	c3psfA	Alignment	not modelled	83.6	10	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259)
66	c2ziuA	Alignment	not modelled	83.3	17	PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
67	d1mpga1	Alignment	not modelled	83.1	15	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
68	d1dgsa1	Alignment	not modelled	83.0	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
69	c4bxoB	Alignment	not modelled	83.0	17	PDB header: hydrolase/dna Chain: B: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
70	c4uobA	Alignment	not modelled	82.6	25	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3
71	c1nomA	Alignment	not modelled	82.3	16	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 mncl2 (5 millimolar)
72	d1cmwa1	Alignment	not modelled	81.7	23	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
73	c2csdB	Alignment	not modelled	81.5	17	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
74	c1ut8B	Alignment	not modelled	80.6	30	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
75	c1rxvA	Alignment	not modelled	80.4	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
76	c2izoA	Alignment	not modelled	79.5	27	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
77	c6c34A	Alignment	not modelled	79.4	22	PDB header: dna binding protein Chain: A: PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
78	c3f10A	Alignment	not modelled	79.4	16	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
79	c5t9jB	Alignment	not modelled	77.8	21	PDB header: hydrolase Chain: B: PDB Molecule: flap endonuclease gen homolog 1; PDBTitle: crystal structure of human gen1 in complex with holliday junction dna2 in the upper interface
80	c1b43A	Alignment	not modelled	77.2	18	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
81	c3oryA	Alignment	not modelled	77.1	17	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus

82	c2zixA	Alignment	not modelled	76.4	14	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: crystal structure of the mus81-eme1 complex
83	c1ul1Y	Alignment	not modelled	75.9	26	PDB header: hydrolase/dna binding protein Chain: Y: PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
84	c2yg8B	Alignment	not modelled	75.8	15	PDB header: hydrolase Chain: B: PDB Molecule: dna-3-methyladenine glycosidase ii, putative; PDBTitle: structure of an unusual 3-methyladenine dna glycosylase ii (alka) from <i>Deinococcus radiodurans</i>
85	c6gmhM	Alignment	not modelled	75.8	13	PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor spt6, transcription PDBTitle: structure of activated transcription complex pol ii-dsif-paf-spt6
86	c2bhnD	Alignment	not modelled	75.6	20	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from <i>Aeropyrum pernix</i>
87	c3zddA	Alignment	not modelled	75.5	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 50v62 oligonucleotide and potassium
88	c4wa8A	Alignment	not modelled	75.1	27	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: methanopyrus kandleri fen-1 nuclease
89	c4ejyA	Alignment	not modelled	75.0	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: 3-methyladenine dna glycosylase; PDBTitle: structure of mbogg1 in complex with high affinity dna ligand
90	c2owoA	Alignment	not modelled	74.8	13	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
91	c3q8IA	Alignment	not modelled	74.8	33	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+
92	c2jhnB	Alignment	not modelled	74.4	19	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from <i>archaeoglobus fulgidus</i>
93	c2bcuA	Alignment	not modelled	74.1	23	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
94	c1vddC	Alignment	not modelled	74.1	14	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
95	c3psiA	Alignment	not modelled	73.9	10	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from <i>saccharomyces2 cerevisiae</i> , form spt6(239-1451)
96	c5zvqA	Alignment	not modelled	73.4	14	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
97	d1vdda	Alignment	not modelled	72.7	14	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
98	c1mpgB	Alignment	not modelled	72.7	16	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from <i>escherichia coli</i>
99	c1ko9A	Alignment	not modelled	72.6	13	PDB header: hydrolase Chain: A: PDB Molecule: 8-oxoguanine dna glycosylase; PDBTitle: native structure of the human 8-oxoguanine dna glycosylase2 hogg1
100	c5z2vB	Alignment	not modelled	72.0	14	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from <i>pseudomonas aeruginosa</i> pao1
101	c1a77A	Alignment	not modelled	70.8	18	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from <i>methanococcus jannaschii</i>
102	c3bqsB	Alignment	not modelled	70.6	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from <i>listeria monocytogenes</i> , trigonal form
103	c1yqmA	Alignment	not modelled	70.2	12	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
104	d1i94m	Alignment	not modelled	69.5	24	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
105	d1szpa1	Alignment	not modelled	68.6	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
106	d1d8ba	Alignment	not modelled	68.4	6	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
107	c3iz6M	Alignment	not modelled	66.6	24	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 <i>triticum aestivum</i> translating 80s ribosome

108	c5oI9A_	Alignment	not modelled	66.6	9	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
109	c2xznM_	Alignment	not modelled	66.2	24	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
110	c1dgsB_	Alignment	not modelled	65.4	15	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
111	c5o5jM_	Alignment	not modelled	64.9	24	PDB header: ribosome Chain: M: PDB Molecule: 30s ribosomal protein s13; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
112	c4glxA_	Alignment	not modelled	64.4	15	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
113	d1wuda1	Alignment	not modelled	63.4	11	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
114	d2bcqa2	Alignment	not modelled	63.4	27	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
115	c3qeaZ_	Alignment	not modelled	62.6	14	PDB header: hydrolase/dna Chain: Z: PDB Molecule: exonuclease 1; PDBTitle: crystal structure of human exonuclease 1 exo1 (wt) in complex with dna2 (complex ii)
116	c5xyiS_	Alignment	not modelled	61.4	28	PDB header: ribosome Chain: S: PDB Molecule: ribosomal protein s13p/s18e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
117	d1nt2b_	Alignment	not modelled	61.3	13	Fold: Nop domain Superfamily: Nop domain Family: Nop domain
118	d1jmsa3	Alignment	not modelled	60.4	19	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
119	d1szpb1	Alignment	not modelled	59.9	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
120	c3j20O_	Alignment	not modelled	59.8	28	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)