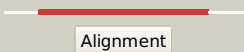

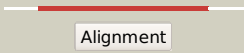

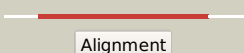








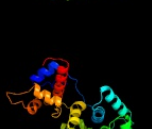
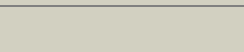

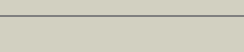
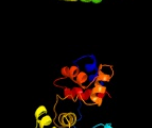












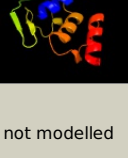


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0142_(-)_167709_168635
Date	Tue Jul 23 14:50:18 BST 2019
Unique Job ID	54c53ee9378cb19e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1mpgB_	 Alignment		100.0	16	PDB header: hydrolase Chain: B; PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli
2	c2jhnB_	 Alignment		100.0	16	PDB header: hydrolase Chain: B; PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
3	c4ejyA_	 Alignment		100.0	14	PDB header: hydrolase/dna Chain: A; PDB Molecule: 3-methyladenine dna glycosylase; PDBTitle: structure of mbogg1 in complex with high affinity dna ligand
4	c3f10A_	 Alignment		100.0	15	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
5	c1yqmA_	 Alignment		100.0	15	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
6	c1ko9A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: 8-oxoguanine dna glycosylase; PDBTitle: native structure of the human 8-oxoguanine dna glycosylase2 hogg1
7	c2y98B_	 Alignment		100.0	21	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
8	d1mpga1	 Alignment		100.0	21	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
9	c3s6iA_	 Alignment		100.0	17	PDB header: hydrolase/dna Chain: A; PDB Molecule: dna-3-methyladenine glycosylase 1; PDBTitle: schizosaccharomyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
10	c4b24A_	 Alignment		100.0	14	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
11	c2h56C_	 Alignment		100.0	15	PDB header: hydrolase Chain: C; PDB Molecule: dna-3-methyladenine glycosidase; PDBTitle: crystal structure of dna-3-methyladenine glycosidase (10174367) from2 bacillus halodurans at 2.55 a resolution

12	d2noha1	Alignment		100.0	19	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
13	c4unfA	Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-1; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-1
14	d1orna	Alignment		100.0	19	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
15	d2abka	Alignment		99.9	18	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
16	d1pu6a	Alignment		99.9	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
17	c3fhgA	Alignment		99.9	14	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)
18	c4uobA	Alignment		99.9	19	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3
19	d1keaa	Alignment		99.9	19	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
20	d1ngna	Alignment		99.9	19	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
21	c3kntC	Alignment	not modelled	99.9	10	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
22	c3n0uB	Alignment	not modelled	99.9	13	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
23	d1rrqa1	Alignment	not modelled	99.9	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
24	d1kg2a	Alignment	not modelled	99.9	19	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
25	c3n5nX	Alignment	not modelled	99.8	17	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
26	c1rrqA	Alignment	not modelled	99.8	13	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
27	d1mpga2	Alignment	not modelled	99.2	6	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: DNA repair glycosylase, N-terminal domain
28	d2noha2	Alignment	not modelled	96.6	10	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: DNA repair glycosylase, N-terminal domain

29	d1vdda_	Alignment	not modelled	92.7	23	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
30	c1vddC_	Alignment	not modelled	92.5	23	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
31	c5z2vB_	Alignment	not modelled	90.5	27	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pa01
32	c5zvqA_	Alignment	not modelled	90.4	27	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
33	c1b22A_	Alignment	not modelled	89.3	14	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
34	d1b22a_	Alignment	not modelled	89.3	14	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
35	c8icZA_	Alignment	not modelled	85.7	19	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 with 2 seven base pairs of dna; soaked in the presence of datp3 (1 millimolar), mnc12 (5 millimolar), and lithium sulfate4 (75 millimolar)
36	d1szpa1	Alignment	not modelled	85.5	11	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
37	d1cuka2	Alignment	not modelled	85.4	40	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
38	c2h5xA_	Alignment	not modelled	85.4	35	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
39	d1bvsa2	Alignment	not modelled	85.0	30	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
40	c1d8IA_	Alignment	not modelled	84.6	42	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking 2 domain iii
41	d2bgwa1	Alignment	not modelled	83.7	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
42	c1ixrB_	Alignment	not modelled	83.5	40	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
43	d1dgsa1	Alignment	not modelled	83.4	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
44	d1x2ia1	Alignment	not modelled	82.9	24	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
45	c1ixrA_	Alignment	not modelled	82.8	40	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
46	c1kdhA_	Alignment	not modelled	81.9	19	PDB header: transferase/dna Chain: A: PDB Molecule: terminal deoxynucleotidyltransferase short PDBTitle: binary complex of murine terminal deoxynucleotidyl 2 transferase with a primer single stranded dna
47	c1dgsB_	Alignment	not modelled	81.6	19	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
48	c2owoA_	Alignment	not modelled	81.4	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 bound 2 to nicked dna-adenylate
49	c2ihmA_	Alignment	not modelled	80.8	16	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: polymerase mu in ternary complex with gapped 11mer dna duplex and 2 bound incoming nucleotide
50	d2a1jb1	Alignment	not modelled	80.7	22	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
51	d2bcqa1	Alignment	not modelled	80.2	24	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
52	c4p4oA_	Alignment	not modelled	79.8	30	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
53	d1ixra1	Alignment	not modelled	79.8	33	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
54	c1kftA_	Alignment	not modelled	79.4	16	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	d1kfta_	Alignment	not modelled	79.4	16	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
56	c2mutA_	Alignment	not modelled	79.0	23	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
57	d2fmpa1_	Alignment	not modelled	78.1	18	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
58	c1hjpA_	Alignment	not modelled	77.7	24	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
59	c1v9pB_	Alignment	not modelled	77.7	19	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
60	d1jmsa1_	Alignment	not modelled	76.8	14	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
61	c4glxA_	Alignment	not modelled	75.7	21	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
62	c1nomA_	Alignment	not modelled	75.7	22	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 mnc12 (5 millimolar)
63	c2csdB_	Alignment	not modelled	75.5	33	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
64	c3auoB_	Alignment	not modelled	73.6	33	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
65	c6h5hA_	Alignment	not modelled	73.0	19	PDB header: unknown function Chain: A: PDB Molecule: polb4; PDBTitle: a computationally designed drp lyase domain reconstructed from two2 heterologous fragments
66	d1nzpa_	Alignment	not modelled	71.5	24	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
67	c2bcuA_	Alignment	not modelled	69.3	13	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
68	d2fmpa2_	Alignment	not modelled	67.7	16	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
69	c5o19A_	Alignment	not modelled	67.4	13	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
70	d2aq0a1_	Alignment	not modelled	67.0	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
71	d2duya1_	Alignment	not modelled	66.0	37	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComeA-like
72	d2hkja1_	Alignment	not modelled	64.9	13	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Topoisomerase VI-B subunit middle domain
73	c6flqF_	Alignment	not modelled	64.3	18	PDB header: transcription Chain: F: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: cryoem structure of e.coli rna polymerase paused elongation complex2 bound to nusa
74	d2vana1_	Alignment	not modelled	64.0	16	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
75	d2ilqa1_	Alignment	not modelled	63.9	18	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
76	c2opfA_	Alignment	not modelled	63.6	15	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
77	d2bcqa2_	Alignment	not modelled	63.5	24	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
78	d1a77a1_	Alignment	not modelled	63.4	31	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
79	c2lyhA_	Alignment	not modelled	61.7	26	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
80	d1ee8a1_	Alignment	not modelled	60.3	29	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins PDB header: dna replication

81	c2w9mB_	Alignment	not modelled	60.2	24	Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
82	d1jmsa3	Alignment	not modelled	60.1	28	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
83	d1mc8a1	Alignment	not modelled	58.3	31	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
84	d1b43a1	Alignment	not modelled	56.3	31	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
85	d1r2za1	Alignment	not modelled	55.6	19	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
86	d1lb2b_	Alignment	not modelled	55.5	22	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
87	c1ee8A_	Alignment	not modelled	55.4	29	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
88	d1rxwa1	Alignment	not modelled	55.0	38	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
89	c1s5lu_	Alignment	not modelled	54.9	17	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
90	d1dk2a_	Alignment	not modelled	54.8	18	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
91	d1xo1a1	Alignment	not modelled	53.9	15	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
92	c3ve5D_	Alignment	not modelled	53.4	25	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
93	d1tdza1	Alignment	not modelled	53.3	14	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
94	d2axtu1	Alignment	not modelled	53.2	17	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: PsbU-like
95	c2kp7A_	Alignment	not modelled	53.1	12	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
96	c4bxoA_	Alignment	not modelled	52.9	16	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
97	d1cooa_	Alignment	not modelled	52.5	22	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
98	d1k82a1	Alignment	not modelled	51.2	29	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
99	d1z3eb1	Alignment	not modelled	50.9	17	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
100	d1szpb1	Alignment	not modelled	49.4	15	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
101	c4itqA_	Alignment	not modelled	48.3	40	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
102	c5n4cF_	Alignment	not modelled	47.7	33	PDB header: hydrolase Chain: F: PDB Molecule: alpha-amanitin proprotein; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 35mer2 hydrolysis and macrocyclization substrate - s577a mutant
103	d1doqa_	Alignment	not modelled	47.3	26	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
104	d1ul1x1	Alignment	not modelled	47.2	23	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
105	d1pzna1	Alignment	not modelled	45.6	23	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
106	c2f5qA_	Alignment	not modelled	44.4	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
107	c2nrzB_	Alignment	not modelled	44.1	19	PDB header: hydrolase Chain: B: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvr bound to its2 catalytic divalent cation
						Fold: SAM domain-like

108	d2csba3	Alignment	not modelled	43.6	40	Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
109	c4bxoB	Alignment	not modelled	41.2	20	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
110	c1ut8B	Alignment	not modelled	41.0	15	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
111	d3bzka1	Alignment	not modelled	39.3	15	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HHH-containing domain-like
112	c5xyiS	Alignment	not modelled	38.2	31	PDB header: ribosome Chain: S: PDB Molecule: ribosomal protein s13p/s18e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
113	c5mmjm	Alignment	not modelled	38.2	20	PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
114	d1cmwa1	Alignment	not modelled	37.3	44	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
115	d1k3xa1	Alignment	not modelled	37.1	24	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
116	d2edua1	Alignment	not modelled	36.9	14	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
117	d1i94m	Alignment	not modelled	36.5	24	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
118	c3c1zA	Alignment	not modelled	35.5	13	PDB header: dna binding protein Chain: A: PDB Molecule: dna integrity scanning protein disa; PDBTitle: structure of the ligand-free form of a bacterial dna damage sensor2 protein
119	c3zddA	Alignment	not modelled	34.4	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
120	d1gm5a2	Alignment	not modelled	33.6	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain