










Phyre2

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 Description RVBD2593c_(ruvA)_2924240_2924830
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2h5xA_	Alignment		100.0	100	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
2	c1ixrB_	Alignment		100.0	37	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
3	c1hjpA_	Alignment		100.0	36	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
4	c1d8IA_	Alignment		100.0	38	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
5	c1ixrA_	Alignment		100.0	41	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
6	d1bvsa2	Alignment		99.9	80	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
7	d1cuka2	Alignment		99.9	33	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
8	d1ixra1	Alignment		99.9	46	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
9	d1cuka3	Alignment		99.8	41	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
10	d1bvsa3	Alignment		99.8	83	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
11	d1ixra2	Alignment		99.8	35	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain

12	d1cuka1	Alignment		98.5	27	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
13	c1kftA	Alignment		98.4	31	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
14	d1kfta	Alignment		98.4	31	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
15	d1x2ia1	Alignment		98.3	22	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
16	d1dgsa1	Alignment		98.2	29	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
17	d2bgwa1	Alignment		98.2	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
18	d2ilqa1	Alignment		98.1	30	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
19	d1ixsa	Alignment		98.0	31	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
20	d1pzna1	Alignment		98.0	25	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
21	c2mutA	Alignment	not modelled	97.9	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
22	d2a1jb1	Alignment	not modelled	97.9	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
23	d1szpa1	Alignment	not modelled	97.6	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
24	c1dgsB	Alignment	not modelled	97.5	26	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
25	c3auoB	Alignment	not modelled	97.5	31	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
26	c1b22A	Alignment	not modelled	97.4	17	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
27	d1b22a	Alignment	not modelled	97.4	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
28	c2w9mB	Alignment	not modelled	97.4	21	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
						PDB header: isomerase

29	c2csdB	Alignment	not modelled	97.4	23	Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
30	c2bhnD	Alignment	not modelled	97.4	26	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
31	c2zj8A	Alignment	not modelled	97.4	24	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
32	c8icZA	Alignment	not modelled	97.3	31	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 dtp3 (1 millimolar), mnc12 (5 millimolar), and lithium sulfate4 (75 millimolar)
33	c4qlxA	Alignment	not modelled	97.3	22	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
34	c2nrzB	Alignment	not modelled	97.3	22	PDB header: hydrolase Chain: B: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrc bound to its 2 catalytic divalent cation
35	c4bxoA	Alignment	not modelled	97.2	11	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
36	c2owoA	Alignment	not modelled	97.2	22	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 to nicked dna-adenylate
37	c1kdhA	Alignment	not modelled	97.0	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
38	c5z2vB	Alignment	not modelled	97.0	41	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
39	c5zvqA	Alignment	not modelled	97.0	50	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
40	c1vddC	Alignment	not modelled	97.0	41	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
41	d1vdda	Alignment	not modelled	97.0	41	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
42	c2ihmA	Alignment	not modelled	96.9	23	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
43	c1v9pB	Alignment	not modelled	96.9	24	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
44	d1szpb1	Alignment	not modelled	96.8	15	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
45	c2ziuA	Alignment	not modelled	96.6	27	PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
46	c2lyhA	Alignment	not modelled	96.5	26	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
47	d2aq0a1	Alignment	not modelled	96.4	17	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
48	c2bcuA	Alignment	not modelled	96.3	18	PDB header: transferase, lyase/dna Chain: A: PDB Molecule: dna polymerase lambda; PDBTitle: dna polymerase lambda in complex with a dna duplex 2 containing an unpaired damp and a t:t mismatch
49	c5ol9A	Alignment	not modelled	96.3	17	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor 2 (tefm) n-terminal domain
50	d2axtu1	Alignment	not modelled	96.3	21	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
51	d2duya1	Alignment	not modelled	96.2	34	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
52	d1a77a1	Alignment	not modelled	96.2	13	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
53	c4ejyA	Alignment	not modelled	96.1	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: 3-methyladenine dna glycosylase; PDBTitle: structure of mbog1 in complex with high affinity dna ligand
54	c1s5lu	Alignment	not modelled	96.1	19	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
						PDB header: transcription

55	c6flqF_	Alignment	not modelled	96.1	24	Chain: F; PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: cryoem structure of e.coli rna polymerase paused elongation complex2 bound to nusa
56	d1b43a1	Alignment	not modelled	96.0	10	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
57	d1bvsa1	Alignment	not modelled	96.0	78	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
58	c4bxoB_	Alignment	not modelled	96.0	23	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
59	c3f10A_	Alignment	not modelled	96.0	17	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
60	d1mc8a1	Alignment	not modelled	95.9	16	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
61	c6c34A_	Alignment	not modelled	95.8	20	PDB header: dna binding protein Chain: A; PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
62	c1yqmA_	Alignment	not modelled	95.7	31	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
63	c1ko9A_	Alignment	not modelled	95.7	30	PDB header: hydrolase Chain: A; PDB Molecule: 8-oxoguanine dna glycosylase; PDBTitle: native structure of the human 8-oxoguanine dna glycosylase2 hogg1
64	d1rxwa1	Alignment	not modelled	95.5	17	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
65	d2edua1	Alignment	not modelled	95.4	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
66	d1ul1x1	Alignment	not modelled	95.4	12	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
67	c2zixA_	Alignment	not modelled	95.3	21	PDB header: hydrolase Chain: A; PDB Molecule: crossover junction endonuclease mus81; PDBTitle: crystal structure of the mus81-eme1 complex
68	d2noha1	Alignment	not modelled	95.2	20	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
69	d3bzka1	Alignment	not modelled	94.9	28	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
70	c2yg8B_	Alignment	not modelled	94.7	25	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
71	c3ve5D_	Alignment	not modelled	94.4	40	PDB header: recombination Chain: D; PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
72	c1a77A_	Alignment	not modelled	94.3	13	PDB header: 5'-3' exo/endo nuclease Chain: A; PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
73	c4wa8A_	Alignment	not modelled	94.2	18	PDB header: hydrolase Chain: A; PDB Molecule: flap endonuclease 1; PDBTitle: methanopyrus kandleri fen-1 nuclease
74	c3fhgA_	Alignment	not modelled	94.2	23	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)
75	c2izoA_	Alignment	not modelled	94.1	11	PDB header: hydrolase Chain: A; PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
76	c1b43A_	Alignment	not modelled	94.1	15	PDB header: transferase Chain: A; PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
77	c2jhnB_	Alignment	not modelled	94.1	24	PDB header: hydrolase Chain: B; PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
78	c4p4oA_	Alignment	not modelled	94.0	19	PDB header: transferase/dna Chain: A; PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
79	d1ngna_	Alignment	not modelled	94.0	16	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
80	c1nomA_	Alignment	not modelled	93.8	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 mncl2 (5 millimolar)
						Fold: DNA-glycosylase

81	d2abka_	Alignment	not modelled	93.7	20	Superfamily: DNA-glycosylase Family: Endonuclease III
82	dlorna_	Alignment	not modelled	93.7	24	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
83	c4b24A_	Alignment	not modelled	93.7	12	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
84	d2p6ra2	Alignment	not modelled	93.5	22	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Achaeal helicase C-terminal domain
85	clut8B_	Alignment	not modelled	93.4	16	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
86	clrxvA_	Alignment	not modelled	93.3	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
87	dlxo1a1	Alignment	not modelled	93.3	14	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
88	dlpu6a_	Alignment	not modelled	93.0	21	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
89	c3s6IA_	Alignment	not modelled	93.0	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.
90	dlkeaa_	Alignment	not modelled	92.9	24	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
91	dlmpga1	Alignment	not modelled	92.7	32	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
92	c3q8IA_	Alignment	not modelled	92.7	13	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+
93	dlrrqa1	Alignment	not modelled	92.6	14	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
94	c3zddA_	Alignment	not modelled	92.1	24	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
95	dlkg2a_	Alignment	not modelled	91.8	18	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
96	clmpgB_	Alignment	not modelled	91.8	30	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli
97	c3c1zA_	Alignment	not modelled	91.5	16	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
98	c3gp8A_	Alignment	not modelled	91.5	28	PDB header: hydrolase/dna Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd, putative; PDBTitle: crystal structure of the binary complex of recd2 with dna
99	c3oryA_	Alignment	not modelled	90.9	20	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
100	clrrqA_	Alignment	not modelled	90.8	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
101	c3n0uB_	Alignment	not modelled	90.6	21	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
102	c4uobA_	Alignment	not modelled	90.5	32	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3
103	c2va8A_	Alignment	not modelled	90.3	26	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
104	c2p6uA_	Alignment	not modelled	90.2	22	PDB header: dna binding protein Chain: A: PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
105	clul1Y_	Alignment	not modelled	90.1	9	PDB header: hydrolase/dna binding protein Chain: Y: PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
106	d2csba3	Alignment	not modelled	89.7	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
107	d2i5ha1	Alignment	not modelled	89.4	25	Fold: AF1531-like Superfamily: AF1531-like Family: AF1531-like

108	c2i5hA_	Alignment	not modelled	89.4	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1531; PDBTitle: crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
109	d2bcqa1	Alignment	not modelled	89.3	40	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
110	c4unfA_	Alignment	not modelled	89.1	35	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-1; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-1
111	c2oceA_	Alignment	not modelled	88.9	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
112	d2fmpa1	Alignment	not modelled	88.7	32	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
113	c3n5nX_	Alignment	not modelled	88.5	21	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
114	c3kntC_	Alignment	not modelled	88.4	21	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
115	d1nzpa_	Alignment	not modelled	87.7	40	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
116	d1cmwa1	Alignment	not modelled	87.6	28	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
117	d1wiva_	Alignment	not modelled	87.1	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
118	c3go5A_	Alignment	not modelled	86.7	8	PDB header: gene regulation Chain: A: PDB Molecule: multidomain protein with s1 rna-binding domains; PDBTitle: crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
119	c6h5hA_	Alignment	not modelled	86.4	30	PDB header: unknown function Chain: A: PDB Molecule: polb4; PDBTitle: a computationally designed drp lyase domain reconstructed from two2 heterologous fragments
120	d1veka_	Alignment	not modelled	86.3	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain