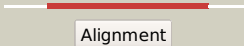

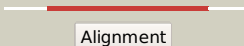

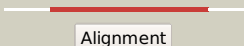


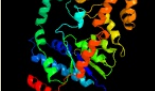




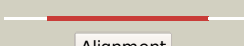















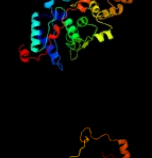
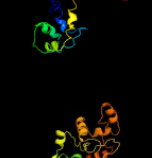



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2090_(-)_2347381_2348562
Date	Mon Aug 5 13:25:20 BST 2019
Unique Job ID	77dfa502b0157edb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1cmwA_	 Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain
2	c6c34A_	 Alignment		100.0	74	PDB header: dna binding protein Chain: A: PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
3	c3zddA_	 Alignment		100.0	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
4	c2ihnA_	 Alignment		100.0	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
5	c1ut8B_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
6	d1cmwa2	 Alignment		100.0	33	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
7	c1rxvA_	 Alignment		100.0	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
8	c3q8IA_	 Alignment		100.0	19	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+
9	c1a77A_	 Alignment		100.0	19	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
10	c4wa8A_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: methanopyrus kandleri fen-1 nuclease
11	c1b43A_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus

12	c3oryA	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
13	c2izoA	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
14	d1xola2	Alignment		100.0	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
15	c3qeaZ	Alignment		100.0	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)
16	c1ul1Y	Alignment		100.0	19	PDB header: hydrolase/dna binding protein Chain: Y: PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
17	d1tfra2	Alignment		100.0	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
18	c4q0rB	Alignment		100.0	19	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna repair protein rad2; PDBTitle: the catalytic core of rad2 (complex i)
19	d1cmwa1	Alignment		100.0	34	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
20	c5t9jB	Alignment		100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: flap endonuclease gen homolog 1; PDBTitle: crystal structure of the holliday junction-resolving enzyme gen1 in complex with holliday junction dna2 in the upper interface
21	d1xola1	Alignment	not modelled	99.9	18	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
22	c5cngA	Alignment	not modelled	99.8	27	PDB header: replication Chain: A: PDB Molecule: nuclease-like protein; PDBTitle: crystal structure of the holliday junction-resolving enzyme gen1 (wt)2 in complex with product dna, mg2+ and mn2+ ions
23	d1a77a1	Alignment	not modelled	99.8	18	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
24	d1ul1x1	Alignment	not modelled	99.8	22	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
25	d1b43a1	Alignment	not modelled	99.7	22	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
26	d1mc8a1	Alignment	not modelled	99.7	23	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
27	d1rxwa1	Alignment	not modelled	99.7	27	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
28	d1a77a2	Alignment	not modelled	99.6	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
29	d1rxwa2	Alignment	not modelled	99.6	16	Fold: PIN domain-like Superfamily: PIN domain-like

						Family: 5' to 3' exonuclease catalytic domain
30	d1mc8a2	Alignment	not modelled	99.6	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
31	d1ul1x2	Alignment	not modelled	99.6	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
32	d1b43a2	Alignment	not modelled	99.5	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
33	c5mq9A_	Alignment	not modelled	98.0	18	PDB header: translation Chain: A: PDB Molecule: uncharacterized protein yacp; PDBTitle: crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
34	c2lyhA_	Alignment	not modelled	97.5	23	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
35	d1x2ia1	Alignment	not modelled	97.4	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
36	d2bgwa1	Alignment	not modelled	97.3	24	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
37	c2nrzB_	Alignment	not modelled	97.3	25	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
38	c1kftA_	Alignment	not modelled	97.3	27	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
39	d1kfta_	Alignment	not modelled	97.3	27	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
40	d2a1jb1	Alignment	not modelled	97.2	28	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
41	c2mutA_	Alignment	not modelled	97.1	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
42	d1dgsa1	Alignment	not modelled	96.8	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD ⁺ -dependent DNA ligase, domain 3
43	c4bxoB_	Alignment	not modelled	96.7	24	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
44	c1d8lA_	Alignment	not modelled	96.6	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
45	d1ixra1	Alignment	not modelled	96.5	27	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
46	d2aq0a1	Alignment	not modelled	96.4	16	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
47	d2i1qa1	Alignment	not modelled	96.2	24	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
48	c2h5xA_	Alignment	not modelled	96.1	24	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
49	d1cuka2	Alignment	not modelled	96.1	22	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
50	d1bvsa2	Alignment	not modelled	96.0	27	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
51	c3fqdA_	Alignment	not modelled	96.0	19	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: 5'-3' exoribonuclease 2; PDBTitle: crystal structure of the s. pombe rat1-rai1 complex
52	c1ixrB_	Alignment	not modelled	95.9	27	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
53	c1ixrA_	Alignment	not modelled	95.9	24	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
54	c1hjpA_	Alignment	not modelled	95.8	21	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
55	d1pzna1	Alignment	not modelled	95.8	21	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
						PDB header: ligase/ligase inhibitor/dna

56	c4glxA	Alignment	not modelled	95.7	30	Chain: A; PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
57	c4bxoA	Alignment	not modelled	95.5	10	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
58	c2owoA	Alignment	not modelled	95.4	30	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
59	c1v9pB	Alignment	not modelled	95.3	25	PDB header: ligase Chain: B; PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
60	c1dgsB	Alignment	not modelled	95.2	25	PDB header: ligase Chain: B; PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
61	c3auoB	Alignment	not modelled	95.2	34	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
62	c5firC	Alignment	not modelled	94.5	20	PDB header: hydrolase Chain: C; PDB Molecule: 5'-3' exoribonuclease 2 homolog; PDBTitle: crystal structure of c. elegans xrn2 in complex with the2 xrn2-binding domain of paxt-1
63	c2bhnD	Alignment	not modelled	94.3	28	PDB header: hydrolase Chain: D; PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
64	c2w9mB	Alignment	not modelled	94.2	22	PDB header: dna replication Chain: B; PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
65	d1szpa1	Alignment	not modelled	94.1	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
66	c4p4oA	Alignment	not modelled	94.0	23	PDB header: transferase/dna Chain: A; PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
67	c2va8A	Alignment	not modelled	93.5	24	PDB header: hydrolase Chain: A; PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
68	c2p6uA	Alignment	not modelled	93.1	11	PDB header: dna binding protein Chain: A; PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
69	c2csdB	Alignment	not modelled	93.0	26	PDB header: isomerase Chain: B; PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
70	c2ihmA	Alignment	not modelled	92.7	23	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
71	c1nomA	Alignment	not modelled	92.1	23	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	c2ziuA	Alignment	not modelled	91.6	32	PDB header: hydrolase Chain: A; PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
73	d2p6ra2	Alignment	not modelled	90.8	16	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Achaeal helicase C-terminal domain
74	c3majA	Alignment	not modelled	90.7	21	PDB header: dna binding protein Chain: A; PDB Molecule: dna processing chain a; PDBTitle: crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
75	d2fyma1	Alignment	not modelled	90.5	13	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
76	c3pifD	Alignment	not modelled	90.2	17	PDB header: hydrolase Chain: D; PDB Molecule: 5'->3' exoribonuclease (xrn1); PDBTitle: crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
77	c3c1zA	Alignment	not modelled	89.4	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
78	c1b22A	Alignment	not modelled	89.1	15	PDB header: dna binding protein Chain: A; PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
79	d1b22a	Alignment	not modelled	89.1	15	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
80	c8icZA	Alignment	not modelled	88.7	21	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)
81	c2zj8A	Alignment	not modelled	88.4	20	PDB header: hydrolase Chain: A; PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
82	d1iyxa1	Alignment	not modelled	88.2	19	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like

						Family: Enolase
83	c4z1yA_	Alignment	not modelled	87.1	17	PDB header: lyase Chain: A: PDB Molecule: enolase; PDBTitle: thermostable enolase from chloroflexus aurantiacus with substrate 2-2 phosphoglycerate
84	c1s5lu_	Alignment	not modelled	86.7	10	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
85	c5dkuB_	Alignment	not modelled	85.8	8	PDB header: transferase Chain: B: PDB Molecule: prex dna polymerase; PDBTitle: c-terminal his tagged appol exonuclease mutant
86	c6flqF_	Alignment	not modelled	85.6	25	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
87	c4ropA_	Alignment	not modelled	85.1	14	PDB header: lyase Chain: A: PDB Molecule: enolase; PDBTitle: crystal structure of enolase from synechococcus elongatus
88	d2vana1	Alignment	not modelled	84.9	23	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
89	d2fmpa2	Alignment	not modelled	84.5	19	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
90	d2bcqa2	Alignment	not modelled	83.9	31	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
91	c3v32B_	Alignment	not modelled	83.7	20	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
92	d2axtu1	Alignment	not modelled	81.5	9	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: PsbU-like
93	d1jmsa3	Alignment	not modelled	81.1	35	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
94	d7reqb2	Alignment	not modelled	80.4	9	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
95	d1szpb1	Alignment	not modelled	79.5	16	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
96	c5yaaD_	Alignment	not modelled	78.7	13	PDB header: hydrolase Chain: D: PDB Molecule: meiosis regulator and mrna stability factor 1; PDBTitle: crystal structure of marf1 nyn domain from mus musculus
97	c2zixA_	Alignment	not modelled	78.2	32	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: crystal structure of the mus81-eme1 complex
98	c2bcuA_	Alignment	not modelled	78.1	31	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
99	d2yvta1	Alignment	not modelled	78.1	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
100	c1kdhA_	Alignment	not modelled	77.5	35	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
101	c2qipA_	Alignment	not modelled	77.4	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function vpa0982; PDBTitle: crystal structure of a protein of unknown function vpa0982 from vibrio2 parahaemolyticus rimd 2210633
102	c1iyxA_	Alignment	not modelled	76.5	18	PDB header: lyase Chain: A: PDB Molecule: enolase; PDBTitle: crystal structure of enolase from enterococcus hirae
103	c3qn3B_	Alignment	not modelled	75.9	16	PDB header: lyase Chain: B: PDB Molecule: enolase; PDBTitle: phosphopyruvate hydratase from campylobacter jejuni.
104	d2csba3	Alignment	not modelled	75.5	38	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
105	d1a4ia1	Alignment	not modelled	74.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
106	c3fhgA_	Alignment	not modelled	74.3	28	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)
107	c3kntC_	Alignment	not modelled	74.0	28	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
108	d2i5ha1	Alignment	not modelled	71.3	20	Fold: AF1531-like Superfamily: AF1531-like

						Family: AF1531-like
109	c2i5hA_	Alignment	not modelled	71.3	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1531; PDBTitle: crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
110	c5o19A_	Alignment	not modelled	71.0	18	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
111	d2duya1	Alignment	not modelled	70.6	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
112	c2fymA_	Alignment	not modelled	70.4	14	PDB header: lyase Chain: A: PDB Molecule: enolase; PDBTitle: crystal structure of e. coli enolase complexed with the minimal2 binding segment of rnae e.
113	d1w6ta1	Alignment	not modelled	70.1	20	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
114	c2y35A_	Alignment	not modelled	69.8	18	PDB header: hydrolase/dna Chain: A: PDB Molecule: ld22664p; PDBTitle: crystal structure of xrn1-substrate complex
115	c3n0uB_	Alignment	not modelled	69.3	33	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
116	d1pu6a_	Alignment	not modelled	64.3	29	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
117	c2pa6A_	Alignment	not modelled	63.8	18	PDB header: lyase Chain: A: PDB Molecule: enolase; PDBTitle: crystal structure of mj0232 from methanococcus jannaschii
118	c1vddC_	Alignment	not modelled	62.8	50	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
119	c3ve5D_	Alignment	not modelled	62.6	19	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
120	c5z2vB_	Alignment	not modelled	62.1	50	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1