























Phyre2

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 Description ASR85459.1_DNA_polymerase_II_exonuclease_[Mycobacterium_phage_Cain]
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qxfa1	 Alignment		100.0	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
2	c4rg8A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease i; PDBTitle: structural and biochemical studies of a moderately thermophilic2 exonuclease i from methylocaldum szegediense
3	c5fkvD_	 Alignment		100.0	20	PDB header: transferase Chain: D: PDB Molecule: dna polymerase iii epsilon; PDBTitle: cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
4	c2p1jB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii polc-type; PDBTitle: crystal structure of a polc-type dna polymerase iii exonuclease domain2 from thermotoga maritima
5	d2guia1	 Alignment		100.0	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
6	d2f96a1	 Alignment		100.0	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
7	c3u6fA_	 Alignment		100.0	20	PDB header: hydrolase/dna Chain: A: PDB Molecule: three prime repair exonuclease 1; PDBTitle: mouse trex1 d200n mutant
8	c3cm6A_	 Alignment		100.0	11	PDB header: hydrolase, apoptosis Chain: A: PDB Molecule: cell death-related nuclease 4; PDBTitle: crystal structure of cell-death related nuclease 4 (crn-4)2 bound with er
9	d1y97a1	 Alignment		100.0	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
10	c1zbuB_	 Alignment		100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: 3'-5' exonuclease eri1; PDBTitle: crystal structure of full-length 3'-exonuclease
11	d3b6oa1	 Alignment		100.0	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease

12	d1w0ha_	Alignment		100.0	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
13	c1zbhA_	Alignment		100.0	13	PDB header: hydrolase/rna Chain: A: PDB Molecule: 3'-5' exonuclease eri1; PDBTitle: 3'-end specific recognition of histone mrna stem-loop by 3'-2 exonuclease
14	c2xriA_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: eri1 exoribonuclease 3; PDBTitle: crystal structure of human eri1 exoribonuclease 3
15	c6n6jB_	Alignment		100.0	18	PDB header: rna binding protein/rna Chain: B: PDB Molecule: rna exonuclease 2 homolog,small fragment nuclease; PDBTitle: human rexo2 bound to paa
16	c6rk6B_	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: oligoribonuclease; PDBTitle: characterization of an intertidal zone metagenome oligoribonuclease2 and the role of the intermolecular disulfide bond for homodimer3 formation and nuclease activity.
17	d1j9aa_	Alignment		100.0	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
18	c3tr8A_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: structure of an oligoribonuclease (orn) from coxiella burnetii
19	c6n6dA_	Alignment		100.0	16	PDB header: rna binding protein/rna Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: vibrio cholerae oligoribonuclease bound to pag
20	c6a4dA_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: pnp-tmp bound oligoribonuclease (orn) from colwellia psychrerythraea2 strain 34h
21	c5cy4C_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: oligoribonuclease; PDBTitle: crystal structure of an oligoribonuclease from acinetobacter baumannii
22	c2gbzA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: the crystal structure of xc847 from xanthomonas campestris: a 3-52 oligoribonuclease of dnaq fold family with a novel opposingly-shifted3 helix
23	c5z9xA_	Alignment	not modelled	100.0	16	PDB header: plant protein/rna Chain: A: PDB Molecule: small rna degrading nuclease 1; PDBTitle: arabidopsis small rna degrading nuclease 1 in complex with an rna2 substrate
24	d2igia1	Alignment	not modelled	100.0	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
25	d1wlja_	Alignment	not modelled	99.9	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
26	c4fzxC_	Alignment	not modelled	99.9	19	PDB header: hydrolase/dna Chain: C: PDB Molecule: exodeoxyribonuclease 10; PDBTitle: exonuclease x in complex with 3' overhanging duplex dna
27	c5l80B_	Alignment	not modelled	99.9	12	PDB header: rna binding protein Chain: B: PDB Molecule: maternal protein exuperantia,maternal protein exuperantia; PDBTitle: structure of exuperantia exo-like and sam-like domains
28	c4wbqA_	Alignment	not modelled	99.9	20	PDB header: rna binding protein Chain: A: PDB Molecule: qde-2-interacting protein; PDBTitle: crystal structure of the exonuclease domain of qip (qde-2 interacting2 protein) solved by native-sad phasing.

29	c2is3B_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease t; PDBTitle: crystal structure of escherichia coli rnase t
30	d1uoca_	Alignment	not modelled	99.8	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF1-like ribonuclease
31	d2d5ra1	Alignment	not modelled	99.7	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF1-like ribonuclease
32	c2p51A_	Alignment	not modelled	99.6	16	PDB header: hydrolase, gene regulation Chain: A: PDB Molecule: spsc18.06c protein; PDBTitle: crystal structure of the s. pombe pop2p deadenylation subunit
33	c4czwA_	Alignment	not modelled	99.6	14	PDB header: gene regulation Chain: A: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan2; PDBTitle: structure of the neurospora crassa pan2 catalytic unit (protease and2 nuclease domain)
34	c4gmjB_	Alignment	not modelled	99.6	19	PDB header: rna binding protein Chain: B: PDB Molecule: ccr4-not transcription complex subunit 7; PDBTitle: structure of human not1 mif4g domain co-crystallized with caf1
35	c4hecB_	Alignment	not modelled	99.5	18	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis
36	c4q8iA_	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: A: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan2; PDBTitle: structure of the saccharomyces cerevisiae pan2-pan3 core complex
37	c3d45B_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: B: PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of mouse parn in complex with m7gpppg
38	c2a1sC_	Alignment	not modelled	99.2	19	PDB header: hydrolase Chain: C: PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of native parn nuclease domain
39	d1kfsa1	Alignment	not modelled	99.2	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
40	d1x9ma1	Alignment	not modelled	99.1	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
41	c2kzzA_	Alignment	not modelled	99.0	18	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: klenow fragment with normal substrate and zinc only
42	c5okiA_	Alignment	not modelled	98.8	19	PDB header: replication Chain: A: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: crystal structure of the ctf18-1-8 module from ctf18-rfc in complex2 with a 63 kda fragment of dna polymerase epsilon
43	c5dkuB_	Alignment	not modelled	98.7	14	PDB header: transferase Chain: B: PDB Molecule: prex dna polymerase; PDBTitle: c-terminal his tagged appol exonuclease mutant
44	c6s1cE_	Alignment	not modelled	98.7	19	PDB header: replication Chain: E: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: p3221 crystal form of the ctf18-1-8/pol2(1-528) complex
45	c6r5kA_	Alignment	not modelled	98.6	17	PDB header: rna binding protein Chain: A: PDB Molecule: pan2-pan3 deadenylation complex catalytic subunit pan2; PDBTitle: cryo-em structure of a poly(a) rnp bound to the pan2-pan3 deadenylase
46	d1wn7a1	Alignment	not modelled	98.6	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
47	c1tk0A_	Alignment	not modelled	98.6	21	PDB header: transferase/electron transport/dna Chain: A: PDB Molecule: dna polymerase; PDBTitle: t7 dna polymerase ternary complex with 8 oxo guanosine and ddctp at2 the insertion site
48	d1qhta1	Alignment	not modelled	98.6	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
49	c4m8oA_	Alignment	not modelled	98.6	18	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: ternary complex of dna polymerase epsilon with an incoming datp
50	d1tgoa1	Alignment	not modelled	98.6	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
51	c6wjvA_	Alignment	not modelled	98.6	21	PDB header: cell cycle Chain: A: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: structure of the saccharomyces cerevisiae polymerase epsilon2 holoenzyme
52	c1njzA_	Alignment	not modelled	98.5	14	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase i; PDBTitle: cytosine-thymine mismatch at the polymerase active site
53	c2gv9A_	Alignment	not modelled	98.5	14	PDB header: transferase Chain: A: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the herpes simplex virus type 1 dna polymerase
						Fold: Ribonuclease H-like motif

54	d1d5aa1	Alignment	not modelled	98.5	14	Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
55	c6fwkB	Alignment	not modelled	98.5	21	PDB header: dna binding protein Chain: B: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: the crystal structure of pol2core-m644g in complex with dna and an2 incoming nucleotide
56	c5mdnB	Alignment	not modelled	98.4	19	PDB header: transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: structure of the family b dna polymerase from the hyperthermophilic2 archaeon pyrobaculum calidifontis
57	c3iayA	Alignment	not modelled	98.4	13	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase delta catalytic subunit; PDBTitle: ternary complex of dna polymerase delta
58	c2qv9B	Alignment	not modelled	98.4	13	PDB header: transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the herpes simplex virus type 1 dna polymerase
59	c4x0pB	Alignment	not modelled	98.4	14	PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase theta; PDBTitle: ternary complex of human dna polymerase theta c-terminal domain2 binding ddatp opposite a tetrahydrofuran ap site analog
60	c5zo4B	Alignment	not modelled	98.4	24	PDB header: hydrolase Chain: B: PDB Molecule: putative 3'-5' exonuclease family protein; PDBTitle: inactive state of the nuclease
61	c6s2fA	Alignment	not modelled	98.3	17	PDB header: replication Chain: A: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: cryo-em structure of ctf18-1-8 in complex with the catalytic domain of2 dna polymerase epsilon (class 2)
62	d2hhva1	Alignment	not modelled	98.3	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
63	d1ih7a1	Alignment	not modelled	98.2	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
64	c2vwkA	Alignment	not modelled	98.1	15	PDB header: dna replication Chain: A: PDB Molecule: dna polymerase; PDBTitle: uracil recognition in archaeal dna polymerases captured by2 x-ray crystallography. v93q polymerase variant
65	c6vddD	Alignment	not modelled	98.1	18	PDB header: transferase/dna Chain: D: PDB Molecule: dna polymerase i; PDBTitle: pol domain of pol1 from m. smegmatis complex with dna primer-template2 and dntp
66	c6p1hA	Alignment	not modelled	98.1	13	PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna polymerase delta catalytic subunit; PDBTitle: cryo-em structure of dna polymerase delta holoenzyme
67	c6tnyA	Alignment	not modelled	98.1	17	PDB header: replication Chain: A: PDB Molecule: dna polymerase delta catalytic subunit; PDBTitle: processive human polymerase delta holoenzyme
68	d1s5ja1	Alignment	not modelled	98.0	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
69	d1q8ia1	Alignment	not modelled	97.9	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
70	c1d5aA	Alignment	not modelled	97.9	15	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase); PDBTitle: crystal structure of an archaeobacterial dna polymerase2 d.tok. deposition of second native structure at 2.43 angstrom
71	c7jw2B	Alignment	not modelled	97.9	14	PDB header: rna binding protein Chain: B: PDB Molecule: exonuclease mut-7 homolog; PDBTitle: crystal structure of aedes aegypti nibbler exo domain
72	c5c0xK	Alignment	not modelled	97.8	17	PDB header: hydrolase/rna Chain: K: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of a 12-subunit nuclear exosome complex bound to structured2 rna
73	c5exrG	Alignment	not modelled	97.8	13	PDB header: replication Chain: G: PDB Molecule: dna polymerase alpha catalytic subunit; PDBTitle: crystal structure of human primosome
74	c5n2hA	Alignment	not modelled	97.8	11	PDB header: transferase Chain: A: PDB Molecule: dna polymerase; PDBTitle: structure of the e9 dna polymerase exonuclease deficient mutant2 (d166a+e168a) from vaccinia virus
75	d1noya	Alignment	not modelled	97.7	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
76	c7jw6A	Alignment	not modelled	97.7	11	PDB header: rna binding protein Chain: A: PDB Molecule: exonuclease mut-7 homolog; PDBTitle: crystal structure of drosophila nibbler exo domain
77	d1yt3a3	Alignment	not modelled	97.7	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
78	c2dtuA	Alignment	not modelled	97.7	13	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the beta hairpin loop deletion variant of rb692 gp43 in complex with dna containing an abasic site analog
79	c1q8iA	Alignment	not modelled	97.6	18	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii; PDBTitle: crystal structure of escherichia coli dna polymerase ii
80	c1c5iA	Alignment	not modelled	97.6	18	PDB header: transferase Chain: A: PDB Molecule: dna polymerase i;

80	c439jA	Alignment	not modelled	97.8	18	PDBTitle: insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfobolus solfataricus PDB header: hydrolase,translation
81	c1yt3A	Alignment	not modelled	97.6	14	Chain: A: PDB Molecule: ribonuclease d; PDBTitle: crystal structure of escherichia coli rnase d, an2 exoribonuclease involved in structured rna processing
82	c2e6mA	Alignment	not modelled	97.5	16	PDB header: hydrolase Chain: A: PDB Molecule: werner syndrome atp-dependent helicase homolog; PDBTitle: structure of mouse werner exonuclease domain
83	c6k1dB	Alignment	not modelled	97.4	17	PDB header: hydrolase Chain: B: PDB Molecule: exonuclease 3'-5' domain-containing protein 2; PDBTitle: crystal structure of exd2 exonuclease domain soaked in mn and gmp
84	c4ktqA	Alignment	not modelled	97.3	21	PDB header: transferase/dna Chain: A: PDB Molecule: protein (large fragment of dna polymerase i); PDBTitle: binary complex of the large fragment of dna polymerase i2 from t. aquaticus bound to a primer/template dna
85	c4oo1j	Alignment	not modelled	97.2	18	PDB header: hydrolase/rna Chain: J: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of an rrp6-rna exosome complex bound to poly(a) rna
86	c4xviA	Alignment	not modelled	97.0	14	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase nu; PDBTitle: binary complex of human polymerase nu and dna with the finger domain2 ajar
87	c4q5vA	Alignment	not modelled	97.0	8	PDB header: transferase/dna/rna Chain: A: PDB Molecule: dna polymerase alpha catalytic subunit; PDBTitle: crystal structure of the catalytic core of human dna polymerase alpha2 in ternary complex with an rna-primed dna template and aphidicolin
88	c4fydA	Alignment	not modelled	96.9	10	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase alpha catalytic subunit a; PDBTitle: crystal structure of yeast dna polymerase alpha bound to dna/rna and2 dgtp
89	c6vdeA	Alignment	not modelled	96.9	20	PDB header: transferase Chain: A: PDB Molecule: dna polymerase i; PDBTitle: full-length m. smegmatis pol1
90	c6v8pA	Alignment	not modelled	96.6	7	PDB header: dna binding protein Chain: A: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: structure of dna polymerase zeta (apo)
91	d2hbka2	Alignment	not modelled	96.5	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
92	d1vk0a	Alignment	not modelled	96.5	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
93	c6v93A	Alignment	not modelled	95.8	8	PDB header: dna binding protein Chain: A: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: structure of dna polymerase zeta/dna/dntp ternary complex
94	c2hbka	Alignment	not modelled	95.4	17	PDB header: hydrolase, gene regulation Chain: A: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of the yeast nuclear exosome component, rrp6p, reveals an2 interplay between the active site and the hrdc domain; protein in3 complex with mn
95	c3cymA	Alignment	not modelled	94.1	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bad_0989; PDBTitle: crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
96	c5v5fA	Alignment	not modelled	93.7	16	PDB header: transferase Chain: A: PDB Molecule: at3g11770; PDBTitle: crystal structure of rice1 (pnt2)
97	c4nlbA	Alignment	not modelled	92.8	15	PDB header: hydrolase Chain: A: PDB Molecule: ribosomal rna processing protein 6; PDBTitle: crystal structure of the catalytic core of rrp6 from trypanosoma2 brucei
98	c3ikmD	Alignment	not modelled	91.5	18	PDB header: transferase Chain: D: PDB Molecule: dna polymerase subunit gamma-1; PDBTitle: crystal structure of human mitochondrial dna polymerase holoenzyme
99	c5fiqE	Alignment	not modelled	90.5	10	PDB header: hydrolase Chain: E: PDB Molecule: exd1; PDBTitle: exonuclease domain-containing 1 (exd1) in the native conformation
100	c5c0wK	Alignment	not modelled	90.1	19	PDB header: hydrolase/rna Chain: K: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of a 12-subunit nuclear exosome complex bound to single-2 stranded rna substrates
101	c4ybgA	Alignment	not modelled	90.0	12	PDB header: hydrolase Chain: A: PDB Molecule: protein maelstrom; PDBTitle: crystal structure of the mael domain of drosophila melanogaster2 maelstrom
102	d2py5a1	Alignment	not modelled	87.8	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
103	c4ztuA	Alignment	not modelled	87.6	16	PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna polymerase subunit gamma-1; PDBTitle: structural basis for processivity and antiviral drug toxicity in human2 mitochondrial dna replicase
104	c3sahA	Alignment	not modelled	82.3	16	PDB header: hydrolase Chain: A: PDB Molecule: exosome component 10; PDBTitle: crystal structure of the human rrp6 catalytic domain with y436a2 mutation in the catalytic site
105	c4o6hA	Alignment	not modelled	78.4	11	PDB header: hydrolase Chain: A: PDB Molecule: nucleoprotein; PDBTitle: 2.8a crystal structure of lymphocytic choriomeningitis

					virus2 nucleoprotein c-terminal domain
106	c7c4cA_	Alignment	not modelled	74.4	16 PDB header: rna binding protein Chain: A: PDB Molecule: cchc-type domain-containing protein; PDBTitle: the crystal structure of trypanosoma brucei rnase d : gmp complex
107	c3q7cA_	Alignment	not modelled	67.5	15 PDB header: hydrolase Chain: A: PDB Molecule: nucleoprotein; PDBTitle: exonuclease domain of lassa virus nucleoprotein bound to manganese
108	c2ex3l_	Alignment	not modelled	47.9	11 PDB header: transferase/replication Chain: I: PDB Molecule: dna polymerase; PDBTitle: bacteriophage phi29 dna polymerase bound to terminal protein
109	c4gveA_	Alignment	not modelled	38.5	15 PDB header: viral protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: tacaribe nucleoprotein structure