

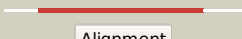













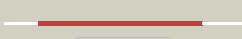







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2511_(orn)_2827167_2827814
Date	Wed Aug 7 12:50:14 BST 2019
Unique Job ID	0aafa4f60f249d1a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6n6jB_	 Alignment		100.0	48	PDB header: rna binding protein/rna Chain: B: PDB Molecule: rna exonuclease 2 homolog,small fragment nuclease; PDBTitle: human rexo2 bound to paa
2	c6n6dA_	 Alignment		100.0	43	PDB header: rna binding protein/rna Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: vibrio cholerae oligoribonuclease bound to pag
3	c5cy4C_	 Alignment		100.0	42	PDB header: oxidoreductase Chain: C: PDB Molecule: oligoribonuclease; PDBTitle: crystal structure of an oligoribonuclease from acinetobacter baumannii
4	c6a4dA_	 Alignment		100.0	41	PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: pnp-tmp bound oligoribonuclease (orn) from colwellia psychrerythraea2 strain 34h
5	c3tr8A_	 Alignment		100.0	41	PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: structure of an oligoribonuclease (orn) from coxiella burnetii
6	d1j9aa_	 Alignment		100.0	42	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
7	d2lgia1	 Alignment		100.0	46	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
8	c2gbzA_	 Alignment		100.0	45	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
9	c5z9xA_	 Alignment		100.0	19	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
10	d2qxfa1	 Alignment		100.0	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
11	d1y97a1	 Alignment		100.0	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease

12	c4rg8A_	Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease i; PDBTitle: structural and biochemical studies of a moderately thermophilic2 exonuclease i from methylocaldum szegediense
13	d3b6oa1	Alignment		100.0	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
14	c3u6fA_	Alignment		99.9	11	PDB header: hydrolase/dna Chain: A: PDB Molecule: three prime repair exonuclease 1; PDBTitle: mouse trex1 d200n mutant
15	c5fkvD_	Alignment		99.9	21	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)
16	d1w0ha_	Alignment		99.9	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
17	d2guia1	Alignment		99.9	23	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
18	d2f96a1	Alignment		99.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
19	c3cm6A_	Alignment		99.9	14	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
20	d1wlja_	Alignment		99.9	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
21	c2p1jB_	Alignment	not modelled	99.9	16	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
22	c2xriA_	Alignment	not modelled	99.9	9	PDB header: hydrolase Chain: A: PDB Molecule: eri1 exoribonuclease 3; PDBTitle: crystal structure of human eri1 exoribonuclease 3
23	c1zbhA_	Alignment	not modelled	99.9	14	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
24	c1zbuB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: 3'-5' exonuclease eri1; PDBTitle: crystal structure of full-length 3'-exonuclease
25	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
26	c4fzxC_	Alignment	not modelled	99.9	16	PDB header: hydrolase/dna Chain: C: PDB Molecule: exodeoxyribonuclease 10; PDBTitle: exonuclease x in complex with 3' overhanging duplex dna
27	c4wbqA_	Alignment	not modelled	99.8	13	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.
28	c2is3B_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease t; PDBTitle: crystal structure of escherichia coli rnase t
						PDB header: gene regulation

29	c4czwA	Alignment	not modelled	99.8	17	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)
30	c4q8jA	Alignment	not modelled	99.7	18	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
31	c6r5kA	Alignment	not modelled	99.6	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
32	c4hecB	Alignment	not modelled	99.3	15	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis
33	d1uoca	Alignment	not modelled	99.1	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF1-like ribonuclease
34	c2kzzA	Alignment	not modelled	98.9	19	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: klenow fragment with normal substrate and zinc only
35	d1kfsa1	Alignment	not modelled	98.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
36	d2d5ra1	Alignment	not modelled	98.9	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF1-like ribonuclease
37	c2p51A	Alignment	not modelled	98.9	20	PDB header: hydrolase, gene regulation Chain: A: PDB Molecule: spcc18.06c protein; PDBTitle: crystal structure of the s. pombe pop2p deadenylation subunit
38	c4gmjB	Alignment	not modelled	98.8	15	PDB header: rna binding protein Chain: B: PDB Molecule: ccc4-not transcription complex subunit 7; PDBTitle: structure of human not1 mif4g domain co-crystallized with caf1
39	d1x9ma1	Alignment	not modelled	98.7	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
40	c3d45B	Alignment	not modelled	98.5	17	PDB header: hydrolase Chain: B: PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of mouse parn in complex with m7gpppg
41	c2a1sC	Alignment	not modelled	98.5	17	PDB header: hydrolase Chain: C: PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of native parn nuclease domain
42	c1tk0A	Alignment	not modelled	98.5	15	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
43	c5dkuB	Alignment	not modelled	98.4	12	PDB header: transferase Chain: B: PDB Molecule: prex dna polymerase; PDBTitle: c-terminal his tagged appol exonuclease mutant
44	c1njzA	Alignment	not modelled	98.3	8	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase i; PDBTitle: cytosine-thymine mismatch at the polymerase active site
45	d2hhva1	Alignment	not modelled	98.2	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
46	c4x0pB	Alignment	not modelled	98.1	12	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
47	c2gv9B	Alignment	not modelled	98.1	18	PDB header: transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the herpes simplex virus type 1 dna polymerase
48	c2gv9A	Alignment	not modelled	98.1	19	PDB header: transferase Chain: A: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the herpes simplex virus type 1 dna polymerase
49	c5okiA	Alignment	not modelled	98.0	14	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
50	d1wn7a1	Alignment	not modelled	98.0	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
51	c3iayA	Alignment	not modelled	98.0	16	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase delta catalytic subunit; PDBTitle: ternary complex of dna polymerase delta
52	d1tgoa1	Alignment	not modelled	97.9	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
53	c6fwkB	Alignment	not modelled	97.9	17	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
						PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase epsilon catalytic subunit

54	c4m8oA_	Alignment	not modelled	97.9	12	a; PDBTitle: ternary complex of dna polymerase epsilon with an incoming datp
55	d1d5aa1	Alignment	not modelled	97.8	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
56	d1qhta1	Alignment	not modelled	97.7	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
57	c5exrG_	Alignment	not modelled	97.5	15	PDB header: replication Chain: G; PDB Molecule: dna polymerase alpha catalytic subunit; PDBTitle: crystal structure of human primosome
58	c2vwkA_	Alignment	not modelled	97.5	12	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
59	c5z04B_	Alignment	not modelled	97.4	20	PDB header: hydrolase Chain: B; PDB Molecule: putative 3'-5' exonuclease family protein; PDBTitle: inactive state of the nuclease
60	d1ih7a1	Alignment	not modelled	97.3	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
61	c5mdnB_	Alignment	not modelled	97.3	20	PDB header: transferase Chain: B; PDB Molecule: dna polymerase; PDBTitle: structure of the family b dna polymerase from the hyperthermophilic2 archaeon pyrobaculum calidifontis
62	c5c0xK_	Alignment	not modelled	97.2	15	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
63	c1d5aA_	Alignment	not modelled	97.2	16	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
64	c4fydA_	Alignment	not modelled	97.2	8	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
65	d1noya_	Alignment	not modelled	97.1	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
66	d1s5ja1	Alignment	not modelled	97.1	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
67	c5n2ha_	Alignment	not modelled	97.1	6	PDB header: transferase Chain: A; PDB Molecule: dna polymerase; PDBTitle: structure of the e9 dna polymerase exonuclease deficient mutant2 (d166a+e168a) from vaccinia virus
68	c4xviA_	Alignment	not modelled	97.0	12	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
69	d1q8ia1	Alignment	not modelled	97.0	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
70	c4q5vA_	Alignment	not modelled	96.9	14	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
71	d1yt3a3	Alignment	not modelled	96.9	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
72	c1s5jA_	Alignment	not modelled	96.8	21	PDB header: transferase Chain: A; PDB Molecule: dna polymerase i; PDBTitle: insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfobolus solfataricus
73	c2e6mA_	Alignment	not modelled	96.7	13	PDB header: hydrolase Chain: A; PDB Molecule: werner syndrome atp-dependent helicase homolog; PDBTitle: structure of mouse werner exonuclease domain
74	c2dtuA_	Alignment	not modelled	96.5	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
75	c6k1dB_	Alignment	not modelled	96.5	16	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
76	c1yt3A_	Alignment	not modelled	96.5	14	PDB header: hydrolase,translation Chain: A; PDB Molecule: ribonuclease d; PDBTitle: crystal structure of escherichia coli rnase d, an2 exoribonuclease involved in structured rna processing
77	c4ktqA_	Alignment	not modelled	96.3	14	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
78	c5af0B_	Alignment	not modelled	96.1	13	PDB header: unknown protein Chain: B; PDB Molecule: maelstrom; PDBTitle: mael domain from bombyx mori maelstrom
79	c4oo1J_	Alignment	not modelled	95.4	17	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

80	c1q8iA_	Alignment	not modelled	94.9	15	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii; PDBTitle: crystal structure of escherichia coli dna polymerase ii
81	d2hbka2	Alignment	not modelled	94.8	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
82	c4ybgA_	Alignment	not modelled	94.4	13	PDB header: hydrolase Chain: A: PDB Molecule: protein maelstrom; PDBTitle: crystal structure of the mael domain of drosophila melanogaster2 maelstrom
83	c3cymA_	Alignment	not modelled	91.5	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bad_0989; PDBTitle: crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
84	c3ikmD_	Alignment	not modelled	91.0	27	PDB header: transferase Chain: D: PDB Molecule: dna polymerase subunit gamma-1; PDBTitle: crystal structure of human mitochondrial dna polymerase holoenzyme
85	c4ztuA_	Alignment	not modelled	90.0	27	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
86	c4nlbA_	Alignment	not modelled	78.2	13	PDB header: hydrolase Chain: A: PDB Molecule: ribosomal rna processing protein 6; PDBTitle: crystal structure of the catalytic core of rrp6 from trypanosoma2 brucei
87	d2py5a1	Alignment	not modelled	70.4	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
88	c2hbka_	Alignment	not modelled	70.3	18	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
89	c5c0wK_	Alignment	not modelled	65.5	17	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
90	d1vk0a_	Alignment	not modelled	58.6	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
91	c3sahA_	Alignment	not modelled	55.0	14	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
92	c2ex3l_	Alignment	not modelled	38.7	19	PDB header: transferase/replication Chain: I: PDB Molecule: dna polymerase; PDBTitle: bacteriophage phi29 dna polymerase bound to terminal protein
93	c5v5fA_	Alignment	not modelled	18.2	11	PDB header: transferase Chain: A: PDB Molecule: at3g11770; PDBTitle: crystal structure of rice1 (pnt2)
94	d3bzka5	Alignment	not modelled	12.9	25	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
95	c3bdvB_	Alignment	not modelled	11.7	19	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein duf1234; PDBTitle: crystal structure of a putative yden-like hydrolase (eca3091) from2 pectobacterium atrosepticum scri1043 at 1.66 a resolution
96	d1hpla2	Alignment	not modelled	8.9	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
97	d1ji8a_	Alignment	not modelled	8.9	13	Fold: DsrC, the gamma subunit of dissimilatory sulfite reductase Superfamily: DsrC, the gamma subunit of dissimilatory sulfite reductase Family: DsrC, the gamma subunit of dissimilatory sulfite reductase
98	c4mf4F_	Alignment	not modelled	8.9	31	PDB header: lyase Chain: F: PDB Molecule: hpch/hpai aldolase/citrate lyase family protein; PDBTitle: crystal structure of a hpch/hpai aldolase/citrate lyase family protein2 from burkholderia cenocepacia j2315
99	d2v4jc1	Alignment	not modelled	8.5	18	Fold: DsrC, the gamma subunit of dissimilatory sulfite reductase Superfamily: DsrC, the gamma subunit of dissimilatory sulfite reductase Family: DsrC, the gamma subunit of dissimilatory sulfite reductase