

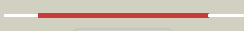
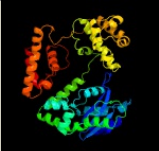

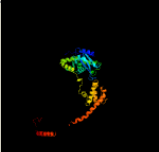

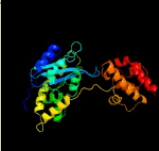

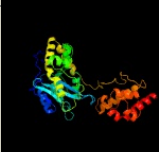



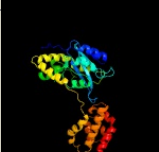














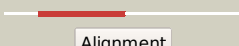
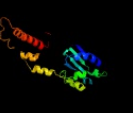
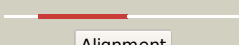











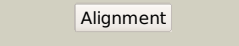


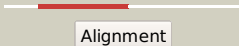
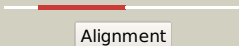
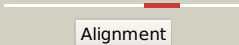


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2681 (-) _2996749_2998065
Date	Wed Aug 7 12:50:33 BST 2019
Unique Job ID	c7fc9386a5d788db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cymA_	 Alignment		100.0	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bad_0989; PDBTitle: crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
2	c1yt3A_	 Alignment		100.0	25	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
3	c5c0wK_	 Alignment		100.0	22	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
4	c4nlbA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: ribosomal rna processing protein 6; PDBTitle: crystal structure of the catalytic core of rrp6 from trypanosoma2 brucei
5	c2hbka_	 Alignment		100.0	23	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
6	c4oo1J_	 Alignment		100.0	25	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
7	c3sahA_	 Alignment		100.0	23	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
8	c5c0xK_	 Alignment		100.0	22	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
9	d2hbka2	 Alignment		100.0	24	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
10	d1yt3a3	 Alignment		100.0	28	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
11	c5fiqE_	 Alignment		100.0	13	PDB header: hydrolase Chain: E: PDB Molecule: exd1; PDBTitle: exonuclease domain-containing 1 (exd1) in the native conformation

12	c5zo4B_	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: putative 3'-5' exonuclease family protein; PDBTitle: inactive state of the nuclease
13	c2e6mA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: werner syndrome atp-dependent helicase homolog; PDBTitle: structure of mouse werner exonuclease domain
14	c5dkuB_	 Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: prex dna polymerase; PDBTitle: c-terminal his tagged appol exonuclease mutant
15	c6k1dB_	 Alignment		100.0	15	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
16	d1vk0a_	 Alignment		100.0	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
17	c5v5fA_	 Alignment		100.0	10	PDB header: transferase Chain: A: PDB Molecule: at3g11770; PDBTitle: crystal structure of rice1 (pnt2)
18	c2kzza_	 Alignment		100.0	18	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: klenow fragment with normal substrate and zinc only
19	d1kfsa1	 Alignment		100.0	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
20	c1njzA_	 Alignment		99.9	12	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase i; PDBTitle: cytosine-thymine mismatch at the polymerase active site
21	d2hhva1	 Alignment	not modelled	99.9	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
22	d1yt3a1	 Alignment	not modelled	99.9	24	Fold: SAM domain-like Superfamily: HRDC-like Family: RNase D C-terminal domains
23	c4x0pB_	 Alignment	not modelled	99.9	15	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
24	d2cpra1	 Alignment	not modelled	99.8	17	Fold: SAM domain-like Superfamily: HRDC-like Family: EXOSC10 HRDC domain-like
25	d2hbka1	 Alignment	not modelled	99.8	22	Fold: SAM domain-like Superfamily: HRDC-like Family: EXOSC10 HRDC domain-like
26	c4xviA_	 Alignment	not modelled	99.7	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
27	c4ktqA_	 Alignment	not modelled	99.5	20	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
28	d1wuda1	 Alignment	not modelled	99.5	20	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases

29	c1tk0A	Alignment	not modelled	99.5	18	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
30	c2rhfA	Alignment	not modelled	99.4	11	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase recq; PDBTitle: d. radiodurans recq hrdc domain 3
31	c2ma1A	Alignment	not modelled	99.4	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna helicase recq; PDBTitle: solution structure of hrdc1 domain of recq helicase from deinococcus2 radiodurans
32	c2rrdA	Alignment	not modelled	99.4	10	PDB header: dna binding protein Chain: A: PDB Molecule: hrdc domain from bloom syndrome protein; PDBTitle: structure of hrdc domain from human bloom syndrome protein, blm
33	d1yt3a2	Alignment	not modelled	99.4	25	Fold: SAM domain-like Superfamily: HRDC-like Family: RNase D C-terminal domains
34	d2e1fa1	Alignment	not modelled	99.3	15	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
35	c1cmwA	Alignment	not modelled	98.9	18	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
36	d1d8ba	Alignment	not modelled	98.7	18	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
37	c4cdgA	Alignment	not modelled	98.7	11	PDB header: hydrolase Chain: A: PDB Molecule: bloom syndrome protein; PDBTitle: crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody
38	d1x9ma1	Alignment	not modelled	98.5	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
39	c2p1jB	Alignment	not modelled	97.9	22	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
40	d1wjja	Alignment	not modelled	97.9	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
41	c4czwA	Alignment	not modelled	97.8	18	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)
42	d2f96a1	Alignment	not modelled	97.7	24	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
43	c2is3B	Alignment	not modelled	97.5	18	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease t; PDBTitle: crystal structure of escherichia coli rnase t
44	c5z9xA	Alignment	not modelled	97.5	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
45	c4q8jA	Alignment	not modelled	97.5	23	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
46	c5fkvD	Alignment	not modelled	97.4	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)
47	c4wbqA	Alignment	not modelled	97.4	14	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.
48	c6r5kA	Alignment	not modelled	97.0	23	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
49	d2guia1	Alignment	not modelled	96.9	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
50	d1y97a1	Alignment	not modelled	96.9	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
51	d1qhta1	Alignment	not modelled	96.8	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
52	d1wn7a1	Alignment	not modelled	96.4	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
53	d1d5aa1	Alignment	not modelled	96.3	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
						Fold: Ribonuclease H-like motif

54	d3b6oa1	Alignment	not modelled	96.3	19	Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
55	d1tgoa1	Alignment	not modelled	96.2	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
56	c3u6fA	Alignment	not modelled	96.2	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: three prime repair exonuclease 1; PDBTitle: mouse trex1 d200n mutant
57	c3ikmD	Alignment	not modelled	96.0	20	PDB header: transferase Chain: D: PDB Molecule: dna polymerase subunit gamma-1; PDBTitle: crystal structure of human mitochondrial dna polymerase holoenzyme
58	c4ztuA	Alignment	not modelled	95.9	19	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
59	c5l80B	Alignment	not modelled	95.8	17	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
60	c3cm6A	Alignment	not modelled	95.0	18	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
61	d2qxfa1	Alignment	not modelled	94.8	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
62	c3d45B	Alignment	not modelled	94.3	21	PDB header: hydrolase Chain: B: PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of mouse parn in complex with m7gpppg
63	c4rg8A	Alignment	not modelled	94.3	19	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease i; PDBTitle: structural and biochemical studies of a moderately thermophilic2 exonuclease i from methylocaldum szegediense
64	d1j9aa	Alignment	not modelled	93.5	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
65	c3tr8A	Alignment	not modelled	93.3	20	PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: structure of an oligoribonuclease (orn) from coxiella burnetii
66	c2xriA	Alignment	not modelled	93.1	14	PDB header: hydrolase Chain: A: PDB Molecule: eri1 exoribonuclease 3; PDBTitle: crystal structure of human eri1 exoribonuclease 3
67	c2vwkA	Alignment	not modelled	91.1	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
68	c1d5aA	Alignment	not modelled	88.8	17	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
69	c2gbzA	Alignment	not modelled	87.1	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
70	d2d5ra1	Alignment	not modelled	86.6	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF1-like ribonuclease
71	d2igia1	Alignment	not modelled	86.4	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
72	c5mdnB	Alignment	not modelled	86.0	14	PDB header: transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: structure of the family b dna polymerase from the hyperthermophilic2 archaeon pyrobaculum calidifontis
73	c6a4dA	Alignment	not modelled	84.5	11	PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: pnp-tmp bound oligoribonuclease (orn) from colwellia psychrerythraea2 strain 34h
74	c1q8iA	Alignment	not modelled	83.9	17	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii; PDBTitle: crystal structure of escherichia coli dna polymerase ii
75	c4fzxC	Alignment	not modelled	83.7	19	PDB header: hydrolase/dna Chain: C: PDB Molecule: exodeoxyribonuclease 10; PDBTitle: exonuclease x in complex with 3' overhanging duplex dna
76	c2p51A	Alignment	not modelled	82.5	19	PDB header: hydrolase, gene regulation Chain: A: PDB Molecule: sppc18.06c protein; PDBTitle: crystal structure of the s. pombe pop2p deadenylation subunit
77	c4gmjB	Alignment	not modelled	81.9	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
78	c2gv9B	Alignment	not modelled	80.3	19	PDB header: transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the herpes simplex virus type 1 dna polymerase
79	c3iayA	Alignment	not modelled	78.0	20	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase delta catalytic subunit; PDBTitle: ternary complex of dna polymerase delta
80	d1q8ia1	Alignment	not modelled	77.6	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like

						Family: DnaQ-like 3'-5' exonuclease
81	c1zbhA	Alignment	not modelled	76.6	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
82	c4m8oA	Alignment	not modelled	76.3	17	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
83	d1s5ja1	Alignment	not modelled	73.9	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
84	c6fwkB	Alignment	not modelled	72.0	18	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
85	d1noya	Alignment	not modelled	70.6	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
86	d1ih7a1	Alignment	not modelled	67.7	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
87	c6n6dA	Alignment	not modelled	67.0	17	PDB header: rna binding protein/rna Chain: A; PDB Molecule: oligoribonuclease; PDBTitle: vibrio cholerae oligoribonuclease bound to pag
88	c2vxdA	Alignment	not modelled	62.5	16	PDB header: nuclear protein Chain: A; PDB Molecule: nucleophosmin; PDBTitle: the structure of the c-terminal domain of nucleophosmin
89	c5cy4C	Alignment	not modelled	57.6	20	PDB header: oxidoreductase Chain: C; PDB Molecule: oligoribonuclease; PDBTitle: crystal structure of an oligoribonuclease from acinetobacter baumannii
90	d1uoca	Alignment	not modelled	56.9	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF1-like ribonuclease
91	c2a1sC	Alignment	not modelled	52.2	23	PDB header: hydrolase Chain: C; PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of native parn nuclease domain
92	c2llhA	Alignment	not modelled	50.3	17	PDB header: dna binding protein, chaperone Chain: A; PDB Molecule: nucleophosmin; PDBTitle: nmr structure of npm1_c70
93	c5okiA	Alignment	not modelled	48.5	15	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
94	c2dtuA	Alignment	not modelled	38.8	15	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
95	c6n6jB	Alignment	not modelled	35.4	13	PDB header: rna binding protein/rna Chain: B; PDB Molecule: rna exonuclease 2 homolog,small fragment nuclease; PDBTitle: human rexo2 bound to paa
96	c3frrA	Alignment	not modelled	33.5	18	PDB header: protein binding Chain: A; PDB Molecule: uncharacterized protein kiaa0174; PDBTitle: structure of human ist1(ntd) - (residues 1-189)(p21)
97	c3ggzC	Alignment	not modelled	28.7	18	PDB header: protein transport, endocytosis Chain: C; PDB Molecule: increased sodium tolerance protein 1; PDBTitle: crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
98	c2of5K	Alignment	not modelled	21.3	16	PDB header: apoptosis Chain: K; PDB Molecule: leucine-rich repeat and death domain-containing protein; PDBTitle: oligomeric death domain complex
99	c4q5vA	Alignment	not modelled	20.0	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