

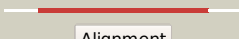

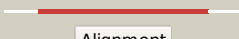











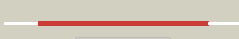







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2179c_(-)_2441819_2442325
Date	Mon Aug 5 13:25:30 BST 2019
Unique Job ID	a095f8b412cb3ed8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4hecB_	 Alignment		100.0	100	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis
2	c5cy4C_	 Alignment		99.6	16	PDB header: oxidoreductase Chain: C: PDB Molecule: oligoribonuclease; PDBTitle: crystal structure of an oligoribonuclease from acinetobacter baumannii
3	d2lgia1	 Alignment		99.6	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
4	d2f96a1	 Alignment		99.6	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
5	c2gbzA_	 Alignment		99.6	16	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
6	c2p1jB_	 Alignment		99.6	19	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
7	c6n6jB_	 Alignment		99.5	14	PDB header: rna binding protein/rna Chain: B: PDB Molecule: rna exonuclease 2 homolog,small fragment nuclease; PDBTitle: human rexo2 bound to paa
8	c3tr8A_	 Alignment		99.5	14	PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: structure of an oligoribonuclease (orn) from coxiella burnetii
9	c6n6dA_	 Alignment		99.5	12	PDB header: rna binding protein/rna Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: vibrio cholerae oligoribonuclease bound to pag
10	c5z9xA_	 Alignment		99.5	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
11	d1wlja_	 Alignment		99.5	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease

12	d1j9aa_	Alignment		99.5	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
13	d1y97a1	Alignment		99.5	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
14	c6a4dA_	Alignment		99.5	10	PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: pnp-tmp bound oligoribonuclease (orn) from colwellia psychrerythraea2 strain 34h
15	d3b6oa1	Alignment		99.5	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
16	d2qxfa1	Alignment		99.4	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
17	c4fzxC_	Alignment		99.4	18	PDB header: hydrolase/dna Chain: C: PDB Molecule: exodeoxyribonuclease 10; PDBTitle: exonuclease x in complex with 3' overhanging duplex dna
18	d2guia1	Alignment		99.4	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
19	c4wbqA_	Alignment		99.4	17	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.
20	c4rg8A_	Alignment		99.4	16	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease i; PDBTitle: structural and biochemical studies of a moderately thermophilic2 exonuclease i from methylocaldum szegediense
21	c3u6fA_	Alignment	not modelled	99.4	18	PDB header: hydrolase/dna Chain: A: PDB Molecule: three prime repair exonuclease 1; PDBTitle: mouse trex1 d200n mutant
22	d1w0ha_	Alignment	not modelled	99.4	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
23	c5fkvD_	Alignment	not modelled	99.4	18	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)
24	c2xriA_	Alignment	not modelled	99.3	13	PDB header: hydrolase Chain: A: PDB Molecule: eri1 exoribonuclease 3; PDBTitle: crystal structure of human eri1 exoribonuclease 3
25	c3cm6A_	Alignment	not modelled	99.1	15	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
26	c1zbhA_	Alignment	not modelled	99.1	12	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
27	c1zbuB_	Alignment	not modelled	99.1	13	PDB header: hydrolase Chain: B: PDB Molecule: 3'-5' exonuclease eri1; PDBTitle: crystal structure of full-length 3'-exonuclease
28	c2is3B_	Alignment	not modelled	99.0	13	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease t; PDBTitle: crystal structure of escherichia coli rnase t PDB header: rna binding protein

29	c5l80B	Alignment	not modelled	98.7	11	Chain: B: PDB Molecule: maternal protein exuperantia,maternal protein exuperantia; PDBTitle: structure of exuperantia exo-like and sam-like domains
30	d1uoca	Alignment	not modelled	98.1	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF1-like ribonuclease
31	d2d5ra1	Alignment	not modelled	97.7	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF1-like ribonuclease
32	c2p51A	Alignment	not modelled	97.6	19	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	97.3	13	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	97.2	17	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
35	d1kfsa1	Alignment	not modelled	97.1	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
36	c2kzza	Alignment	not modelled	96.9	21	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: klenow fragment with normal substrate and zinc only
37	c1njzA	Alignment	not modelled	96.2	27	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase i; PDBTitle: cytosine-thymine mismatch at the polymerase active site
38	d1x9ma1	Alignment	not modelled	96.2	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
39	c4x0pB	Alignment	not modelled	95.9	13	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
40	c5dkuB	Alignment	not modelled	93.9	10	PDB header: transferase Chain: B: PDB Molecule: prex dna polymerase; PDBTitle: c-terminal his tagged appol exonuclease mutant
41	c5zo4B	Alignment	not modelled	92.5	20	PDB header: hydrolase Chain: B: PDB Molecule: putative 3'-5' exonuclease family protein; PDBTitle: inactive state of the nuclease
42	d2hhva1	Alignment	not modelled	91.2	25	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
43	c4xviA	Alignment	not modelled	91.2	9	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
44	c1tk0A	Alignment	not modelled	88.9	19	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
45	c4q8jA	Alignment	not modelled	87.7	13	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	d2ajta1	Alignment	not modelled	86.5	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Fucl/AraA C-terminal domain-like Family: AraA C-terminal domain-like
47	c1yt3A	Alignment	not modelled	85.3	20	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
48	d1s5ja1	Alignment	not modelled	83.7	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
49	c2e6mA	Alignment	not modelled	79.0	15	PDB header: hydrolase Chain: A: PDB Molecule: werner syndrome atp-dependent helicase homolog; PDBTitle: structure of mouse werner exonuclease domain
50	c6k1dB	Alignment	not modelled	72.8	21	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
51	c1s5jA	Alignment	not modelled	68.1	18	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 sulfolobus solfataricus
52	c1d5aA	Alignment	not modelled	67.8	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
53	d2g3ra2	Alignment	not modelled	60.0	33	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
54	d1ih7a1	Alignment	not modelled	57.0	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease

55	c4r1oF	Alignment	not modelled	56.9	21	PDB header: isomerase Chain: F; PDB Molecule: l-arabinose isomerase; PDBTitle: crystal structure of thermophilic geobacillus kaustophilus l-arabinose2 isomerase
56	c2hxgB	Alignment	not modelled	55.7	20	PDB header: isomerase Chain: B; PDB Molecule: l-arabinose isomerase; PDBTitle: crystal structure of mn2+ bound ecai
57	d1noya	Alignment	not modelled	51.0	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
58	c5c0xK	Alignment	not modelled	50.8	11	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
59	d1yt3a3	Alignment	not modelled	50.5	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
60	d1tgoa1	Alignment	not modelled	42.6	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
61	d1d5aa1	Alignment	not modelled	39.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
62	c3d45B	Alignment	not modelled	34.8	13	PDB header: hydrolase Chain: B; PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of mouse parn in complex with m7gpppgg
63	c4oo1J	Alignment	not modelled	34.4	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
64	d1wn7a1	Alignment	not modelled	31.1	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
65	c2gv9A	Alignment	not modelled	28.9	11	PDB header: transferase Chain: A; PDB Molecule: dna polymerase; PDBTitle: crystal structure of the herpes simplex virus type 1 dna polymerase
66	d1qhta1	Alignment	not modelled	26.2	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
67	d1kkoa2	Alignment	not modelled	24.9	16	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
68	d2hbka2	Alignment	not modelled	21.9	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
69	d1q8ia1	Alignment	not modelled	20.6	25	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
70	c3r8rJ	Alignment	not modelled	17.5	43	PDB header: transferase Chain: J; PDB Molecule: transaldolase; PDBTitle: transaldolase from bacillus subtilis
71	d1l6wa	Alignment	not modelled	16.2	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
72	d2fe1a1	Alignment	not modelled	15.8	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
73	c2fe1A	Alignment	not modelled	15.8	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
74	c2gv9B	Alignment	not modelled	15.4	13	PDB header: transferase Chain: B; PDB Molecule: dna polymerase; PDBTitle: crystal structure of the herpes simplex virus type 1 dna polymerase
75	d1vpxa	Alignment	not modelled	14.8	43	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
76	c2m7oA	Alignment	not modelled	13.9	35	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein np_346341.1 from streptococcus pneumoniae
77	c3iayA	Alignment	not modelled	13.5	18	PDB header: transferase/dna Chain: A; PDB Molecule: dna polymerase delta catalytic subunit; PDBTitle: ternary complex of dna polymerase delta
78	d1wx0a1	Alignment	not modelled	12.8	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
79	d1kcza2	Alignment	not modelled	12.7	19	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
80	c6nklA	Alignment	not modelled	11.9	43	PDB header: antitoxin Chain: A; PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
81	c3s1vD	Alignment	not modelled	11.8	43	PDB header: transferase Chain: D; PDB Molecule: probable transaldolase; PDBTitle: transaldolase from thermoplasma acidophilum in complex with d-fructose2 6-phosphate schiff-base intermediate

82	c3zvkc	Alignment	not modelled	11.7	29	PDB header: antitoxin/toxin/dna Chain: C: PDB Molecule: toxin of toxin-antitoxin system; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
83	c2jz7A	Alignment	not modelled	11.6	17	PDB header: selenium-binding protein Chain: A: PDB Molecule: selenium binding protein; PDBTitle: solution nmr structure of selenium-binding protein from2 methanococcus vannielii
84	c6s7qG	Alignment	not modelled	11.5	16	PDB header: lyase Chain: G: PDB Molecule: ergothionase; PDBTitle: crystal structure of ergothioneine degrading enzyme ergothionase from2 treponema denticola in complex with desmethyl-ergothioneine sulfonic3 acid
85	c2dtuA	Alignment	not modelled	11.4	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
86	c3bsuF	Alignment	not modelled	11.1	13	PDB header: hydrolase/rna/dna Chain: F: PDB Molecule: ribonuclease h1; PDBTitle: hybrid-binding domain of human rnase h1 in complex with 12-2 mer rna/dna
87	c2vwkA	Alignment	not modelled	10.8	18	PDB header: dna replication Chain: A: PDB Molecule: dna polymerase; PDBTitle: uracil recognition in archaean dna polymerases captured by2 x-ray crystallography. v93q polymerase variant
88	d2py5a1	Alignment	not modelled	9.6	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
89	d2dsya1	Alignment	not modelled	9.3	26	Fold: TTHA1013/TTHA0281-like Superfamily: TTHA1013/TTHA0281-like Family: TTHA0281-like
90	d1e3ha6	Alignment	not modelled	9.2	32	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
91	c5yvqB	Alignment	not modelled	8.8	25	PDB header: viral protein Chain: B: PDB Molecule: tail fiber assembly protein u; PDBTitle: complex of mu phage tail fiber and its chaperone
92	c5n2hA	Alignment	not modelled	8.6	7	PDB header: transferase Chain: A: PDB Molecule: dna polymerase; PDBTitle: structure of the e9 dna polymerase exonuclease deficient mutant2 (d166a+e168a) from vaccinia virus
93	c3cymA	Alignment	not modelled	8.6	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
94	c3tndC	Alignment	not modelled	8.4	29	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
95	d1khba2	Alignment	not modelled	7.5	14	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
96	c4uzmA	Alignment	not modelled	7.3	50	PDB header: structural protein Chain: A: PDB Molecule: putative membrane protein igaa homolog; PDBTitle: shotgun proteolysis: a practical application
97	c3vhjA	Alignment	not modelled	7.3	17	PDB header: membrane protein Chain: A: PDB Molecule: bfpC; PDBTitle: crystal structure of the cytoplasmic domain of bfpC
98	c2kcdA	Alignment	not modelled	7.2	45	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ssp0047; PDBTitle: solution nmr structure of ssp0047 from staphylococcus2 saprophyticus. northeast structural genomics consortium3 target syr6.
99	c2xetB	Alignment	not modelled	7.1	33	PDB header: transport protein Chain: B: PDB Molecule: f1 capsule-anchoring protein; PDBTitle: conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly