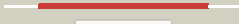



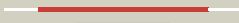


















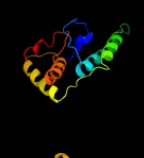

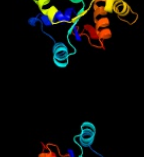
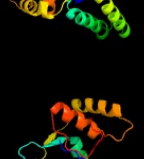
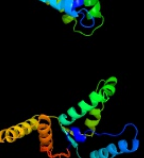
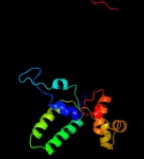
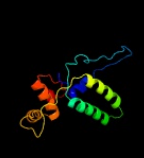
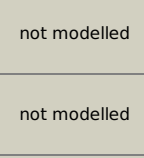


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2872_(-)_3183392_3183835
Date	Wed Aug 7 12:50:54 BST 2019
Unique Job ID	88275f2eace87ccb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3zvkc_	 Alignment		99.9	18	PDB header: antitoxin/toxin/dna Chain: C; PDB Molecule: toxin of toxin-antitoxin system; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to a dna fragment from their promoter
2	d2h1ca1	 Alignment		99.9	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
3	c5wzfb_	 Alignment		99.9	14	PDB header: hydrolase Chain: B; PDB Molecule: 23s rrna-specific endonuclease vapc20; PDBTitle: crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
4	c6nk1a_	 Alignment		99.9	14	PDB header: antitoxin Chain: A; PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
5	c5l6mC_	 Alignment		99.8	14	PDB header: hydrolase Chain: C; PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
6	c3tndC_	 Alignment		99.8	12	PDB header: translation, toxin Chain: C; PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
7	c4xqrG_	 Alignment		99.8	16	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
8	c5x3tD_	 Alignment		99.8	23	PDB header: antitoxin/toxin Chain: D; PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
9	c6a7vG_	 Alignment		99.8	13	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
10	c4chgC_	 Alignment		99.7	20	PDB header: toxin/antitoxin Chain: C; PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
11	c3h87B_	 Alignment		99.7	16	PDB header: toxin/antitoxin Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis

12	d1v96a1	Alignment		99.6	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
13	c3dboB	Alignment		99.6	19	PDB header: toxin/antitoxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a member of the vapbc family of toxin-antitoxin systems, vapbc-5, from mycobacterium tuberculosis
14	c5sv2A	Alignment		99.6	19	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
15	c2fe1A	Alignment		99.6	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
16	d2fe1a1	Alignment		99.6	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	d1w8ia	Alignment		99.6	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	d1y82a1	Alignment		99.6	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	d1v8pa	Alignment		98.9	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c1v8pK	Alignment		98.9	14	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
21	c3i8oA	Alignment	not modelled	98.4	18	PDB header: rna binding protein Chain: A: PDB Molecule: kh domain-containing protein mj1533; PDBTitle: a domain of a functionally unknown protein from methanocaldococcus2 jannaschii dsm 2661.
22	c3ix7A	Alignment	not modelled	98.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ttha0540; PDBTitle: crystal structure of a domain of functionally unknown protein from2 thermus thermophilus hb8
23	d1o4wa	Alignment	not modelled	97.8	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c2lcqA	Alignment	not modelled	97.6	23	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
25	c5ywwA	Alignment	not modelled	97.4	15	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
26	c5f4hF	Alignment	not modelled	97.2	14	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
27	c2hwwC	Alignment	not modelled	96.9	15	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
28	c5yz4A	Alignment	not modelled	96.7	12	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
						PDB header: ribosome

29	c5jppd_	Alignment	not modelled	96.6	18	Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c3zddA_	Alignment	not modelled	93.7	20	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
31	c4mj7B_	Alignment	not modelled	92.1	13	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
32	d1cmwa2	Alignment	not modelled	91.8	24	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
33	c2hwyB_	Alignment	not modelled	91.4	25	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
34	d1tfra2	Alignment	not modelled	90.1	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
35	c6g5iy_	Alignment	not modelled	88.8	8	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
36	c3v32B_	Alignment	not modelled	79.4	26	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpip1 n-terminal conserved domain
37	c2ihnA_	Alignment	not modelled	76.8	18	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
38	c3v33A_	Alignment	not modelled	75.1	22	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpip1 conserved domain with zinc-finger motif
39	d1xo1a2	Alignment	not modelled	72.0	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
40	c1ut8B_	Alignment	not modelled	67.8	13	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
41	c1cmwA_	Alignment	not modelled	62.2	24	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
42	c4g25A_	Alignment	not modelled	29.2	9	PDB header: rna binding protein Chain: A: PDB Molecule: pentatricopeptide repeat-containing protein at2g32230, PDBTitle: crystal structure of proteinaceous rnase p 1 (prorp1) from a.2 thaliana, semet substituted form with sr
43	c5dizB_	Alignment	not modelled	23.9	10	PDB header: hydrolase Chain: B: PDB Molecule: proteinaceous rnase p 2; PDBTitle: crystal structure of nuclear proteinaceous rnase p 2 (prorp2) from a.2 thaliana
44	d1ul1x2	Alignment	not modelled	19.2	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
45	c3q8IA_	Alignment	not modelled	18.9	18	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+
46	c1b43A_	Alignment	not modelled	16.5	21	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
47	c2izoA_	Alignment	not modelled	14.8	19	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaean pcna1-pcna2-fen1 complex
48	d1rxwa2	Alignment	not modelled	13.8	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
49	d1a77a2	Alignment	not modelled	13.5	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
50	c3shpA_	Alignment	not modelled	11.4	44	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase sthe_0691; PDBTitle: crystal structure of putative acetyltransferase from sphaerobacter2 thermophilus dsm 20745
51	d1liba1	Alignment	not modelled	10.1	18	Fold: Sm-like fold Superfamily: YhbC-like, C-terminal domain Family: YhbC-like, C-terminal domain
52	c3dy0B_	Alignment	not modelled	9.8	56	PDB header: blood clotting, hydrolase inhibitor Chain: B: PDB Molecule: c-terminus plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved pci bound to heparin
53	c1lq8H_	Alignment	not modelled	9.4	56	PDB header: blood clotting Chain: H: PDB Molecule: plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved protein c inhibitor
54	c4wa8A_	Alignment	not modelled	9.3	14	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: methanopyrus kandleri fen-1 nuclease
55	d1jx4a1	Alignment	not modelled	8.6	16	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger

					domain
56	c6c34A_	Alignment	not modelled	8.5	17 PDB header: dna binding protein Chain: A: PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
57	c2gksB_	Alignment	not modelled	8.4	14 PDB header: transferase Chain: B: PDB Molecule: bifunctional sat/aps kinase; PDBTitle: crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
58	d1k1sa1	Alignment	not modelled	8.2	14 Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
59	c1ul1Y_	Alignment	not modelled	8.2	18 PDB header: hydrolase/dna binding protein Chain: Y: PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
60	c5i4rA_	Alignment	not modelled	7.9	20 PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
61	c1jqsB_	Alignment	not modelled	7.6	8 PDB header: ribosome Chain: B: PDB Molecule: elongation factor g; PDBTitle: fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
62	c1a77A_	Alignment	not modelled	7.6	16 PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
63	c3oryA_	Alignment	not modelled	7.4	18 PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
64	c1rxvA_	Alignment	not modelled	7.0	22 PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
65	d1jx7a_	Alignment	not modelled	6.8	17 Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
66	c3qeaZ_	Alignment	not modelled	6.7	22 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)
67	c4b2uA_	Alignment	not modelled	6.5	29 PDB header: toxin Chain: A: PDB Molecule: s67; PDBTitle: s67, a spider venom toxin peptide from sicarius dolichocephalus
68	d1mc8a2	Alignment	not modelled	6.1	21 Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
69	c1kjkA_	Alignment	not modelled	5.9	27 PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: solution structure of the lambda integrase amino-terminal2 domain
70	d1z1ba1	Alignment	not modelled	5.9	27 Fold: DNA-binding domain Superfamily: DNA-binding domain Family: lambda integrase N-terminal domain
71	d1y1la1	Alignment	not modelled	5.3	23 Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: PA5104-like