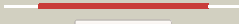



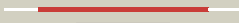




















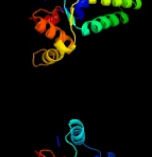

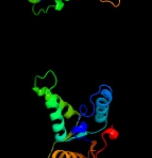
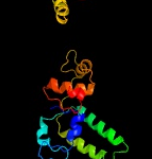
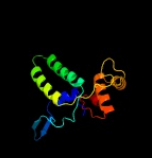
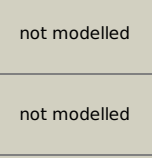


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2103c_(-)_2364094_2364528
Date	Mon Aug 5 13:25:22 BST 2019
Unique Job ID	5c7fce3e9abbdade

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3zvkc_	 Alignment		99.9	15	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
2	d2h1ca1	 Alignment		99.9	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
3	c5wzfb_	 Alignment		99.9	17	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	c516mC_	 Alignment		99.9	17	PDB header: hydrolase Chain: C; PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
6	c3tndC_	 Alignment		99.9	15	PDB header: translation, toxin Chain: C; PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
7	c5x3td_	 Alignment		99.9	22	PDB header: antitoxin/toxin Chain: D; PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
8	c4xgrG_	 Alignment		99.9	14	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
9	c6a7vG_	 Alignment		99.8	20	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
10	c4chgC_	 Alignment		99.8	21	PDB header: toxin/antitoxin Chain: C; PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
11	c3h87B_	 Alignment		99.8	18	PDB header: toxin/antitoxin Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis

12	c3dboB	Alignment		99.8	17	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
13	c5sv2A	Alignment		99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
14	d1v96a1	Alignment		99.7	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
15	c2fe1A	Alignment		99.7	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		99.7	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	d1w8ia	Alignment		99.6	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	d1y82a1	Alignment		99.6	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	d1v8pa	Alignment		99.1	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c1v8pK	Alignment		99.1	16	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
21	c3ix7A	Alignment	not modelled	98.6	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
22	c3i8oA	Alignment	not modelled	98.6	9	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.
23	d1o4wa	Alignment	not modelled	98.0	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c2lcqA	Alignment	not modelled	97.9	17	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	97.8	18	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
26	c5f4hF	Alignment	not modelled	97.7	18	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
27	c2hwwC	Alignment	not modelled	97.5	13	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	96.9	10	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	96.8	16	Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c2hwyB_	Alignment	not modelled	94.1	13	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c4mj7B_	Alignment	not modelled	91.0	18	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	c6g5iy_	Alignment	not modelled	86.3	15	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
33	d1cmwa2	Alignment	not modelled	85.1	32	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
34	d1tfra2	Alignment	not modelled	83.2	32	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
35	c3zdda_	Alignment	not modelled	82.1	18	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
36	c3v32B_	Alignment	not modelled	81.6	36	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
37	c3v33A_	Alignment	not modelled	80.6	36	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
38	d1xo1a2	Alignment	not modelled	60.3	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
39	c2ihna_	Alignment	not modelled	40.1	28	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
40	c1ut8B_	Alignment	not modelled	39.7	18	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
41	c1cmwA_	Alignment	not modelled	21.0	16	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	19.1	27	PDB header: rna binding protein Chain: A: PDB Molecule: pentatricopeptide repeat-containing protein at2g32230, PDBTitle: crystal structure of proteinaceous rnase p 1 (prop1) from a.2 thaliana, semet substituted form with sr
43	c2mdtA_	Alignment	not modelled	16.3	26	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfobolus solfataricus p2
44	c5dizB_	Alignment	not modelled	15.7	22	PDB header: hydrolase Chain: B: PDB Molecule: proteinaceous rnase p 2; PDBTitle: crystal structure of nuclear proteinaceous rnase p 2 (prop2) from a.2 thaliana
45	d1ul1x2	Alignment	not modelled	13.8	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
46	c2izoA_	Alignment	not modelled	12.0	25	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
47	c3q8IA_	Alignment	not modelled	8.5	22	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+
48	c1b43A_	Alignment	not modelled	7.8	22	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
49	d1k1sa1	Alignment	not modelled	6.5	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
50	c1a77A_	Alignment	not modelled	6.3	22	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
51	d1a77a2	Alignment	not modelled	6.1	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain