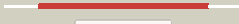



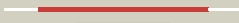

























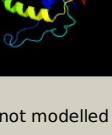


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1838c (-) _2087264_2087659
Date	Fri Aug 2 13:30:45 BST 2019
Unique Job ID	93cd86ec17bf04a9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5wzfB_	 Alignment		99.9	27	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
2	c3zvkc_	 Alignment		99.8	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
3	c5l6mC_	 Alignment		99.8	15	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
4	c5x3tD_	 Alignment		99.8	17	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
5	c6nklA_	 Alignment		99.8	15	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
6	c3tndC_	 Alignment		99.7	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		99.7	11	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
8	c6a7vG_	 Alignment		99.7	15	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
9	d2h1ca1	 Alignment		99.7	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
10	c4chgC_	 Alignment		99.7	13	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
11	c3h87B_	 Alignment		99.6	15	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis

12	d1w8ia_	Alignment		99.6	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
13	d2fe1a1	Alignment		99.6	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
14	c2fe1A_	Alignment		99.6	17	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
15	c3dboB_	Alignment		99.6	16	PDB header: toxin/antitoxin Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis
16	c5sv2A_	Alignment		99.5	15	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
17	d1v96a1	Alignment		99.5	10	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	d1y82a1	Alignment		99.2	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	d1v8pa_	Alignment		98.4	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c1v8pK_	Alignment		98.4	15	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	98.3	11	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	d1o4wa_	Alignment	not modelled	98.0	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
23	c3ix7A_	Alignment	not modelled	97.9	12	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
24	c2hwwC_	Alignment	not modelled	97.2	16	PDB header: rna binding protein Chain: C; PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
25	c5ywwA_	Alignment	not modelled	97.1	11	PDB header: hydrolase Chain: A; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
26	c5yz4A_	Alignment	not modelled	97.0	14	PDB header: hydrolase Chain: A; PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
27	c2lcqA_	Alignment	not modelled	97.0	16	PDB header: metal binding protein Chain: A; PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
28	c5jppd_	Alignment	not modelled	96.9	20	PDB header: ribosome Chain: D; PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
						PDB header: hydrolase

29	c5f4hF_	Alignment	not modelled	96.8	11	Chain: F; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archaeal ruvb-like holiday junction helicase
30	c4mj7B_	Alignment	not modelled	95.8	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
31	c3v32B_	Alignment	not modelled	88.0	14	PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
32	c2hwyB_	Alignment	not modelled	80.8	13	PDB header: rna binding protein Chain: B; PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
33	c6g5iy_	Alignment	not modelled	79.9	23	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
34	c3v33A_	Alignment	not modelled	72.3	17	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
35	c3zddA_	Alignment	not modelled	55.3	17	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	d1tfra2	Alignment	not modelled	54.3	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
37	d1cmwa2	Alignment	not modelled	52.3	11	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	c3q8IA_	Alignment	not modelled	43.8	13	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+
39	d1a77a2	Alignment	not modelled	40.3	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
40	d1ul1x2	Alignment	not modelled	39.0	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
41	d1xo1a2	Alignment	not modelled	38.5	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
42	c1ut8B_	Alignment	not modelled	33.8	21	PDB header: hydrolase Chain: B; PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
43	c1jqsB_	Alignment	not modelled	27.8	15	PDB header: ribosome Chain: B; PDB Molecule: elongation factor g; PDBTitle: fitting of I11 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
44	d1mc8a2	Alignment	not modelled	27.4	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
45	c1rxvA_	Alignment	not modelled	25.0	21	PDB header: hydrolase/dna Chain: A; PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
46	c1b43A_	Alignment	not modelled	24.5	17	PDB header: transferase Chain: A; PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
47	c2ihnA_	Alignment	not modelled	23.7	12	PDB header: hydrolase/dna Chain: A; PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
48	d1rxwa2	Alignment	not modelled	22.0	25	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
49	c2izoA_	Alignment	not modelled	20.1	9	PDB header: hydrolase Chain: A; PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
50	c4wa8A_	Alignment	not modelled	17.0	17	PDB header: hydrolase Chain: A; PDB Molecule: flap endonuclease 1; PDBTitle: methanopyrus kandleri fen-1 nuclease
51	c3qeaZ_	Alignment	not modelled	16.2	13	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)
52	c3oryA_	Alignment	not modelled	14.3	17	PDB header: hydrolase Chain: A; PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amyolyticus
53	d1u9ya1	Alignment	not modelled	13.2	7	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
54	d1b43a2	Alignment	not modelled	10.6	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
55	c1a77A_	Alignment	not modelled	10.3	15	PDB header: 5'-3' exo/endo nuclease Chain: A; PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii

56	c4q0rB_	Alignment	not modelled	9.2	9	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna repair protein rad2; PDBTitle: the catalytic core of rad2 (complex i)
57	c4g25A_	Alignment	not modelled	9.2	18	PDB header: rna binding protein Chain: A: PDB Molecule: pentatricopeptide repeat-containing protein at2g32230, PDBTitle: crystal structure of proteinaceous rna p 1 (prorp1) from a.2 thaliana, semet substituted form with sr
58	c3esgA_	Alignment	not modelled	9.1	31	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hutd from pseudomonas fluorescens sbw25
59	d1ylla1	Alignment	not modelled	8.8	25	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: PA5104-like
60	c1cmwA_	Alignment	not modelled	8.0	11	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
61	c5t9jB_	Alignment	not modelled	7.5	13	PDB header: hydrolase Chain: B: PDB Molecule: flap endonuclease gen homolog 1; PDBTitle: crystal structure of human gen1 in complex with holliday junction dna2 in the upper interface
62	c6c34A_	Alignment	not modelled	6.0	14	PDB header: dna binding protein Chain: A: PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
63	c4ixoB_	Alignment	not modelled	5.9	17	PDB header: protein binding Chain: B: PDB Molecule: nifs-like protein; PDBTitle: x-ray structure of nifs-like protein from rickettsia africae esf-5