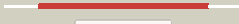



















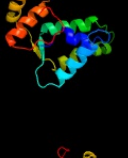

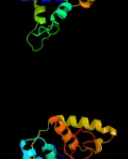



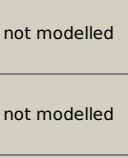


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0277c_(-)_332708_333136
Date	Tue Jul 23 14:50:34 BST 2019
Unique Job ID	c4aa9664794fcb79

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5wzfB_	 Alignment		99.9	16	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		99.9	9	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	d2h1ca1	 Alignment		99.9	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
4	c6nklA_	 Alignment		99.9	9	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		99.9	15	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
6	c5x3tD_	 Alignment		99.9	22	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
7	c4xqrG_	 Alignment		99.9	13	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
8	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
9	c6a7vG_	 Alignment		99.8	14	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	22	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	22	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis

12	d2fe1a1	Alignment		99.7	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
13	c2fe1A	Alignment		99.7	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
14	d1w8ia	Alignment		99.7	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
15	c3dboB	Alignment		99.7	15	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	d1v96a1	Alignment		99.7	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c5sv2A	Alignment		99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
18	d1y82a1	Alignment		99.6	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	d1v8pa	Alignment		99.1	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c1v8pK	Alignment		99.1	19	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	98.7	17	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	98.6	20	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	98.0	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c2lcqA	Alignment	not modelled	98.0	18	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	97.9	13	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	13	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	14	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
28	c5jppd	Alignment	not modelled	97.3	20	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
						PDB header: hydrolase

29	c5yz4A_	Alignment	not modelled	97.2	16	Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
30	c4mj7B_	Alignment	not modelled	95.5	16	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	c6g5iy_	Alignment	not modelled	91.0	13	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
32	c2hwyB_	Alignment	not modelled	91.0	17	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
33	c3v32B_	Alignment	not modelled	85.7	38	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 n-terminal conserved domain
34	c3v33A_	Alignment	not modelled	84.8	38	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 conserved domain with zinc-finger motif
35	c3zddA_	Alignment	not modelled	83.2	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	d1cmwa2	Alignment	not modelled	76.0	26	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
37	d1tfra2	Alignment	not modelled	73.5	24	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	d1xo1a2	Alignment	not modelled	38.4	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
39	c2ihnA_	Alignment	not modelled	37.4	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	d1ul1x2	Alignment	not modelled	23.6	24	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
41	c1cmwA_	Alignment	not modelled	22.5	26	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	21.6	36	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	d1a77a2	Alignment	not modelled	17.2	30	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
44	c2izoA_	Alignment	not modelled	16.7	22	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
45	c3q8IA_	Alignment	not modelled	14.9	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+
46	c1jqsB_	Alignment	not modelled	13.9	19	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
47	c1ut8B_	Alignment	not modelled	13.9	18	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
48	d1rxwa2	Alignment	not modelled	12.5	27	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
49	c1a77A_	Alignment	not modelled	11.8	28	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
50	c1b43A_	Alignment	not modelled	11.7	26	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
51	d1mc8a2	Alignment	not modelled	9.7	30	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
52	c1rxvA_	Alignment	not modelled	9.7	27	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
53	c6a68A_	Alignment	not modelled	8.8	9	PDB header: exocytosis Chain: A: PDB Molecule: calcium-dependent secretion activator 1; PDBTitle: the crystal structure of rat calcium-dependent activator protein for2 secretion (caps) damh domain
54	c3dy0B_	Alignment	not modelled	6.8	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
55	c1lq8H_	Alignment	not modelled	6.5	56	PDB header: blood clotting Chain: H: PDB Molecule: plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved protein c inhibitor

56 [d1w96a2](#)

Alignment

not modelled

6.4

29

Fold:PreATP-grasp domain
Superfamily:PreATP-grasp domain
Family:BC N-terminal domain-like