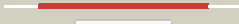



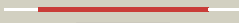



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2602_(-)_2930354_2930794
Date	Wed Aug 7 12:50:24 BST 2019
Unique Job ID	8cb90ce99909c3b8

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	c6nklA_	 Alignment		99.9	18	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
3	c4chgC_	 Alignment		99.9	21	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
4	c3tndC_	 Alignment		99.9	20	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
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	d2h1ca1	 Alignment		99.9	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
7	c6a7vG_	 Alignment		99.9	17	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
8	c5x3tD_	 Alignment		99.9	15	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
9	c5wzfB_	 Alignment		99.9	24	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
10	c3h87B_	 Alignment		99.8	15	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
11	c5sv2A_	 Alignment		99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis

12	c4xgrG_	Alignment		99.8	19	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
13	d1v96a1	Alignment		99.8	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
14	c3dboB_	Alignment		99.8	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
15	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
16	d2fe1a1	Alignment		99.7	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	d1y82a1	Alignment		99.7	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	d1w8ia_	Alignment		99.7	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	c3ix7A_	Alignment		98.7	17	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
20	d1v8pa_	Alignment		98.7	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
21	c1v8pK_	Alignment	not modelled	98.7	22	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
22	c3i8oA_	Alignment	not modelled	98.6	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.
23	c5ywwA_	Alignment	not modelled	98.0	18	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
24	c2lcqA_	Alignment	not modelled	97.9	12	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
25	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
26	d1o4wa_	Alignment	not modelled	97.7	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
27	c2hwwC_	Alignment	not modelled	97.2	19	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	95.3	19	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	94.9	17	Chain: A; PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
30	c2hwyB_	Alignment	not modelled	94.5	24	PDB header: rna binding protein Chain: B; PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c6g5iy_	Alignment	not modelled	91.5	12	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	c4mj7B_	Alignment	not modelled	80.8	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
33	c3v33A_	Alignment	not modelled	72.4	22	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpi1 conserved domain with zinc-finger motif
34	c3zddA_	Alignment	not modelled	70.1	29	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
35	c3v32B_	Alignment	not modelled	69.8	22	PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpi1 n-terminal conserved domain
36	d1cmwa2	Alignment	not modelled	67.2	24	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
37	c2mdtA_	Alignment	not modelled	30.6	8	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfolobus solfataricus p2
38	d1tfra2	Alignment	not modelled	30.1	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
39	c1ut8B_	Alignment	not modelled	29.2	15	PDB header: hydrolase Chain: B; PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
40	c1cmwA_	Alignment	not modelled	27.1	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
41	d1xo1a2	Alignment	not modelled	18.9	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
42	c2izoA_	Alignment	not modelled	14.2	19	PDB header: hydrolase Chain: A; PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
43	c3q81A_	Alignment	not modelled	13.3	26	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+
44	c4g25A_	Alignment	not modelled	13.1	21	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
45	d1jx4a1	Alignment	not modelled	10.6	10	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
46	c1b43A_	Alignment	not modelled	9.8	23	PDB header: transferase Chain: A; PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
47	c5z6vA_	Alignment	not modelled	9.7	15	PDB header: protein transport Chain: A; PDB Molecule: abc-type uncharacterized transport system periplasmic PDBTitle: crystal structure of a substrate-binding protein from rhodothermus2 marinus
48	d1ul1x2	Alignment	not modelled	9.5	26	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
49	d2j01s1	Alignment	not modelled	8.0	34	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
50	c3dy0B_	Alignment	not modelled	7.7	44	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
51	c1lq8H_	Alignment	not modelled	7.3	44	PDB header: blood clotting Chain: H; PDB Molecule: plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved protein c inhibitor
52	c1a77A_	Alignment	not modelled	7.2	23	PDB header: 5'-3' exo/endo nuclease Chain: A; PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
53	c5dizB_	Alignment	not modelled	7.1	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
54	c2j18S_	Alignment	not modelled	7.0	34	PDB header: ribosome Chain: S; PDB Molecule: 50s ribosomal protein l18; PDBTitle: insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.

55	d1a77a2	Alignment	not modelled	6.9	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
56	c6c34A	Alignment	not modelled	6.4	14	PDB header: dna binding protein Chain: A: PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
57	c2qipA	Alignment	not modelled	5.9	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function vpa0982; PDBTitle: crystal structure of a protein of unknown function vpa0982 from vibrio2 paraohaemolyticus rimd 2210633