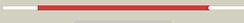
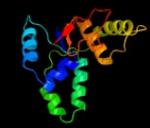
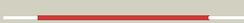
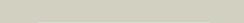


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1561 (-) _1764985_1765389
Date	Fri Aug 2 13:30:15 BST 2019
Unique Job ID	fa9361a524b19a32

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6a7vG_	 Alignment		100.0	100	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
2	c4chgC_	 Alignment		100.0	31	PDB header: toxin/antitoxin Chain: C; PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
3	c3h87B_	 Alignment		99.9	25	PDB header: toxin/antitoxin Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
4	c5sv2A_	 Alignment		99.9	25	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
5	c3zvkc_	 Alignment		99.9	19	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
6	c6nkiA_	 Alignment		99.9	20	PDB header: antitoxin Chain: A; PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
7	d1v96a1	 Alignment		99.9	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
8	d2h1ca1	 Alignment		99.9	24	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
9	c3tndC_	 Alignment		99.9	19	PDB header: translation, toxin Chain: C; PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
10	c5l6mC_	 Alignment		99.9	23	PDB header: hydrolase Chain: C; PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
11	c3dboB_	 Alignment		99.8	24	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

12	d1y82a1	Alignment		99.8	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
13	c4xgrG	Alignment		99.8	20	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
14	c5x3tD	Alignment		99.7	18	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
15	c5wzfB	Alignment		99.7	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
16	d2fe1a1	Alignment		99.4	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c2fe1A	Alignment		99.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
18	c3i8oA	Alignment		98.8	12	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.
19	c3ix7A	Alignment		98.8	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
20	d1w8ia	Alignment		98.5	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
21	d1o4wa	Alignment	not modelled	98.3	10	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
22	c5ywwA	Alignment	not modelled	98.3	15	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
23	c5f4hF	Alignment	not modelled	98.2	16	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
24	c2lcqA	Alignment	not modelled	98.0	17	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
25	d1v8pa	Alignment	not modelled	97.9	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
26	c1v8pK	Alignment	not modelled	97.9	18	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
27	c2hwwC	Alignment	not modelled	97.5	17	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
28	c5jpd	Alignment	not modelled	97.1	14	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
29	c5yz4A	Alignment	not modelled	96.9	13	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1;

						PDBTitle: structure of the pin domain endonuclease utp24
30	c2hwyB_	Alignment	not modelled	91.3	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	87.5	12	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	c3v33A_	Alignment	not modelled	87.4	17	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 conserved domain with zinc-finger motif
33	c3v32B_	Alignment	not modelled	87.0	22	PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 n-terminal conserved domain
34	c6g5iy_	Alignment	not modelled	76.3	16	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
35	c2mdtA_	Alignment	not modelled	53.5	14	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
36	c4g25A_	Alignment	not modelled	52.4	20	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
37	d1cmwa2	Alignment	not modelled	52.2	31	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	c3zddA_	Alignment	not modelled	42.0	38	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
39	d1tfra2	Alignment	not modelled	41.7	29	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
40	c5dizB_	Alignment	not modelled	33.5	21	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
41	c6md3F_	Alignment	not modelled	29.3	15	PDB header: hydrolase/rna Chain: F; PDB Molecule: rrp44p homologue; PDBTitle: structure of t. brucei rrp44 pin domain
42	d1xo1a2	Alignment	not modelled	21.2	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
43	c2ihnA_	Alignment	not modelled	19.4	26	PDB header: hydrolase/dna Chain: A; PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
44	c1ut8B_	Alignment	not modelled	14.7	19	PDB header: hydrolase Chain: B; PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
45	c1cmwA_	Alignment	not modelled	11.5	31	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
46	c6d6rK_	Alignment	not modelled	11.3	14	PDB header: hydrolase Chain: K; PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
47	c3dy0B_	Alignment	not modelled	7.8	22	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
48	c1lq8H_	Alignment	not modelled	7.4	22	PDB header: blood clotting Chain: H; PDB Molecule: plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved protein c inhibitor
49	c1jqsB_	Alignment	not modelled	7.3	12	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
50	d1zcca2	Alignment	not modelled	5.5	20	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC