







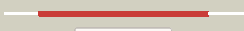















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2530c_(-)_2854277_2854696
Date	Wed Aug 7 12:50:16 BST 2019
Unique Job ID	90d878129da6bfb8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3zvkc_	 Alignment		99.8	12	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	c6a7vG_	 Alignment		99.8	18	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
3	c5wzfb_	 Alignment		99.8	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
4	c5x3tD_	 Alignment		99.8	16	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
5	c3tndC_	 Alignment		99.8	14	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
6	c2fe1A_	 Alignment		99.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
7	d2fe1a1	 Alignment		99.8	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
8	d2h1ca1	 Alignment		99.8	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
9	c4chgC_	 Alignment		99.8	12	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
10	c5sv2A_	 Alignment		99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
11	c3h87B_	 Alignment		99.8	12	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis

12	c6nkIA_	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
13	c4xgrG_	Alignment		99.7	10	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
14	c5l6mC_	Alignment		99.7	18	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
15	d1v96a1	Alignment		99.6	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
16	c3dboB_	Alignment		99.6	20	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
17	d1w8ia_	Alignment		99.5	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	d1y82a1	Alignment		99.5	10	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	d1v8pa_	Alignment		99.3	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c1v8pK_	Alignment		99.3	19	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	99.3	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	99.2	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.
23	d1o4wa_	Alignment	not modelled	98.8	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c5ywwA_	Alignment	not modelled	98.7	16	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
25	c5f4hF_	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
26	c2hwwC_	Alignment	not modelled	98.6	18	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
27	c2lcqA_	Alignment	not modelled	98.2	20	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	97.7	15	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	97.6	9	Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
30	c4mj7B_	Alignment	not modelled	97.0	14	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	c2hwyB_	Alignment	not modelled	95.4	17	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
32	c6g5iy_	Alignment	not modelled	89.8	18	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	c2mdtA_	Alignment	not modelled	85.1	15	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
34	c3v33A_	Alignment	not modelled	73.7	30	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
35	c3v32B_	Alignment	not modelled	72.2	26	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
36	c6d6rK_	Alignment	not modelled	32.8	13	PDB header: hydrolase Chain: K: PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
37	c3zddA_	Alignment	not modelled	26.2	16	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
38	c3ibzA_	Alignment	not modelled	14.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative tellurium resistant like protein terd; PDBTitle: crystal structure of putative tellurium resistant like protein (terd)2 from streptomyces coelicolor a3(2)
39	c2q4pA_	Alignment	not modelled	12.3	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein rs21-c6; PDBTitle: ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
40	d2a3qa1	Alignment	not modelled	12.3	26	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
41	c6a68A_	Alignment	not modelled	12.2	28	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
42	d1k1sa1	Alignment	not modelled	12.1	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
43	c4g25A_	Alignment	not modelled	10.2	32	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
44	c2kxvA_	Alignment	not modelled	7.6	13	PDB header: unknown function Chain: A: PDB Molecule: tellurite resistance protein; PDBTitle: nmr structure and calcium-binding properties of the tellurite2 resistance protein terd from klebsiella pneumoniae
45	c5dizB_	Alignment	not modelled	6.1	37	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
46	d1l5ja1	Alignment	not modelled	5.4	16	Fold: alpha-alpha superhelix Superfamily: Aconitase B, N-terminal domain Family: Aconitase B, N-terminal domain