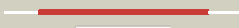




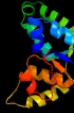


















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2596 (-) _2925744_2926148
Date	Wed Aug 7 12:50:23 BST 2019
Unique Job ID	3c1161247076144d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5l6mC_	 Alignment		99.9	16	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
2	c3tndC_	 Alignment		99.9	14	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
3	c6nkIA_	 Alignment		99.9	11	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
4	d2h1ca1	 Alignment		99.9	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
5	c3zvkc_	 Alignment		99.9	12	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	c5x3tD_	 Alignment		99.8	14	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
7	c5wzfb_	 Alignment		99.8	21	PDB header: hydrolase Chain: B: PDB Molecule: 23s rna-specific endonuclease vapc20; PDBTitle: crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
8	d1v96a1	 Alignment		99.8	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
9	c4xgrG_	 Alignment		99.8	15	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
10	c3dboB_	 Alignment		99.8	19	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
11	c3h87B_	 Alignment		99.7	16	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis

12	c6a7vG_	Alignment		99.7	21	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
13	d2fe1a1	Alignment		99.7	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
14	c2fe1A_	Alignment		99.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
15	d1y82a1	Alignment		99.7	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
16	c4chgC_	Alignment		99.7	17	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
17	c5sv2A_	Alignment		99.6	9	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
18	d1v8pa_	Alignment		99.5	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	c1v8pK_	Alignment		99.5	20	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
20	d1w8ia_	Alignment		99.2	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
21	c3i8oA_	Alignment	not modelled	98.7	14	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	98.7	21	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	98.3	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c5ywwA_	Alignment	not modelled	98.1	11	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
25	c5f4hF_	Alignment	not modelled	97.9	12	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
26	c2lcqA_	Alignment	not modelled	97.6	14	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
27	c2hwwC_	Alignment	not modelled	97.5	16	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	96.4	18	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	95.9	14	Chain: A; PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
30	c2hwyB_	Alignment	not modelled	88.9	14	PDB header: rna binding protein Chain: B; PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c4mj7B_	Alignment	not modelled	85.6	10	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	c2mdtA_	Alignment	not modelled	76.5	20	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
33	c6g5iy_	Alignment	not modelled	71.6	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
34	c3v33A_	Alignment	not modelled	58.0	16	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	56.4	12	PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
36	c2kebA_	Alignment	not modelled	42.6	11	PDB header: dna binding protein Chain: A; PDB Molecule: dna polymerase subunit alpha b; PDBTitle: nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
37	c4e2i3_	Alignment	not modelled	36.2	11	PDB header: hydrolase/dna binding protein Chain: 3; PDB Molecule: dna polymerase alpha subunit b; PDBTitle: the complex structure of the sv40 helicase large t antigen and p682 subunit of dna polymerase alpha-primase
38	d2bz1a1	Alignment	not modelled	17.5	18	Fold: RibA-like Superfamily: RibA-like Family: RibA-like
39	d1rhya1	Alignment	not modelled	9.3	33	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
40	c1jqsB_	Alignment	not modelled	7.6	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
41	c4g25A_	Alignment	not modelled	7.6	26	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
42	d2czca2	Alignment	not modelled	5.8	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
43	d2ae8a1	Alignment	not modelled	5.8	19	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
44	d2f1da1	Alignment	not modelled	5.5	14	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase