







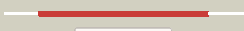














Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2863_(-)_3175002_3175382
Date	Wed Aug 7 12:50:53 BST 2019
Unique Job ID	6fcb691b22125ea

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5wzfB_	 Alignment		99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: 23s rrna-specific endonuclease vapp20; PDBTitle: crystal structure of mycobacterium tuberculosis vappc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
2	c5x3tD_	 Alignment		99.8	22	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vappc26; PDBTitle: vappc from mycobacterium tuberculosis
3	d1w8ia_	 Alignment		99.8	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
4	c3zvkc_	 Alignment		99.6	18	PDB header: antitoxin/toxin/dna Chain: C: PDB Molecule: toxin of toxin-antitoxin system; PDBTitle: crystal structure of vappc2 from rickettsia felis bound to 2 a dna fragment from their promoter
5	d2fe1a1	 Alignment		99.6	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
6	c2fe1A_	 Alignment		99.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
7	c4xqrG_	 Alignment		99.6	13	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vappc30; PDBTitle: crystal structure of addiction module from mycobacterial species
8	c6nkIA_	 Alignment		99.6	16	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vappc; PDBTitle: 2.2 a resolution structure of vappc-1 from nontypeable haemophilus2 influenzae
9	c6a7vG_	 Alignment		99.6	19	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vappc11; PDBTitle: crystal structure of mycobacterium tuberculosis vappc11 toxin-2 antitoxin complex
10	d2h1ca1	 Alignment		99.6	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
11	c3tndC_	 Alignment		99.5	15	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vappc; PDBTitle: crystal structure of shigella flexneri vappc toxin-antitoxin complex

12	c5l6mC_	Alignment		99.4	15	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
13	c4chgC_	Alignment		99.3	18	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
14	d1v96a1	Alignment		99.3	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
15	c3h87B_	Alignment		99.3	12	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
16	d1v82a1	Alignment		99.2	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c5sv2A_	Alignment		99.2	14	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
18	d1v8pa_	Alignment		99.1	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	c1v8pK_	Alignment		99.1	15	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
20	c3dboB_	Alignment		99.0	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
21	c3ix7A_	Alignment	not modelled	98.1	22	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	98.0	13	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	97.7	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c5yz4A_	Alignment	not modelled	97.6	21	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
25	c5jpdq_	Alignment	not modelled	97.5	26	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
26	c2hwwC_	Alignment	not modelled	96.9	19	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
27	c2lqqa_	Alignment	not modelled	96.4	15	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
28	c5ywwA_	Alignment	not modelled	96.1	15	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
						PDB header: hydrolase

29	c5f4hF_	Alignment	not modelled	96.1	15	Chain: F; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
30	c4mj7B_	Alignment	not modelled	95.3	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	91.1	10	PDB header: rna binding protein Chain: B; PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
32	c3v32B_	Alignment	not modelled	33.3	10	PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
33	c6g5iy_	Alignment	not modelled	32.9	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	30.1	10	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
35	c4mcjC_	Alignment	not modelled	14.1	23	PDB header: transferase Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative nucleoside deoxyribosyltransferase2 (bdi_0649) from parabacteroides distasonis atcc 8503 at 2.40 a3 resolution
36	c4ixoB_	Alignment	not modelled	10.5	22	PDB header: protein binding Chain: B; PDB Molecule: nifs-like protein; PDBTitle: x-ray structure of nifs-like protein from rickettsia africae esf-5
37	c1jqsB_	Alignment	not modelled	9.4	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
38	d1u9ya1	Alignment	not modelled	5.0	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like