



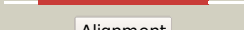

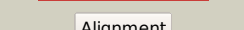

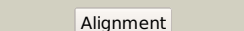





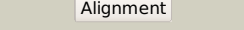

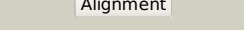
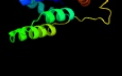
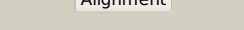

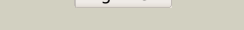
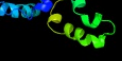


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3320c_(-)_3707813_3708241
Date	Thu Aug 8 16:20:53 BST 2019
Unique Job ID	c6d46a3805d394fb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3zvkc_	 Alignment		99.9	11	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	d2fe1a1	 Alignment		99.8	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
3	c2fe1A_	 Alignment		99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
4	c3tndC_	 Alignment		99.8	10	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
5	c6nkIA_	 Alignment		99.8	11	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
6	c5x3tD_	 Alignment		99.8	16	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
7	c5wzfB_	 Alignment		99.8	11	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	d2h1ca1	 Alignment		99.8	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
9	c6a7vG_	 Alignment		99.8	12	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
10	c5sv2A_	 Alignment		99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
11	c3h87B_	 Alignment		99.8	13	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis

12	c5l6mC_	Alignment		99.8	22	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
13	c4chgC_	Alignment		99.8	10	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
14	c4xgrG_	Alignment		99.8	16	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
15	d1v96a1	Alignment		99.7	10	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	d1v8pa_	Alignment		99.5	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	c1v8pK_	Alignment		99.5	17	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
19	d1y82a1	Alignment		99.5	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	d1w8ia_	Alignment		99.4	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
21	c3ix7A_	Alignment	not modelled	99.1	19	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	98.9	9	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	98.7	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c2hwwC_	Alignment	not modelled	98.3	15	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
25	c5ywwA_	Alignment	not modelled	98.2	20	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
26	c5f4hF_	Alignment	not modelled	98.1	20	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
27	c2lcqA_	Alignment	not modelled	97.6	17	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	97.1	14	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	96.9	12	Chain: A; PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
30	c2hwyB_	Alignment	not modelled	95.9	12	PDB header: rna binding protein Chain: B; PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c4mj7B_	Alignment	not modelled	94.9	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
32	c3v32B_	Alignment	not modelled	79.2	30	PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpip1 n-terminal conserved domain
33	c3v33A_	Alignment	not modelled	78.6	30	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpip1 conserved domain with zinc-finger motif
34	c6g5iy_	Alignment	not modelled	61.7	17	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	d1k1sa1	Alignment	not modelled	11.6	16	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
36	d1l5ja1	Alignment	not modelled	8.1	17	Fold: alpha-alpha superhelix Superfamily: Aconitase B, N-terminal domain Family: Aconitase B, N-terminal domain