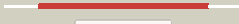



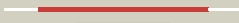




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2527 (-)_2851325_2851726
Date	Wed Aug 7 12:50:16 BST 2019
Unique Job ID	94ed09c53cfd661

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h87B_	 Alignment		99.9	30	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
2	c5sv2A_	 Alignment		99.9	29	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
3	c4chgC_	 Alignment		99.9	18	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
4	c3tndC_	 Alignment		99.9	15	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
5	d1v96a1	 Alignment		99.8	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
6	c6nkiA_	 Alignment		99.8	18	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
7	c3dboB_	 Alignment		99.8	21	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
8	c3zvkc_	 Alignment		99.8	16	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
9	c6a7vG_	 Alignment		99.8	23	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
10	c5l6mC_	 Alignment		99.8	19	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
11	d1y82a1	 Alignment		99.8	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain

12	d2h1ca1	Alignment		99.8	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
13	c4xqrG_	Alignment		99.7	15	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
14	c5x3tD_	Alignment		99.4	18	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
15	c5wzfB_	Alignment		99.4	11	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	c2fe1A_	Alignment		99.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
17	d2fe1a1	Alignment		99.3	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	c3ix7A_	Alignment		98.2	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
19	d1v8pa_	Alignment		98.2	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	d1o4wa_	Alignment		98.2	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
21	c1v8pK_	Alignment	not modelled	98.1	16	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
22	c3i8oA_	Alignment	not modelled	97.9	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	c5ywwA_	Alignment	not modelled	97.6	15	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
24	d1w8ia_	Alignment	not modelled	97.6	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
25	c5f4hF_	Alignment	not modelled	97.5	17	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
26	c2lcqA_	Alignment	not modelled	97.1	17	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	94.9	20	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
28	c5yz4A_	Alignment	not modelled	93.1	14	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
						PDB header: ribosome

29	c5jppd_	Alignment	not modelled	93.0	20	Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c2hwyB_	Alignment	not modelled	84.1	9	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c3v32B_	Alignment	not modelled	72.6	36	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 n-terminal conserved domain
32	c3v33A_	Alignment	not modelled	70.1	36	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 conserved domain with zinc-finger motif
33	c4mj7B_	Alignment	not modelled	65.2	17	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
34	c6g5iy_	Alignment	not modelled	63.4	12	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	d1cmwa2	Alignment	not modelled	57.9	26	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
36	c3zdda_	Alignment	not modelled	52.1	23	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
37	c2qipA_	Alignment	not modelled	21.9	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function vpa0982; PDBTitle: crystal structure of a protein of unknown function vpa0982 from vibrio2 parahaemolyticus rimd 2210633
38	c1ut8B_	Alignment	not modelled	21.8	22	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
39	d1tfra2	Alignment	not modelled	17.7	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
40	c1cmwA_	Alignment	not modelled	17.2	26	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
41	d1xo1a2	Alignment	not modelled	15.5	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
42	c2ihnA_	Alignment	not modelled	14.8	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
43	d1a77a2	Alignment	not modelled	10.7	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
44	c4qtkB_	Alignment	not modelled	10.2	8	PDB header: transcription/dna Chain: B: PDB Molecule: white-opaque regulator 1; PDBTitle: complex of wopr domain of wor1 in candida albicans with the 17bp dsdna
45	c3q8IA_	Alignment	not modelled	8.7	13	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+
46	c2iswB_	Alignment	not modelled	8.7	22	PDB header: lyase Chain: B: PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
47	d1ul1x2	Alignment	not modelled	8.4	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
48	c1zpd_	Alignment	not modelled	8.3	13	PDB header: oxidoreductase Chain: D: PDB Molecule: small cytochrome binding protein; PDBTitle: crystal structure of mitochondrial respiratory complex ii2 bound with 3-nitropropionate and 2-thenoyltrifluoroacetone
49	c2murA_	Alignment	not modelled	8.0	10	PDB header: protein binding Chain: A: PDB Molecule: fanconi anemia-associated protein of 20 kda; PDBTitle: solution structure of the human faap20 ubz-ubiquitin complex
50	c2muqA_	Alignment	not modelled	8.0	10	PDB header: ubiquitin binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 20 kda; PDBTitle: solution structure of the human faap20 ubz
51	c2n22B_	Alignment	not modelled	7.9	38	PDB header: transcription Chain: B: PDB Molecule: transcription factor p65; PDBTitle: nmr structure of the complex between the ph domain of the tfb1 subunit2 from tfiih and the transactivation domain of p65
52	c3wmqA_	Alignment	not modelled	7.0	8	PDB header: sugar binding protein Chain: A: PDB Molecule: galactose-binding lectin; PDBTitle: crystal structure of the complex between sli-2 and galnac.
53	c4m8bR_	Alignment	not modelled	6.5	16	PDB header: transcription/dna Chain: R: PDB Molecule: yhr177w; PDBTitle: fungal protein
54	c2ihuA_	Alignment	not modelled	6.0	33	PDB header: structural protein Chain: A: PDB Molecule: mybpc3 protein; PDBTitle: structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
						PDB header: transcription

55	c5urnB_	Alignment	not modelled	6.0	38	Chain: B: PDB Molecule: transcription factor pb5; PDBTitle: nmr structure of the complex between the ph domain of the tfb1 subunit2 from tfiih and the transactivation domain 1 of p65
56	d1q0qa2	Alignment	not modelled	6.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
57	c2izoA_	Alignment	not modelled	5.9	13	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
58	c4mitG_	Alignment	not modelled	5.7	25	PDB header: signaling protein Chain: G: PDB Molecule: serine/threonine protein kinase pak, putative; PDBTitle: crystal structure of e. histolytica racc bound to the ehpk4 pbd
59	c5v76A_	Alignment	not modelled	5.3	36	PDB header: structural protein Chain: A: PDB Molecule: microcompartments protein; PDBTitle: structure of haliangium ochraceum bmc-t ho-3341