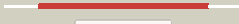



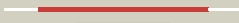




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0627 (-)_718285_718692
Date	Fri Jul 26 01:50:19 BST 2019
Unique Job ID	baa41669744f0e07

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dboB	 Alignment		100.0	94	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
2	c3h87B	 Alignment		99.9	23	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
3	d2h1ca1	 Alignment		99.9	29	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
4	c3zvkc	 Alignment		99.9	19	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
5	d1v96a1	 Alignment		99.9	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
6	c3tndC	 Alignment		99.9	27	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
7	c6nklA	 Alignment		99.9	25	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
8	c5l6mC	 Alignment		99.9	25	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
9	c5sv2A	 Alignment		99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
10	d1y82a1	 Alignment		99.9	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
11	c4chgC	 Alignment		99.9	26	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis

12	c4xgrG_	Alignment		99.8	17	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
13	c6a7vG_	Alignment		99.8	24	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
14	c5x3tD_	Alignment		99.6	22	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
15	c5wzfB_	Alignment		99.6	20	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
16	d2fe1a1	Alignment		99.5	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c2fe1A_	Alignment		99.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
18	c3ix7A_	Alignment		98.6	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
19	d1w8ia_	Alignment		98.5	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c3i8oA_	Alignment		98.3	18	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.
21	d1v8pa_	Alignment	not modelled	98.3	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
22	c1v8pK_	Alignment	not modelled	98.3	22	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
23	d1o4wa_	Alignment	not modelled	98.0	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c5ywwA_	Alignment	not modelled	98.0	13	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	13	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
26	c2lcqA_	Alignment	not modelled	97.8	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	96.9	17	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	93.7	17	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
29	c5jpd_	Alignment	not modelled	92.5	20	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins;

						PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c2hwyB_	Alignment	not modelled	90.4	14	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c3v32B_	Alignment	not modelled	71.4	25	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 n-terminal conserved domain
32	c3v33A_	Alignment	not modelled	67.4	25	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	66.4	15	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	66.0	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	63.3	27	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
36	d1tfra2	Alignment	not modelled	49.8	26	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
37	d1xo1a2	Alignment	not modelled	36.1	27	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	c3zddA_	Alignment	not modelled	34.2	17	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
39	c2qipA_	Alignment	not modelled	23.2	23	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
40	c2ihnA_	Alignment	not modelled	22.9	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
41	c1ut8B_	Alignment	not modelled	13.8	21	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
42	c1cmwA_	Alignment	not modelled	12.6	27	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
43	d1q0qa2	Alignment	not modelled	9.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
44	c4mitG_	Alignment	not modelled	8.6	22	PDB header: signaling protein Chain: G: PDB Molecule: serine/threonine protein kinase pak, putative; PDBTitle: crystal structure of e. histolytica racc bound to the ehpak4 pbd
45	c2mdtA_	Alignment	not modelled	7.5	18	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
46	c5yaaD_	Alignment	not modelled	7.4	33	PDB header: hydrolase Chain: D: PDB Molecule: meiosis regulator and mrna stability factor 1; PDBTitle: crystal structure of marf1 nyn domain from mus musculus
47	d2hi6a1	Alignment	not modelled	6.9	19	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: AF0055-like
48	c3iefA_	Alignment	not modelled	6.2	30	PDB header: transferase, rna binding protein Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna guanine-n1-methyltransferase from bartonella2 henselae using mpccs.
49	c5urnB_	Alignment	not modelled	5.9	23	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 1 of p65
50	c1jqsB_	Alignment	not modelled	5.7	15	PDB header: ribosome Chain: B: PDB Molecule: elongation factor g; PDBTitle: fitting of I11 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
51	c4g25A_	Alignment	not modelled	5.7	21	PDB header: rna binding protein Chain: A: PDB Molecule: pentatricopeptide repeat-containing protein at2g32230, PDBTitle: crystal structure of proteinaceous rnase p 1 (prop1) from a.2 thaliana, semet substituted form with sr
52	d1r0ka2	Alignment	not modelled	5.4	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
53	c5dizB_	Alignment	not modelled	5.3	26	PDB header: hydrolase Chain: B: PDB Molecule: proteinaceous rnase p 2; PDBTitle: crystal structure of nuclear proteinaceous rnase p 2 (prop2) from a.2 thaliana