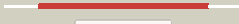



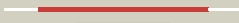



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0582 (-)_677925_678332
Date	Fri Jul 26 01:50:13 BST 2019
Unique Job ID	10d996a22d8fb7f0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5x3tD_	 Alignment		100.0	99	PDB header: antitoxin/toxin Chain: D; PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
2	c5wzfB_	 Alignment		99.9	20	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
3	c4xgrG_	 Alignment		99.8	21	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
4	d1w8ia_	 Alignment		99.8	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
5	c5l6mC_	 Alignment		99.8	17	PDB header: hydrolase Chain: C; PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
6	c3tndC_	 Alignment		99.8	18	PDB header: translation, toxin Chain: C; PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
7	c6nkIA_	 Alignment		99.7	17	PDB header: antitoxin Chain: A; PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
8	c6a7vG_	 Alignment		99.7	18	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
9	c3zvkc_	 Alignment		99.7	15	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
10	d2h1ca1	 Alignment		99.7	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
11	d1v96a1	 Alignment		99.7	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain

12	c3h87B_	Alignment		99.7	21	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
13	c4chgC_	Alignment		99.7	18	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
14	d1y82a1	Alignment		99.7	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
15	c5sv2A_	Alignment		99.6	11	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
16	c3dboB_	Alignment		99.6	24	PDB header: toxin/antitoxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a member of the vapbc family of toxin-antitoxin systems, vapbc-5, from mycobacterium tuberculosis
17	d2fe1a1	Alignment		99.6	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	c2fe1A_	Alignment		99.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
19	d1v8pa_	Alignment		98.7	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c1v8pK_	Alignment		98.7	17	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
21	c3i8oA_	Alignment	not modelled	97.9	15	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	97.8	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
23	d1o4wa_	Alignment	not modelled	97.5	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c2lcqA_	Alignment	not modelled	97.4	16	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
25	c5jpdq_	Alignment	not modelled	96.7	18	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
26	c5ywwA_	Alignment	not modelled	96.6	18	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archaeal ruvb-like holiday junction helicase
27	c2hwwC_	Alignment	not modelled	96.4	23	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	96.4	21	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
						PDB header: hydrolase

29	c5f4hF_	Alignment	not modelled	96.3	18	Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
30	c2hwyB_	Alignment	not modelled	92.4	19	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c6g5iy_	Alignment	not modelled	91.5	19	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
32	c4mj7B_	Alignment	not modelled	84.3	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
33	c3v32B_	Alignment	not modelled	70.9	25	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 n-terminal conserved domain
34	c3v33A_	Alignment	not modelled	64.0	22	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 conserved domain with zinc-finger motif
35	d1zcza2	Alignment	not modelled	39.0	20	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
36	d1g8ma2	Alignment	not modelled	34.5	17	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
37	d1s1da_	Alignment	not modelled	22.2	27	Fold: 5-bladed beta-propeller Superfamily: Apyrase Family: Apyrase
38	d1pkxa2	Alignment	not modelled	20.0	20	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
39	d1tfra2	Alignment	not modelled	19.1	29	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
40	d1a77a2	Alignment	not modelled	18.3	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
41	d1cmwa2	Alignment	not modelled	17.0	39	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
42	c3q8lA_	Alignment	not modelled	15.8	21	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+
43	c1zcza_	Alignment	not modelled	14.9	17	PDB header: transferase/hydrolase Chain: A: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
44	d1ul1x2	Alignment	not modelled	14.1	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
45	c1thza_	Alignment	not modelled	14.0	20	PDB header: transferase, hydrolase Chain: A: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
46	c4g25A_	Alignment	not modelled	12.0	18	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
47	c4ehiB_	Alignment	not modelled	11.8	33	PDB header: hydrolase,transferase Chain: B: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: an x-ray crystal structure of a putative bifunctional2 phosphoribosylaminoimidazolecarboxamide formyltransferase/imp3 cyclohydrolase
48	c4a1oB_	Alignment	not modelled	11.5	23	PDB header: transferase-hydrolase Chain: B: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfar, at 2.48 a resolution.
49	d1rxwa2	Alignment	not modelled	10.6	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
50	d1mc8a2	Alignment	not modelled	9.7	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
51	c1rxvA_	Alignment	not modelled	9.4	13	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
52	d1xo1a2	Alignment	not modelled	9.1	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
53	c3zddA_	Alignment	not modelled	8.9	30	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
54	c3al0B_	Alignment	not modelled	8.6	22	PDB header: ligase/rna Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) PDBTitle: crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
55	c3kfuF_	Alignment	not modelled	8.5	17	PDB header: ligase/rna Chain: F: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) PDBTitle: crystal structure of the transamidosome
56	c4wj3K_	Alignment	not modelled	8.4	22	PDB header: ligase/rna Chain: K: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
57	c3kful_	Alignment	not modelled	8.3	17	PDB header: ligase/rna Chain: I: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) PDBTitle: crystal structure of the transamidosome
58	c4wj3H_	Alignment	not modelled	8.2	22	PDB header: ligase/rna Chain: H: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
59	c4wj3E_	Alignment	not modelled	8.2	22	PDB header: ligase/rna Chain: E: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
60	c4wj3B_	Alignment	not modelled	8.2	22	PDB header: ligase/rna Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
61	c1qsb_	Alignment	not modelled	8.0	23	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
62	c2g5iB_	Alignment	not modelled	8.0	22	PDB header: ligase Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) PDBTitle: structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
63	c1a77A_	Alignment	not modelled	7.7	13	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
64	c2izoA_	Alignment	not modelled	7.6	13	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
65	c3h0mE_	Alignment	not modelled	7.5	22	PDB header: ligase Chain: E: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) PDBTitle: structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
66	d1oy5a_	Alignment	not modelled	7.4	13	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
67	c1oy5B_	Alignment	not modelled	7.4	13	PDB header: transferase Chain: B: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus
68	c1b43A_	Alignment	not modelled	7.1	13	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
69	c4n0iB_	Alignment	not modelled	6.8	31	PDB header: ligase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit b, PDBTitle: crystal structure of s. cerevisiae mitochondrial gatfab in complex2 with glutamine
70	c3ip4B_	Alignment	not modelled	6.2	22	PDB header: ligase Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) PDBTitle: the high resolution structure of gatcab