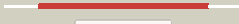



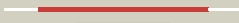



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0595c (- )_694842_695234
Date	Fri Jul 26 01:50:15 BST 2019
Unique Job ID	bd915ffeedd106d2

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dboB</a>	 Alignment		99.9	38	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis
2	<a href="#">c3h87B</a>	 Alignment		99.9	19	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
3	<a href="#">c3tndC</a>	 Alignment		99.9	20	<b>PDB header:</b> translation, toxin <b>Chain:</b> C: <b>PDB Molecule:</b> trna(fmet)-specific endonuclease vapc; <b>PDBTitle:</b> crystal structure of shigella flexneri vapbc toxin-antitoxin complex
4	<a href="#">c3zvkc</a>	 Alignment		99.9	19	<b>PDB header:</b> antitoxin/toxin/dna <b>Chain:</b> C: <b>PDB Molecule:</b> toxin of toxin-antitoxin system; <b>PDBTitle:</b> crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
5	<a href="#">d1v96a1</a>	 Alignment		99.9	14	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
6	<a href="#">c6nkiA</a>	 Alignment		99.9	19	<b>PDB header:</b> antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease vapc; <b>PDBTitle:</b> 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
7	<a href="#">d2h1ca1</a>	 Alignment		99.9	26	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
8	<a href="#">c5sv2A</a>	 Alignment		99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease vapc21; <b>PDBTitle:</b> toxin vapc21 from mycobacterium tuberculosis
9	<a href="#">c5l6mC</a>	 Alignment		99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ribonuclease vapc; <b>PDBTitle:</b> structure of caulobacter crescentus vapbc1 (vapb1delta;vapc1 form)
10	<a href="#">c4chgC</a>	 Alignment		99.8	24	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> C: <b>PDB Molecule:</b> probable ribonuclease vapc15; <b>PDBTitle:</b> crystal structure of vapbc15 complex from mycobacterium tuberculosis
11	<a href="#">d1y82a1</a>	 Alignment		99.8	15	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain

12	<a href="#">c6a7vG_</a>	Alignment		99.8	23	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> G; <b>PDB Molecule:</b> ribonuclease vapc11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
13	<a href="#">c4xgrG_</a>	Alignment		99.8	17	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> G; <b>PDB Molecule:</b> ribonuclease vapc30; <b>PDBTitle:</b> crystal structure of addition module from mycobacterial species
14	<a href="#">c5x3tD_</a>	Alignment		99.6	22	<b>PDB header:</b> antitoxin/toxin <b>Chain:</b> D; <b>PDB Molecule:</b> ribonuclease vapc26; <b>PDBTitle:</b> vapbc from mycobacterium tuberculosis
15	<a href="#">c5wzfB_</a>	Alignment		99.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> 23s rna-specific endonuclease vapc20; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
16	<a href="#">d2fe1a1</a>	Alignment		99.6	16	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
17	<a href="#">c2fe1A_</a>	Alignment		99.6	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> conserved hypothetical protein pae0151; <b>PDBTitle:</b> crystal structure of pae0151 from pyrobaculum aerophilum
18	<a href="#">d1w8ia_</a>	Alignment		98.8	15	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
19	<a href="#">d1v8pa_</a>	Alignment		98.6	19	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
20	<a href="#">c3ix7A_</a>	Alignment		98.6	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein ttha0540; <b>PDBTitle:</b> crystal structure of a domain of functionally unknown protein from2 thermus thermophilus hb8
21	<a href="#">c1v8pK_</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> K; <b>PDB Molecule:</b> hypothetical protein pae2754; <b>PDBTitle:</b> crystal structure of pae2754 from pyrobaculum aerophilum
22	<a href="#">d1o4wa_</a>	Alignment	not modelled	98.5	22	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
23	<a href="#">c3i8oA_</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> kh domain-containing protein mj1533; <b>PDBTitle:</b> a domain of a functionally unknown protein from methanocaldococcus2 jannaschii dsm 2661.
24	<a href="#">c5ywwA_</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> nucleotide binding protein pinc; <b>PDBTitle:</b> archael ruvb-like holiday junction helicase
25	<a href="#">c5f4hF_</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> nucleotide binding protein pinc; <b>PDBTitle:</b> archael ruvb-like holiday junction helicase
26	<a href="#">c2lcqA_</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative toxin vapc6; <b>PDBTitle:</b> solution structure of the endonuclease nob1 from p.horikoshii
27	<a href="#">c2hwwC_</a>	Alignment	not modelled	97.3	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> telomerase-binding protein est1a; <b>PDBTitle:</b> structure of pin domain of human smg6
28	<a href="#">c5jppd_</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> ribosome <b>Chain:</b> D; <b>PDB Molecule:</b> wd40 domain proteins; <b>PDBTitle:</b> cryo-em structure of the 90s pre-ribosome
						<b>PDB header:</b> hydrolase

29	<a href="#">c5yz4A_</a>	Alignment	not modelled	96.7	17	<b>Chain:</b> A: <b>PDB Molecule:</b> rrna-processing protein fcf1; <b>PDBTitle:</b> structure of the pin domain endonuclease utp24
30	<a href="#">c4mj7B_</a>	Alignment	not modelled	93.4	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> rrna-processing protein utp23; <b>PDBTitle:</b> crystal structure of the pin domain of saccharomyces cerevisiae utp23
31	<a href="#">c2hwyB_</a>	Alignment	not modelled	86.8	8	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein smg5; <b>PDBTitle:</b> structure of pin domain of human smg5.
32	<a href="#">c6g5iy_</a>	Alignment	not modelled	79.4	18	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 40s ribosomal protein s24; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state r
33	<a href="#">c3v33A_</a>	Alignment	not modelled	72.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease zc3h12a; <b>PDBTitle:</b> crystal structure of mcpi1 conserved domain with zinc-finger motif
34	<a href="#">c3v32B_</a>	Alignment	not modelled	71.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonuclease zc3h12a; <b>PDBTitle:</b> crystal structure of mcpi1 n-terminal conserved domain
35	<a href="#">d1cmwa2</a>	Alignment	not modelled	68.6	35	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
36	<a href="#">d1tfra2</a>	Alignment	not modelled	45.2	32	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
37	<a href="#">c3zddA_</a>	Alignment	not modelled	38.3	19	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein xni; <b>PDBTitle:</b> structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
38	<a href="#">d1xo1a2</a>	Alignment	not modelled	35.8	16	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
39	<a href="#">c4hecB_</a>	Alignment	not modelled	25.5	33	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis
40	<a href="#">c1ut8B_</a>	Alignment	not modelled	24.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exodeoxyribonuclease; <b>PDBTitle:</b> divalent metal ions (zinc) bound to t5 5'-exonuclease
41	<a href="#">c2ihnA_</a>	Alignment	not modelled	24.2	28	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease h; <b>PDBTitle:</b> co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
42	<a href="#">c1cmwA_</a>	Alignment	not modelled	22.3	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase i); <b>PDBTitle:</b> crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain
43	<a href="#">d1hdoa_</a>	Alignment	not modelled	18.2	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
44	<a href="#">c2izoA_</a>	Alignment	not modelled	16.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flap structure-specific endonuclease; <b>PDBTitle:</b> structure of an archaeal pcna1-pcna2-fen1 complex
45	<a href="#">d1ul1x2</a>	Alignment	not modelled	16.5	21	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
46	<a href="#">c2qipA_</a>	Alignment	not modelled	14.2	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function vpa0982; <b>PDBTitle:</b> crystal structure of a protein of unknown function vpa0982 from vibrio2 parahaemolyticus rimd 2210633
47	<a href="#">c4mitG_</a>	Alignment	not modelled	13.2	20	<b>PDB header:</b> signaling protein <b>Chain:</b> G: <b>PDB Molecule:</b> serine/threonine protein kinase pak, putative; <b>PDBTitle:</b> crystal structure of e. histolytica racc bound to the ehpak4 pbd
48	<a href="#">c3q8IA_</a>	Alignment	not modelled	13.2	21	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> flap endonuclease 1; <b>PDBTitle:</b> crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+
49	<a href="#">d1a77a2</a>	Alignment	not modelled	12.1	18	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
50	<a href="#">c1b43A_</a>	Alignment	not modelled	10.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (fen-1); <b>PDBTitle:</b> fen-1 from p. furiosus
51	<a href="#">c1a77A_</a>	Alignment	not modelled	10.0	18	<b>PDB header:</b> 5'-3' exo/endo nuclease <b>Chain:</b> A: <b>PDB Molecule:</b> flap endonuclease-1 protein; <b>PDBTitle:</b> flap endonuclease-1 from methanococcus jannaschii
52	<a href="#">d1rxwa2</a>	Alignment	not modelled	8.5	15	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
53	<a href="#">c2c40B_</a>	Alignment	not modelled	8.3	0	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> inosine-uridine preferring nucleoside hydrolase family <b>PDBTitle:</b> crystal structure of inosine-uridine preferring nucleoside2 hydrolase from bacillus anthracis at 2.2a resolution
54	<a href="#">c3t8iC_</a>	Alignment	not modelled	8.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> purine nucleosidase, (iunh-2); <b>PDBTitle:</b> structural analysis of thermostable s. solfataricus purine-specific2 nucleoside hydrolase
55	<a href="#">c6dxdD_</a>	Alignment	not modelled	7.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase; <b>PDBTitle:</b> the crystal structure of an fmn-dependent nadh-

						azoreductase from2 klebsiella pneumoniae
56	<a href="#">c3t8jA_</a>	Alignment	not modelled	7.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleosidase, (iunh-1); <b>PDBTitle:</b> structural analysis of thermostable s. solfataricus pyrimidine-2 specific nucleoside hydrolase
57	<a href="#">c5dzB_</a>	Alignment	not modelled	7.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> proteinaceous rnase p 2; <b>PDBTitle:</b> crystal structure of nuclear proteinaceous rnase p 2 (prorp2) from a.2 thaliana
58	<a href="#">d1mc8a2</a>	Alignment	not modelled	7.1	21	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
59	<a href="#">c4mitE_</a>	Alignment	not modelled	7.1	25	<b>PDB header:</b> signaling protein <b>Chain:</b> E: <b>PDB Molecule:</b> serine/threonine protein kinase pak, putative; <b>PDBTitle:</b> crystal structure of e. histolytica racc bound to the ehpak4 pbd
60	<a href="#">c4g25A_</a>	Alignment	not modelled	6.9	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pentatricopeptide repeat-containing protein at2g32230, <b>PDBTitle:</b> crystal structure of proteinaceous rnase p 1 (prorp1) from a.2 thaliana, semet substituted form with sr
61	<a href="#">c1rxvA_</a>	Alignment	not modelled	6.8	15	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> flap structure-specific endonuclease; <b>PDBTitle:</b> crystal structure of a. fulgidus fen-1 bound to dna
62	<a href="#">c2hsnA_</a>	Alignment	not modelled	6.7	13	<b>PDB header:</b> ligase/rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> structural basis of yeast aminoacyl-trna synthetase complex2 formation revealed by crystal structures of two binary sub-3 complexes
63	<a href="#">c6c34A_</a>	Alignment	not modelled	6.1	8	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-3' exonuclease; <b>PDBTitle:</b> mycobacterium smegmatis dna flap endonuclease mutant d125n
64	<a href="#">c6ba0D_</a>	Alignment	not modelled	5.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cytidine/uridine-specific hydrolase; <b>PDBTitle:</b> pyrimidine-specific ribonucleoside hydrolase from gardnerella2 vaginalis
65	<a href="#">c1zp0D_</a>	Alignment	not modelled	5.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> small cytochrome binding protein; <b>PDBTitle:</b> crystal structure of mitochondrial respiratory complex ii2 bound with 3-nitropropionate and 2-thenyltrifluoroacetone
66	<a href="#">c3ofeB_</a>	Alignment	not modelled	5.2	18	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> ldlr chaperone boca; <b>PDBTitle:</b> structured domain of drosophila melanogaster boca p41 2 2 crystal form
67	<a href="#">c2i9sA_</a>	Alignment	not modelled	5.1	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> mesoderm development candidate 2; <b>PDBTitle:</b> the solution structure of the core of mesoderm development2 (mesd).