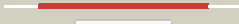



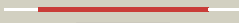



















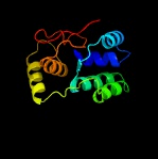




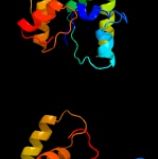
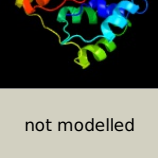


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2010_(-) _2258281_2258679
Date	Mon Aug 5 13:25:11 BST 2019
Unique Job ID	41cfc5d7a296ac94

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4chgC_</a>	 Alignment		100.0	98	<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
2	<a href="#">c6a7vG_</a>	 Alignment		100.0	31	<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
3	<a href="#">c3h87B_</a>	 Alignment		99.9	23	<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
4	<a href="#">c5sv2A_</a>	 Alignment		99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease vapc21; <b>PDBTitle:</b> toxin vapc21 from mycobacterium tuberculosis
5	<a href="#">d1v96a1</a>	 Alignment		99.9	24	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
6	<a href="#">c3zvkcC_</a>	 Alignment		99.9	13	<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
7	<a href="#">c6nklA_</a>	 Alignment		99.9	11	<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
8	<a href="#">c3tndC_</a>	 Alignment		99.9	19	<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
9	<a href="#">c5l6mC_</a>	 Alignment		99.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ribonuclease vapc; <b>PDBTitle:</b> structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
10	<a href="#">c3dboB_</a>	 Alignment		99.8	24	<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
11	<a href="#">d2h1ca1</a>	 Alignment		99.8	21	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain

12	<a href="#">d1y82a1</a>	Alignment		99.8	24	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
13	<a href="#">c4xgrG</a>	Alignment		99.8	18	<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="#">c5wzfB</a>	Alignment		99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 23s rrna-specific endonuclease vapc20; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
15	<a href="#">c5x3tD</a>	Alignment		99.8	19	<b>PDB header:</b> antitoxin/toxin <b>Chain:</b> D: <b>PDB Molecule:</b> ribonuclease vapc26; <b>PDBTitle:</b> vapbc from mycobacterium tuberculosis
16	<a href="#">c2fe1A</a>	Alignment		99.5	15	<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
17	<a href="#">d2fe1a1</a>	Alignment		99.5	15	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
18	<a href="#">c3i8oA</a>	Alignment		99.2	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.
19	<a href="#">c3ix7A</a>	Alignment		98.9	19	<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
20	<a href="#">d1w8ia</a>	Alignment		98.8	13	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
21	<a href="#">c5ywwA</a>	Alignment	not modelled	98.6	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
22	<a href="#">c5f4hF</a>	Alignment	not modelled	98.5	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
23	<a href="#">d1o4wa</a>	Alignment	not modelled	98.5	14	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
24	<a href="#">c2lqA</a>	Alignment	not modelled	98.3	21	<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
25	<a href="#">d1v8pa</a>	Alignment	not modelled	98.2	19	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
26	<a href="#">c1v8pK</a>	Alignment	not modelled	98.2	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
27	<a href="#">c2hwwC</a>	Alignment	not modelled	97.9	16	<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="#">c5jpd</a>	Alignment	not modelled	97.3	21	<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
29	<a href="#">c5yz4A</a>	Alignment	not modelled	97.3	21	<b>PDB header:</b> hydrolase <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	96.1	15	<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="#">c6g5iy_</a>	Alignment	not modelled	94.6	22	<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
32	<a href="#">c2hwyB_</a>	Alignment	not modelled	93.0	27	<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.
33	<a href="#">c3v32B_</a>	Alignment	not modelled	74.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonuclease zc3h12a; <b>PDBTitle:</b> crystal structure of mcip1 n-terminal conserved domain
34	<a href="#">c3v33A_</a>	Alignment	not modelled	70.6	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease zc3h12a; <b>PDBTitle:</b> crystal structure of mcip1 conserved domain with zinc-finger motif
35	<a href="#">c2mdtA_</a>	Alignment	not modelled	67.2	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfolobus solfataricus p2
36	<a href="#">d1cmwa2</a>	Alignment	not modelled	49.2	26	<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	37.9	22	<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="#">d1tfra2</a>	Alignment	not modelled	32.7	15	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
39	<a href="#">d1xo1a2</a>	Alignment	not modelled	26.3	27	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
40	<a href="#">c2ihnA_</a>	Alignment	not modelled	20.5	9	<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
41	<a href="#">c2qipA_</a>	Alignment	not modelled	18.4	17	<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
42	<a href="#">c4g25A_</a>	Alignment	not modelled	12.0	23	<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
43	<a href="#">c1jqsB_</a>	Alignment	not modelled	10.1	18	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> 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
44	<a href="#">c1ut8B_</a>	Alignment	not modelled	8.8	22	<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
45	<a href="#">d1a77a2</a>	Alignment	not modelled	8.6	35	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
46	<a href="#">c1cmwA_</a>	Alignment	not modelled	8.2	26	<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
47	<a href="#">c2n22B_</a>	Alignment	not modelled	7.5	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor p65; <b>PDBTitle:</b> nmr structure of the complex between the ph domain of the tfb1 subunit2 from tfiih and the transactivation domain of p65
48	<a href="#">c3q8lA_</a>	Alignment	not modelled	7.3	30	<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="#">d1ul1x2</a>	Alignment	not modelled	6.7	30	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain