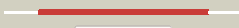























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0665 (-) _758804_759142
Date	Fri Jul 26 01:50:23 BST 2019
Unique Job ID	8ae97aef5370a277

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dboB_</a>	 Alignment		99.9	40	<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="#">d1v96a1</a>	 Alignment		99.8	21	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
3	<a href="#">c3h87B_</a>	 Alignment		99.8	20	<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="#">d2h1ca1</a>	 Alignment		99.8	29	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
5	<a href="#">c5sv2A_</a>	 Alignment		99.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease vapc21; <b>PDBTitle:</b> toxin vapc21 from mycobacterium tuberculosis
6	<a href="#">d1y82a1</a>	 Alignment		99.7	24	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
7	<a href="#">c3tndC_</a>	 Alignment		99.7	18	<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
8	<a href="#">c3zvkc_</a>	 Alignment		99.6	21	<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
9	<a href="#">c6nklA_</a>	 Alignment		99.6	20	<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
10	<a href="#">c4chgC_</a>	 Alignment		99.6	25	<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="#">c5l6mC_</a>	 Alignment		99.6	26	<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)

12	<a href="#">c4xgrG_</a>	Alignment		99.5	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
13	<a href="#">c6a7vG_</a>	Alignment		99.4	25	<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
14	<a href="#">c5x3tD_</a>	Alignment		99.0	19	<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		98.9	21	<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
16	<a href="#">d2fe1a1</a>	Alignment		98.4	18	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
17	<a href="#">c2fe1A_</a>	Alignment		98.4	18	<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="#">c3ix7A_</a>	Alignment		95.3	20	<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
19	<a href="#">c2lcqA_</a>	Alignment		90.3	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
20	<a href="#">d1o4wa_</a>	Alignment		89.7	17	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
21	<a href="#">c3i8oA_</a>	Alignment	not modelled	89.4	15	<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.
22	<a href="#">d1w8ia_</a>	Alignment	not modelled	87.7	17	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
23	<a href="#">c2hwwC_</a>	Alignment	not modelled	85.7	18	<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
24	<a href="#">c2hwyB_</a>	Alignment	not modelled	75.9	13	<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.
25	<a href="#">c5ywwA_</a>	Alignment	not modelled	68.3	13	<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
26	<a href="#">c5f4hF_</a>	Alignment	not modelled	66.1	17	<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
27	<a href="#">c6g5iy_</a>	Alignment	not modelled	52.8	14	<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
28	<a href="#">d1v8pa_</a>	Alignment	not modelled	50.8	18	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
29	<a href="#">c1v8nK_</a>	Alignment	not modelled	50.8	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> K: <b>PDB Molecule:</b> hypothetical protein pae2754;

29	<a href="#">c1v6pk_</a>	Alignment	not modelled	30.8	18	<b>PDBTitle:</b> crystal structure of pae2754 from pyrobaculum aerophilum
30	<a href="#">c5yz4A_</a>	Alignment	not modelled	33.7	17	<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
31	<a href="#">c5jppd_</a>	Alignment	not modelled	31.4	14	<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
32	<a href="#">c4mj7B_</a>	Alignment	not modelled	16.2	18	<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
33	<a href="#">c4jx2B_</a>	Alignment	not modelled	10.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative secreted protein (lpg1979) from2 legionella pneumophila subsp. pneumophila str. philadelphia 1 at 2.653 a resolution
34	<a href="#">d1qe0a1</a>	Alignment	not modelled	9.4	13	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
35	<a href="#">c3htuE_</a>	Alignment	not modelled	8.2	55	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> vacuolar protein-sorting-associated protein 25; <b>PDBTitle:</b> crystal structure of the human vps25-vps20 subcomplex
36	<a href="#">d1qf6a1</a>	Alignment	not modelled	7.4	13	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
37	<a href="#">d1wu7a1</a>	Alignment	not modelled	7.2	13	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS