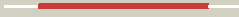























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1953 (-) _2200945_2201256
Date	Mon Aug 5 13:25:05 BST 2019
Unique Job ID	61cb4f5ee23a7636

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2h1ca1</a>	 Alignment		99.5	27	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
2	<a href="#">c6nklA</a>	 Alignment		99.3	14	<b>PDB header:</b> antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease vapbc; <b>PDBTitle:</b> 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
3	<a href="#">c3zvkc</a>	 Alignment		99.1	14	<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
4	<a href="#">c3h87B</a>	 Alignment		99.1	12	<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
5	<a href="#">c3tndC</a>	 Alignment		99.1	15	<b>PDB header:</b> translation, toxin <b>Chain:</b> C: <b>PDB Molecule:</b> trna(fmet)-specific endonuclease vapbc; <b>PDBTitle:</b> crystal structure of shigella flexneri vapbc toxin-antitoxin complex
6	<a href="#">c5sv2A</a>	 Alignment		99.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease vapc21; <b>PDBTitle:</b> toxin vapc21 from mycobacterium tuberculosis
7	<a href="#">c5l6mC</a>	 Alignment		98.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ribonuclease vapbc; <b>PDBTitle:</b> structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
8	<a href="#">d1v96a1</a>	 Alignment		98.8	7	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
9	<a href="#">c4chgC</a>	 Alignment		98.8	16	<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
10	<a href="#">c3dboB</a>	 Alignment		98.7	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="#">d1y82a1</a>	 Alignment		98.4	5	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain

12	<a href="#">c6a7vG_</a>	Alignment		98.3	15	<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		97.9	11	<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="#">d2fe1a1</a>	Alignment		97.5	17	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
15	<a href="#">c2fe1A_</a>	Alignment		97.5	17	<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
16	<a href="#">c5x3tD_</a>	Alignment		97.1	14	<b>PDB header:</b> antitoxin/toxin <b>Chain:</b> D: <b>PDB Molecule:</b> ribonuclease vapc26; <b>PDBTitle:</b> vapbc from mycobacterium tuberculosis
17	<a href="#">c5wzfB_</a>	Alignment		95.9	18	<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
18	<a href="#">c2hwwC_</a>	Alignment		93.8	21	<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
19	<a href="#">c1v8pK_</a>	Alignment		88.1	14	<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
20	<a href="#">d1v8pa_</a>	Alignment		88.0	14	<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	83.3	16	<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="#">c2hwyB_</a>	Alignment	not modelled	80.4	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.
23	<a href="#">c3ix7A_</a>	Alignment	not modelled	80.0	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
24	<a href="#">d1o4wa_</a>	Alignment	not modelled	77.6	21	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
25	<a href="#">c5jpdq_</a>	Alignment	not modelled	52.0	17	<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
26	<a href="#">c4mj7B_</a>	Alignment	not modelled	41.6	5	<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
27	<a href="#">c5yz4A_</a>	Alignment	not modelled	37.1	15	<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
28	<a href="#">d2ckaa1</a>	Alignment	not modelled	30.1	15	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
						<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chromodomain-helicase-dna-binding

29	<a href="#">c2ckaA_</a>	Alignment	not modelled	30.1	15	protein 8; <b>PDBTitle:</b> solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
30	<a href="#">c4gwpC_</a>	Alignment	not modelled	17.5	21	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 8; <b>PDBTitle:</b> structure of the mediator head module from s. cerevisiae
31	<a href="#">c2lqA_</a>	Alignment	not modelled	17.4	28	<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
32	<a href="#">c6hsdB_</a>	Alignment	not modelled	14.3	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rff2 family transcriptional regulator; <b>PDBTitle:</b> crystal structure of the oxidized form of the transcription regulator2 rsrr
33	<a href="#">c2dmnA_</a>	Alignment	not modelled	14.2	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein tgif2lx; <b>PDBTitle:</b> the solution structure of the homeobox domain of human2 homeobox protein tgif2lx
34	<a href="#">d2dl6a1</a>	Alignment	not modelled	13.1	17	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
35	<a href="#">c2mdvB_</a>	Alignment	not modelled	12.0	31	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> nmr structure of beta alpha alpha 38
36	<a href="#">c6dlhA_</a>	Alignment	not modelled	9.1	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,4-endofucoidanase; <b>PDBTitle:</b> endo-fucoidan hydrolase mffcna4 from glycoside hydrolase family 107
37	<a href="#">c2lk2A_</a>	Alignment	not modelled	9.0	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein tgif1; <b>PDBTitle:</b> solution nmr structure of homeobox domain (171-248) of human homeobox2 protein tgif1, northeast structural genomics consortium target3 hr4411b
38	<a href="#">c6bmtB_</a>	Alignment	not modelled	8.2	21	<b>PDB header:</b> oxidoreductase/inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a recombinant form of human myeloperoxidase bound2 to an inhibitor from staphylococcus delphini
39	<a href="#">d2r5yb1</a>	Alignment	not modelled	7.7	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
40	<a href="#">d1lfup_</a>	Alignment	not modelled	7.4	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
41	<a href="#">d1x2na1</a>	Alignment	not modelled	6.6	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
42	<a href="#">c3btnA_</a>	Alignment	not modelled	6.1	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> antizyme inhibitor 1; <b>PDBTitle:</b> crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
43	<a href="#">c5j5vC_</a>	Alignment	not modelled	6.0	35	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> immunity protein cdii; <b>PDBTitle:</b> cdia-ct from uropathogenic escherichia coli in complex with cognate2 immunity protein and cysk
44	<a href="#">d1yrnb_</a>	Alignment	not modelled	5.7	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
45	<a href="#">c5houA_</a>	Alignment	not modelled	5.7	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> cellular tumor antigen p53,creb-binding protein fusion <b>PDBTitle:</b> solution structure of p53tad-taz1
46	<a href="#">d2v0fa1</a>	Alignment	not modelled	5.6	29	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
47	<a href="#">c2lndA_</a>	Alignment	not modelled	5.4	44	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed protein, pfk fold; <b>PDBTitle:</b> solution nmr structure of de novo designed protein, pfk fold,2 northeast structural genomics consortium target or134