










# Phyre2

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Description	RVBD1561 (-) _1764985_1765389
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6a7vG_</a>	Alignment		100.0	100	<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
2	<a href="#">c4chgC_</a>	Alignment		100.0	31	<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
3	<a href="#">c3h87B_</a>	Alignment		99.9	25	<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	25	<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="#">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 to a dna fragment from their promoter
6	<a href="#">c6nkiA_</a>	Alignment		99.9	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
7	<a href="#">d1v96a1</a>	Alignment		99.9	17	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
8	<a href="#">d2h1ca1</a>	Alignment		99.9	24	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
9	<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
10	<a href="#">c5l6mC_</a>	Alignment		99.9	23	<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)
11	<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

12	<a href="#">d1y82a1</a>	Alignment		99.8	20	<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	20	<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		99.7	18	<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		99.7	16	<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		99.4	16	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
17	<a href="#">c2fe1A</a>	Alignment		99.4	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="#">c3i8oA</a>	Alignment		98.8	12	<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		98.8	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
20	<a href="#">d1w8ia</a>	Alignment		98.5	16	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
21	<a href="#">d1o4wa</a>	Alignment	not modelled	98.3	10	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
22	<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
23	<a href="#">c5f4hF</a>	Alignment	not modelled	98.2	16	<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
24	<a href="#">c2lqA</a>	Alignment	not modelled	98.0	17	<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	97.9	20	<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	97.9	18	<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	97.5	17	<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	97.1	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
29	<a href="#">c5yz4A</a>	Alignment	not modelled	96.9	13	<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="#">c2hwyB_</a>	Alignment	not modelled	91.3	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.
31	<a href="#">c4mj7B_</a>	Alignment	not modelled	87.5	12	<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
32	<a href="#">c3v33A_</a>	Alignment	not modelled	87.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonuclease zc3h12a; <b>PDBTitle:</b> crystal structure of mczip1 conserved domain with zinc-finger motif
33	<a href="#">c3v32B_</a>	Alignment	not modelled	87.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> ribonuclease zc3h12a; <b>PDBTitle:</b> crystal structure of mczip1 n-terminal conserved domain
34	<a href="#">c6g5iy_</a>	Alignment	not modelled	76.3	16	<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
35	<a href="#">c2mdtA_</a>	Alignment	not modelled	53.5	14	<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 sulfobolus solfataricus p2
36	<a href="#">c4g25A_</a>	Alignment	not modelled	52.4	20	<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
37	<a href="#">d1cmwa2</a>	Alignment	not modelled	52.2	31	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
38	<a href="#">c3zddA_</a>	Alignment	not modelled	42.0	38	<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
39	<a href="#">d1tfra2</a>	Alignment	not modelled	41.7	29	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
40	<a href="#">c5dizB_</a>	Alignment	not modelled	33.5	21	<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
41	<a href="#">c6md3F_</a>	Alignment	not modelled	29.3	15	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> F; <b>PDB Molecule:</b> rrp44p homologue; <b>PDBTitle:</b> structure of t. brucei rrp44 pin domain
42	<a href="#">d1xo1a2</a>	Alignment	not modelled	21.2	19	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
43	<a href="#">c2ihnA_</a>	Alignment	not modelled	19.4	26	<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
44	<a href="#">c1ut8B_</a>	Alignment	not modelled	14.7	19	<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="#">c1cmwA_</a>	Alignment	not modelled	11.5	31	<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
46	<a href="#">c6d6rK_</a>	Alignment	not modelled	11.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> K; <b>PDB Molecule:</b> exosome complex exonuclease rrp44; <b>PDBTitle:</b> human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
47	<a href="#">c3dy0B_</a>	Alignment	not modelled	7.8	22	<b>PDB header:</b> blood clotting, hydrolase inhibitor <b>Chain:</b> B; <b>PDB Molecule:</b> c-terminus plasma serine protease inhibitor; <b>PDBTitle:</b> crystal structure of cleaved pci bound to heparin
48	<a href="#">c1lq8H_</a>	Alignment	not modelled	7.4	22	<b>PDB header:</b> blood clotting <b>Chain:</b> H; <b>PDB Molecule:</b> plasma serine protease inhibitor; <b>PDBTitle:</b> crystal structure of cleaved protein c inhibitor
49	<a href="#">c1jqsB_</a>	Alignment	not modelled	7.3	12	<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
50	<a href="#">d1zcca2</a>	Alignment	not modelled	5.5	20	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC