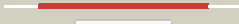



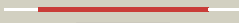


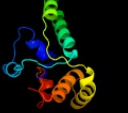
















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1720c_(-)_1947037_1947426
Date	Fri Aug 2 13:30:32 BST 2019
Unique Job ID	101fa08956153f70

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1v8pa_</a>	 Alignment		99.9	18	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
2	<a href="#">c1v8pK_</a>	 Alignment		99.9	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
3	<a href="#">d2fe1a1</a>	 Alignment		99.8	27	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
4	<a href="#">c2fe1A_</a>	 Alignment		99.8	27	<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
5	<a href="#">c4xgrG_</a>	 Alignment		99.7	13	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> G: <b>PDB Molecule:</b> ribonuclease vapc30; <b>PDBTitle:</b> crystal structure of addiction module from mycobacterial species
6	<a href="#">c3zvK_</a>	 Alignment		99.6	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="#">c3tndC_</a>	 Alignment		99.5	13	<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="#">c6nkIA_</a>	 Alignment		99.5	14	<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
9	<a href="#">c5l6mC_</a>	 Alignment		99.5	16	<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="#">c5wzfB_</a>	 Alignment		99.5	14	<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
11	<a href="#">d2h1ca1</a>	 Alignment		99.4	20	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain

12	<a href="#">c3h87B_</a>	Alignment		99.4	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
13	<a href="#">c5x3tD_</a>	Alignment		99.4	14	<b>PDB header:</b> antitoxin/toxin <b>Chain:</b> D: <b>PDB Molecule:</b> ribonuclease vapc26; <b>PDBTitle:</b> vapbc from mycobacterium tuberculosis
14	<a href="#">c4chgC_</a>	Alignment		99.4	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
15	<a href="#">c6a7vG_</a>	Alignment		99.3	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
16	<a href="#">c5sv2A_</a>	Alignment		99.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease vapc21; <b>PDBTitle:</b> toxin vapc21 from mycobacterium tuberculosis
17	<a href="#">c3dboB_</a>	Alignment		99.2	15	<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
18	<a href="#">d1v96a1</a>	Alignment		99.1	17	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
19	<a href="#">d1y82a1</a>	Alignment		99.0	17	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
20	<a href="#">c3i8oA_</a>	Alignment		98.5	11	<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.
21	<a href="#">c3ix7A_</a>	Alignment	not modelled	98.4	18	<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
22	<a href="#">c5ywwA_</a>	Alignment	not modelled	98.2	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="#">d1w8ia_</a>	Alignment	not modelled	98.1	14	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
24	<a href="#">c5f4hF_</a>	Alignment	not modelled	98.1	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
25	<a href="#">c2lcqA_</a>	Alignment	not modelled	97.6	13	<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
26	<a href="#">d1o4wa_</a>	Alignment	not modelled	97.4	16	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
27	<a href="#">c2hwwC_</a>	Alignment	not modelled	96.5	14	<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="#">c6g5iy_</a>	Alignment	not modelled	87.9	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
						<b>PDB header:</b> ribosome

29	<a href="#">c5jppd_</a>	Alignment	not modelled	79.6	11	<b>Chain:</b> D: <b>PDB Molecule:</b> wd40 domain proteins; <b>PDBTitle:</b> cryo-em structure of the 90s pre-ribosome
30	<a href="#">c2mdtA_</a>	Alignment	not modelled	75.1	13	<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
31	<a href="#">c2hwyB_</a>	Alignment	not modelled	73.8	24	<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="#">c5yz4A_</a>	Alignment	not modelled	71.7	16	<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
33	<a href="#">c3v33A_</a>	Alignment	not modelled	58.3	22	<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
34	<a href="#">c3v32B_</a>	Alignment	not modelled	48.6	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
35	<a href="#">d2gpra_</a>	Alignment	not modelled	9.2	17	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
36	<a href="#">c3iz5t_</a>	Alignment	not modelled	8.9	19	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 60s ribosomal protein l19 (l19e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
37	<a href="#">d1qlaf_</a>	Alignment	not modelled	8.2	21	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
38	<a href="#">c1jqsB_</a>	Alignment	not modelled	7.9	6	<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
39	<a href="#">c4mj7B_</a>	Alignment	not modelled	7.5	13	<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
40	<a href="#">c4behA_</a>	Alignment	not modelled	6.8	29	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> 60s acidic ribosomal protein p1; <b>PDBTitle:</b> solution structure of human ribosomal protein p1.p2 heterodimer
41	<a href="#">d2f3ga_</a>	Alignment	not modelled	6.4	21	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
42	<a href="#">d1cmwa2</a>	Alignment	not modelled	6.2	30	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
43	<a href="#">c3izct_</a>	Alignment	not modelled	6.1	19	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 60s ribosomal protein rpl19 (l19e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
44	<a href="#">c2lbfA_</a>	Alignment	not modelled	5.9	29	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 60s acidic ribosomal protein p1; <b>PDBTitle:</b> solution structure of the dimerization domain of human ribosomal2 protein p1/p2 heterodimer
45	<a href="#">d1gxja_</a>	Alignment	not modelled	5.9	27	<b>Fold:</b> Smc hinge domain <b>Superfamily:</b> Smc hinge domain <b>Family:</b> Smc hinge domain
46	<a href="#">d1gpra_</a>	Alignment	not modelled	5.9	17	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
47	<a href="#">c2wd5A_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> structural maintenance of chromosomes protein 1a; <b>PDBTitle:</b> smc hinge heterodimer (mouse) <b>PDB header:</b> cell cycle
48	<a href="#">c3l51B_</a>	Alignment	not modelled	5.4	17	<b>Chain:</b> B: <b>PDB Molecule:</b> structural maintenance of chromosomes protein 4; <b>PDBTitle:</b> crystal structure of the mouse condensin hinge domain
49	<a href="#">d1gxla_</a>	Alignment	not modelled	5.2	27	<b>Fold:</b> Smc hinge domain <b>Superfamily:</b> Smc hinge domain <b>Family:</b> Smc hinge domain