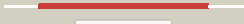



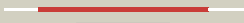




























Phyre2

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Description	RVBD0240 (-) _289345_289782
Date	Tue Jul 23 14:50:30 BST 2019
Unique Job ID	73ee794efda7ec32

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2h1ca1	 Alignment		99.9	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
2	c5wzfB_	 Alignment		99.8	18	PDB header: hydrolase Chain: B: PDB Molecule: 23s rrna-specific endonuclease vapc20; PDBTitle: crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
3	c3zvkc_	 Alignment		99.8	16	PDB header: antitoxin/toxin/dna Chain: C: PDB Molecule: toxin of toxin-antitoxin system; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to 2 a dna fragment from their promoter
4	c6nkiA_	 Alignment		99.8	13	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
5	c5l6mC_	 Alignment		99.8	16	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
6	c5x3tD_	 Alignment		99.8	17	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
7	c3tndC_	 Alignment		99.8	17	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
8	c4xgrG_	 Alignment		99.7	16	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
9	c4chgC_	 Alignment		99.7	18	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
10	c6a7vG_	 Alignment		99.6	15	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
11	c3h87B_	 Alignment		99.6	13	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis

12	d1v96a1	Alignment		99.6	7	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
13	c5sv2A_	Alignment		99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
14	d1y82a1	Alignment		99.5	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
15	c3dboB_	Alignment		99.5	15	PDB header: toxin/antitoxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis
16	d2fe1a1	Alignment		99.4	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c2fe1A_	Alignment		99.4	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
18	d1w8ia_	Alignment		99.2	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	d1v8pa_	Alignment		98.3	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c1v8pK_	Alignment		98.3	15	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
21	c3ix7A_	Alignment	not modelled	97.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ttha0540; PDBTitle: crystal structure of a domain of functionally unknown protein from2 thermus thermophilus hb8
22	c3i8oA_	Alignment	not modelled	97.8	13	PDB header: rna binding protein Chain: A: PDB Molecule: kh domain-containing protein mj1533; PDBTitle: a domain of a functionally unknown protein from methanocaldococcus2 jannaschii dsm 2661.
23	c2hwwC_	Alignment	not modelled	96.7	19	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
24	c5ywwA_	Alignment	not modelled	96.6	16	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
25	d1o4wa_	Alignment	not modelled	96.5	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
26	c5f4hF_	Alignment	not modelled	96.5	16	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
27	c2lcqA_	Alignment	not modelled	93.5	11	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
28	c2hwyB_	Alignment	not modelled	91.1	17	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
						PDB header: transferase

29	c1b43A_	Alignment	not modelled	85.6	15	Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
30	c5jpdq_	Alignment	not modelled	83.1	18	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
31	c5yz4A_	Alignment	not modelled	75.2	13	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
32	c3oryA_	Alignment	not modelled	71.6	14	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
33	c4mj7B_	Alignment	not modelled	70.9	13	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
34	d1ul1x2	Alignment	not modelled	70.2	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
35	d1a77a2	Alignment	not modelled	70.1	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
36	c3q8IA_	Alignment	not modelled	68.1	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+
37	d1tfra2	Alignment	not modelled	63.4	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	d1rxwa2	Alignment	not modelled	63.3	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
39	c3qeaZ_	Alignment	not modelled	62.0	26	PDB header: hydrolase/dna Chain: Z: PDB Molecule: exonuclease 1; PDBTitle: crystal structure of human exonuclease 1 exo1 (wt) in complex with dna2 (complex ii)
40	d1b43a2	Alignment	not modelled	60.4	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
41	c2izoA_	Alignment	not modelled	59.6	18	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
42	c3zddA_	Alignment	not modelled	56.6	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
43	c1rxvA_	Alignment	not modelled	54.6	15	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
44	c1ul1Y_	Alignment	not modelled	53.8	21	PDB header: hydrolase/dna binding protein Chain: Y: PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
45	c5t9jB_	Alignment	not modelled	52.6	16	PDB header: hydrolase Chain: B: PDB Molecule: flap endonuclease gen homolog 1; PDBTitle: crystal structure of human gen1 in complex with holliday junction dna2 in the upper interface
46	d1mc8a2	Alignment	not modelled	52.2	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
47	c1a77A_	Alignment	not modelled	52.0	14	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
48	c4q0rB_	Alignment	not modelled	40.0	19	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna repair protein rad2; PDBTitle: the catalytic core of rad2 (complex i)
49	c1ut8B_	Alignment	not modelled	31.3	9	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
50	c4wa8A_	Alignment	not modelled	28.9	21	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: methanopyrus kandleri fen-1 nuclease
51	c2q5xA_	Alignment	not modelled	20.8	13	PDB header: protein transport Chain: A: PDB Molecule: nuclear pore complex protein nup98; PDBTitle: crystal structure of the c-terminal domain of hnup98
52	c2r8rB_	Alignment	not modelled	20.2	21	PDB header: transferase Chain: B: PDB Molecule: sensor protein; PDBTitle: crystal structure of the n-terminal region (19..243) of sensor protein2 kdpg from pseudomonas syringae pv. tomato str. dc3000
53	d1cmwa2	Alignment	not modelled	19.3	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
54	d1jx4a1	Alignment	not modelled	13.6	8	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
55	c5cngA_	Alignment	not modelled	12.6	16	PDB header: replication Chain: A: PDB Molecule: nuclease-like protein; PDBTitle: crystal structure of the holliday junction-resolving enzyme gen1 (wt)2 in complex with product dna, mg2+ and mn2+ ions

56	d1g8sa_	Alignment	not modelled	12.5	33	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Fibrillarlin homologue
57	d1k1sa1	Alignment	not modelled	11.8	14	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
58	c2ipxA_	Alignment	not modelled	11.4	50	PDB header: transferase Chain: A: PDB Molecule: rrna 2'-o-methyltransferase fibrillarlin; PDBTitle: human fibrillarlin
59	c2m7oA_	Alignment	not modelled	11.1	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein np_346341.1 from streptococcus pneumoniae
60	d1xo1a2	Alignment	not modelled	10.7	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
61	c2p0a_	Alignment	not modelled	10.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein duf871; PDBTitle: crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
62	c3v33A_	Alignment	not modelled	10.3	5	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
63	c6g5iy_	Alignment	not modelled	10.3	9	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
64	c3b8iF_	Alignment	not modelled	10.2	13	PDB header: lyase Chain: F: PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+
65	c3cuqA_	Alignment	not modelled	9.8	7	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
66	d1e9ya2	Alignment	not modelled	8.8	19	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
67	c5b04G_	Alignment	not modelled	8.8	12	PDB header: translation Chain: G: PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
68	d2gy9p1	Alignment	not modelled	8.6	22	Fold: Ribosomal protein S16 Superfamily: Ribosomal protein S16 Family: Ribosomal protein S16
69	d1xmba2	Alignment	not modelled	8.3	12	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
70	d1g8ma2	Alignment	not modelled	8.1	13	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
71	c2ihnA_	Alignment	not modelled	7.8	18	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
72	c2zmeA_	Alignment	not modelled	7.8	7	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
73	c3iwcD_	Alignment	not modelled	7.6	20	PDB header: lyase Chain: D: PDB Molecule: s-adenosylmethionine decarboxylase; PDBTitle: t. maritima adometdc complex with s-adenosylmethionine methyl ester
74	d1zcza2	Alignment	not modelled	7.5	16	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
75	c2vhhA_	Alignment	not modelled	7.4	17	PDB header: hydrolase Chain: A: PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
76	d1pkxa2	Alignment	not modelled	7.4	16	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
77	c1thzA_	Alignment	not modelled	6.7	13	PDB header: transferase, hydrolase Chain: A: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
78	c3v32B_	Alignment	not modelled	6.6	12	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
79	c3efaA_	Alignment	not modelled	6.3	14	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of putative n-acetyltransferase from lactobacillus2 plantarum
80	c2aivA_	Alignment	not modelled	6.3	9	PDB header: transport protein Chain: A: PDB Molecule: fragment of nucleoporin nup116/hsp116; PDBTitle: multiple conformations in the ligand-binding site of the yeast nuclear2 pore targeting domain of nup116p PDB header: lyase

81	c3mwbA_	Alignment	not modelled	6.0	11	Chain: A; PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aureus to 2.0a
82	d1m3ua_	Alignment	not modelled	5.7	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
83	c4mg4G_	Alignment	not modelled	5.5	27	PDB header: unknown function Chain: G; PDB Molecule: phosphonmutase; PDBTitle: crystal structure of a putative phosphonmutase from burkholderia2 cenocepacia j2315
84	c3w15A_	Alignment	not modelled	5.1	33	PDB header: protein transport Chain: A; PDB Molecule: peroxisomal targeting signal 2 receptor; PDBTitle: structure of peroxisomal targeting signal 2 (pts2) of saccharomyces2 cerevisiae 3-ketoacyl-coa thiolase in complex with pex7p and pex21p