

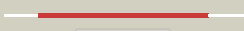





















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1397c_(-)_1574118_1574519
Date	Wed Jul 31 22:05:50 BST 2019
Unique Job ID	8678687cf930d4e6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6nkIA_	 Alignment		99.9	24	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
2	c3tndC_	 Alignment		99.9	22	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
3	c3zvkc_	 Alignment		99.9	19	PDB header: antitoxin/toxin/dna Chain: C: PDB Molecule: toxin of toxin-antitoxin system; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
4	c3h87B_	 Alignment		99.9	24	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
5	d2h1ca1	 Alignment		99.9	25	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
6	d1v96a1	 Alignment		99.9	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
7	c5l6mC_	 Alignment		99.9	22	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
8	c5sv2A_	 Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
9	d1y82a1	 Alignment		99.8	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
10	c4chgC_	 Alignment		99.8	25	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
11	c3dboB_	 Alignment		99.8	27	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

12	c4xgrG_	Alignment		99.8	16	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
13	c6a7vG_	Alignment		99.8	18	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
14	c5x3tD_	Alignment		99.7	17	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
15	c5wzfB_	Alignment		99.6	16	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
16	d2fe1a1	Alignment		99.5	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c2fe1A_	Alignment		99.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
18	c3ix7A_	Alignment		98.4	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
19	d1w8ia_	Alignment		98.3	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	d1v8pa_	Alignment		98.2	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
21	c1v8pK_	Alignment	not modelled	98.1	18	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
22	c3i8oA_	Alignment	not modelled	98.0	18	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	d1o4wa_	Alignment	not modelled	98.0	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c5ywwA_	Alignment	not modelled	97.9	13	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
25	c5f4hF_	Alignment	not modelled	97.8	16	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
26	c5yz4A_	Alignment	not modelled	97.5	15	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
27	c5jppd_	Alignment	not modelled	97.4	12	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
28	c2lcqA_	Alignment	not modelled	97.3	14	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
						PDB header: rna binding protein

29	c2hwwC_	Alignment	not modelled	95.9	26	Chain: C; PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
30	c4mj7B_	Alignment	not modelled	95.5	10	PDB header: rna binding protein Chain: B; PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
31	c2hwyB_	Alignment	not modelled	91.2	24	PDB header: rna binding protein Chain: B; PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
32	c6g5iy_	Alignment	not modelled	49.5	14	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
33	c3v33A_	Alignment	not modelled	41.9	18	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
34	c3v32B_	Alignment	not modelled	39.4	20	PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
35	c1jqsB_	Alignment	not modelled	11.3	24	PDB header: ribosome Chain: B; PDB Molecule: elongation factor g; PDBTitle: fitting of I11 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
36	c6hc2L_	Alignment	not modelled	11.0	67	PDB header: cell cycle Chain: L; PDB Molecule: nuclear mitotic apparatus protein 1; PDBTitle: crystal structure of numa/Ign hetero-hexamers
37	d1cmwa2	Alignment	not modelled	9.9	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	c6nkoA_	Alignment	not modelled	9.9	4	PDB header: unknown function Chain: A; PDB Molecule: forh; PDBTitle: crystal structure of forh
39	c3zddA_	Alignment	not modelled	9.9	14	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
40	d1pkxa1	Alignment	not modelled	9.7	12	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
41	d1zcza2	Alignment	not modelled	8.3	10	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
42	c4mitG_	Alignment	not modelled	8.2	10	PDB header: signaling protein Chain: G; PDB Molecule: serine/threonine protein kinase pak, putative; PDBTitle: crystal structure of e. histolytica racc bound to the ehpk4 pbd
43	d1g8ma1	Alignment	not modelled	7.5	12	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
44	d1g8ma2	Alignment	not modelled	7.4	14	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
45	c5xv8A_	Alignment	not modelled	7.3	18	PDB header: nuclear protein Chain: A; PDB Molecule: uv-stimulated scaffold protein a; PDBTitle: solution structure of the complex between uvssa acidic region and2 tfih p62 ph domain
46	d1pkxa2	Alignment	not modelled	7.1	21	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
47	c1dgrX_	Alignment	not modelled	6.8	19	PDB header: plant protein Chain: X; PDB Molecule: canavalin; PDBTitle: refined crystal structure of canavalin from jack bean
48	d1tfra2	Alignment	not modelled	6.7	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
49	d1ofcx1	Alignment	not modelled	5.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
50	d1gyxa_	Alignment	not modelled	5.8	30	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
51	d1ebfa1	Alignment	not modelled	5.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
52	c4rl4B_	Alignment	not modelled	5.8	14	PDB header: hydrolase Chain: B; PDB Molecule: gtp cyclohydrolase-2; PDBTitle: crystal structure of gtp cyclohydrolase ii from helicobacter pylori2 26695
53	d1a3qa1	Alignment	not modelled	5.6	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
54	d1u36a_	Alignment	not modelled	5.6	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain