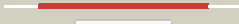



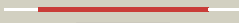



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2494 (-) _2808320_2808745
Date	Wed Aug 7 12:50:12 BST 2019
Unique Job ID	6c497e4a95aaf3fc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2h1ca1	 Alignment		99.8	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
2	c3zvkc_	 Alignment		99.8	13	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
3	c6a7vG_	 Alignment		99.8	16	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
4	c5x3tD_	 Alignment		99.8	18	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
5	c6nkIA_	 Alignment		99.8	10	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
6	c4chgC_	 Alignment		99.8	16	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
7	c2fe1A_	 Alignment		99.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
8	d2fe1a1	 Alignment		99.7	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
9	c3tndC_	 Alignment		99.7	14	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
10	c3h87B_	 Alignment		99.7	14	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
11	c5wzFB_	 Alignment		99.7	14	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

12	c4xgrG_	Alignment		99.7	15	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
13	d1v96a1	Alignment		99.7	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
14	c5sv2A_	Alignment		99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
15	c5l6mC_	Alignment		99.6	15	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
16	d1y82a1	Alignment		99.6	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c3dboB_	Alignment		99.6	13	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
18	d1w8ia_	Alignment		99.3	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	d1v8pa_	Alignment		99.3	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c1v8pK_	Alignment		99.2	22	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	99.1	20	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	99.1	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	d1o4wa_	Alignment	not modelled	98.6	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c2hwwC_	Alignment	not modelled	98.4	12	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
25	c5f4hF_	Alignment	not modelled	98.2	17	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
26	c5ywwA_	Alignment	not modelled	98.2	16	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
27	c2lcqA_	Alignment	not modelled	97.5	17	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
28	c5jppd_	Alignment	not modelled	97.0	16	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
						PDB header: hydrolase

29	c5yz4A_	Alignment	not modelled	96.8	12	Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
30	c2hwyB_	Alignment	not modelled	95.0	23	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c4mj7B_	Alignment	not modelled	94.3	6	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
32	c3v33A_	Alignment	not modelled	84.5	22	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
33	c3v32B_	Alignment	not modelled	83.5	25	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
34	c2mdtA_	Alignment	not modelled	58.9	20	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfolobus solfataricus p2
35	c6chgE_	Alignment	not modelled	30.9	26	PDB header: transferase Chain: E: PDB Molecule: klla0e03521p; PDBTitle: crystal structure of the yeast compass catalytic module
36	c3g36D_	Alignment	not modelled	24.9	42	PDB header: nuclear protein Chain: D: PDB Molecule: protein dpy-30 homolog; PDBTitle: crystal structure of the human dpy-30-like c-terminal domain
37	c6bx3N_	Alignment	not modelled	21.8	37	PDB header: gene regulation/transferase Chain: N: PDB Molecule: compass component sdc1; PDBTitle: structure of histone h3k4 methyltransferase
38	c5b52B_	Alignment	not modelled	21.7	22	PDB header: transcription Chain: B: PDB Molecule: h-ns family protein mvat; PDBTitle: crystal structure of the n-terminal domain of h-ns family protein turb
39	c4rtaB_	Alignment	not modelled	17.1	42	PDB header: protein binding Chain: B: PDB Molecule: protein dpy-30 homolog; PDBTitle: crystal structure of the dpy30 for ml/set1 compass h3k4 trimethylation
40	c6d6rK_	Alignment	not modelled	11.1	15	PDB header: hydrolase Chain: K: PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
41	c3dy0B_	Alignment	not modelled	10.3	33	PDB header: blood clotting, hydrolase inhibitor Chain: B: PDB Molecule: c-terminus plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved pci bound to heparin
42	c6nmiD_	Alignment	not modelled	9.9	19	PDB header: transcription Chain: D: PDB Molecule: general transcription factor iih subunit 4, p52; PDBTitle: cryo-em structure of the human tfiih core complex
43	c1lq8H_	Alignment	not modelled	9.7	33	PDB header: blood clotting Chain: H: PDB Molecule: plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved protein c inhibitor
44	d1cmwa2	Alignment	not modelled	9.7	35	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
45	c4g25A_	Alignment	not modelled	8.7	37	PDB header: rna binding protein Chain: A: PDB Molecule: pentatricopeptide repeat-containing protein at2g32230, PDBTitle: crystal structure of proteinaceous rna p 1 (prorp1) from a.2 thaliana, semet substituted form with sr
46	c2lr8A_	Alignment	not modelled	7.8	30	PDB header: apoptosis Chain: A: PDB Molecule: casp8-associated protein 2; PDBTitle: solution nmr structure of casp8-associated protein 2 from homo2 sapiens, northeast structural genomics consortium (nesg) target3 hr8150a
47	d1k1sa1	Alignment	not modelled	7.8	17	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
48	c1jb0M_	Alignment	not modelled	7.1	43	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem 1 reaction centre subunit xii; PDBTitle: crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
49	c4fe1M_	Alignment	not modelled	7.1	43	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: improving the accuracy of macromolecular structure refinement at 7 a2 resolution
50	d1jb0m_	Alignment	not modelled	7.1	43	Fold: Single transmembrane helix Superfamily: Subunit XII of photosystem I reaction centre, Psam Family: Subunit XII of photosystem I reaction centre, Psam
51	d2a3qa1	Alignment	not modelled	6.2	26	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
52	c2q4pA_	Alignment	not modelled	6.2	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein rs21-c6; PDBTitle: ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
53	d3by5a1	Alignment	not modelled	6.1	12	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
54	c3by5A_	Alignment	not modelled	6.1	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: cobalamin biosynthesis protein; PDBTitle: crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58

55	d2a7wa1	Alignment	not modelled	5.4	18	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)
56	c2a7wF_	Alignment	not modelled	5.4	18	PDB header: hydrolase Chain: F; PDB Molecule: phosphoribosyl-atp pyrophosphatase; PDBTitle: crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7