



















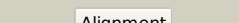



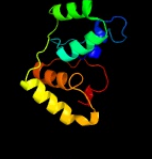

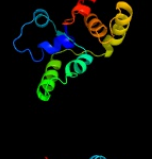
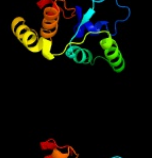
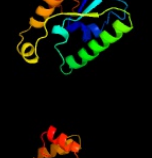
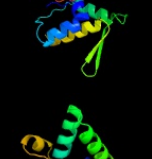
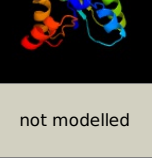


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1114 (-)_1239615_1239989
Date	Wed Jul 31 22:05:19 BST 2019
Unique Job ID	a3f8afd5c3cf7eec

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h87B_	 Alignment		99.9	19	PDB header: toxin/antitoxin Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
2	c5sv2A_	 Alignment		99.9	16	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
3	d1v96a1	 Alignment		99.9	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
4	c4chgC_	 Alignment		99.9	23	PDB header: toxin/antitoxin Chain: C; PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
5	c6a7vG_	 Alignment		99.9	22	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
6	c3zvkc_	 Alignment		99.9	23	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
7	c6nklA_	 Alignment		99.8	18	PDB header: antitoxin Chain: A; PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
8	c3dboB_	 Alignment		99.8	25	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
9	d2h1ca1	 Alignment		99.8	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
10	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
11	c5l6mC_	 Alignment		99.8	16	PDB header: hydrolase Chain: C; PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)

12	d1y82a1	Alignment		99.8	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
13	c4xqrG_	Alignment		99.8	17	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
14	c5x3tD_	Alignment		99.6	17	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
15	c5wzfB_	Alignment		99.6	23	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	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
17	d2fe1a1	Alignment		99.5	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	c3i8oA_	Alignment		99.1	19	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.
19	c3ix7A_	Alignment		98.9	24	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
20	c5ywwA_	Alignment		98.7	16	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
21	c5f4hF_	Alignment	not modelled	98.7	16	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
22	d1v8pa_	Alignment	not modelled	98.5	25	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
23	d1o4wa_	Alignment	not modelled	98.5	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c1v8pK_	Alignment	not modelled	98.5	25	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
25	d1w8ia_	Alignment	not modelled	98.3	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
26	c2hwwC_	Alignment	not modelled	98.0	25	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
27	c2lcqA_	Alignment	not modelled	97.7	13	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
28	c5jpdq_	Alignment	not modelled	97.7	20	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
29	c5yz4A_	Alignment	not modelled	97.4	17	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1;

						PDBTitle: structure of the pin domain endonuclease utp24
30	c4mj7B_	Alignment	not modelled	95.3	15	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	93.3	21	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
32	c6g5iy_	Alignment	not modelled	75.1	16	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	c2mdtA_	Alignment	not modelled	65.2	33	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
34	c3v33A_	Alignment	not modelled	59.4	14	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpi1 conserved domain with zinc-finger motif
35	c3v32B_	Alignment	not modelled	51.7	14	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpi1 n-terminal conserved domain
36	d1cmwa2	Alignment	not modelled	30.9	39	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
37	d1tfra2	Alignment	not modelled	29.0	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	d1xo1a2	Alignment	not modelled	21.1	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
39	c2ihnA_	Alignment	not modelled	12.5	4	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
40	d1rfma_	Alignment	not modelled	9.7	28	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
41	c3zddA_	Alignment	not modelled	9.3	30	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
42	c6dy3G_	Alignment	not modelled	7.1	37	PDB header: hydrolase Chain: G: PDB Molecule: n-acylethanolamine-hydrolyzing acid amidase alpha-subunit; PDBTitle: caenorhabditis elegans n-acylethanolamine-hydrolyzing acid amidase2 (naaa) ortholog
43	c2n7iA_	Alignment	not modelled	6.7	83	PDB header: hormone receptor Chain: A: PDB Molecule: prolactin receptor; PDBTitle: nmr structure of the prolactin receptor transmembrane domain
44	c6dy2C_	Alignment	not modelled	5.2	11	PDB header: hydrolase Chain: C: PDB Molecule: n-acylethanolamine acid amidase alpha-subunit; PDBTitle: guinea pig n-acylethanolamine-hydrolyzing acid amidase (naaa)2 covalently bound to beta-lactam inhibitor arn726
45	c2x5eA_	Alignment	not modelled	5.2	25	PDB header: unknown function Chain: A: PDB Molecule: upf0271 protein pa4511; PDBTitle: crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
46	c5zwoW_	Alignment	not modelled	5.2	20	PDB header: splicing Chain: W: PDB Molecule: 23 kda u4/u6.u5 small nuclear ribonucleoprotein component; PDBTitle: cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom