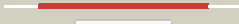



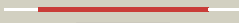



















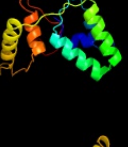


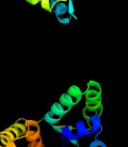


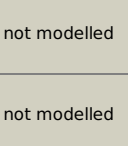


Phyre2


Email	mdejesus@rockefeller.edu
Description	RVBD0609 (-) _703489_703890
Date	Fri Jul 26 01:50:16 BST 2019
Unique Job ID	fa753aacfcc2f746

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xgrG_	 Alignment		100.0	41	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
2	d2h1ca1	 Alignment		99.9	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
3	c3h87B_	 Alignment		99.9	21	PDB header: toxin/antitoxin Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
4	c3zvkc_	 Alignment		99.9	10	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
5	c5wzfb_	 Alignment		99.8	20	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
6	c3dboB_	 Alignment		99.8	19	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
7	c5l6mC_	 Alignment		99.8	17	PDB header: hydrolase Chain: C; PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
8	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
9	c5sv2A_	 Alignment		99.8	14	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
10	c3tndC_	 Alignment		99.8	15	PDB header: translation, toxin Chain: C; PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
11	d1v96a1	 Alignment		99.8	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain

12	c6a7vG_	Alignment		99.8	21	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
13	c4chgC_	Alignment		99.8	23	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
14	c5x3tD_	Alignment		99.8	16	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
15	d1y82a1	Alignment		99.8	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
16	d2fe1a1	Alignment		99.7	25	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c2fe1A_	Alignment		99.7	25	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		99.4	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	d1v8pa_	Alignment		99.2	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c1v8pK_	Alignment		99.1	19	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	98.4	16	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	98.0	14	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	c2lcqA_	Alignment	not modelled	97.7	16	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
24	d1o4wa_	Alignment	not modelled	97.7	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
25	c5ywwA_	Alignment	not modelled	97.4	10	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archaeal ruvb-like holiday junction helicase
26	c5f4hF_	Alignment	not modelled	97.2	10	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archaeal ruvb-like holiday junction helicase
27	c2hwwC_	Alignment	not modelled	95.7	15	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
28	c5yz4A_	Alignment	not modelled	95.2	19	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
						PDB header: ribosome

29	c5jppd_	Alignment	not modelled	94.9	21	Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c2hwyB_	Alignment	not modelled	92.9	17	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c4mj7B_	Alignment	not modelled	89.7	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
32	c6g5iy_	Alignment	not modelled	88.3	27	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	c3v32B_	Alignment	not modelled	69.1	10	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 n-terminal conserved domain
34	c3v33A_	Alignment	not modelled	64.9	13	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 conserved domain with zinc-finger motif
35	d1cmwa2	Alignment	not modelled	50.2	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
36	d1xo1a2	Alignment	not modelled	31.8	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
37	c3zddA_	Alignment	not modelled	27.7	15	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
38	d1tfra2	Alignment	not modelled	24.9	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
39	d2reta1	Alignment	not modelled	13.0	11	Fold: Pili subunits Superfamily: Pili subunits Family: GPSII I/J protein-like
40	d1qd1a1	Alignment	not modelled	11.9	22	Fold: Ferredoxin-like Superfamily: Formiminotransferase domain of formiminotransferase-cyclodeaminase. Family: Formiminotransferase domain of formiminotransferase-cyclodeaminase.
41	c2retE_	Alignment	not modelled	11.0	11	PDB header: protein transport Chain: E: PDB Molecule: pseudopilin epsi; PDBTitle: the crystal structure of a binary complex of two pseudopilins: epsi2 and epsj from the type 2 secretion system of vibrio vulnificus
42	c2kebA_	Alignment	not modelled	10.3	15	PDB header: dna binding protein Chain: A: PDB Molecule: dna polymerase subunit alpha b; PDBTitle: nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
43	c4e2i3_	Alignment	not modelled	10.3	15	PDB header: hydrolase/dna binding protein Chain: 3: PDB Molecule: dna polymerase alpha subunit b; PDBTitle: the complex structure of the sv40 helicase large t antigen and p682 subunit of dna polymerase alpha-primase
44	c1ut8B_	Alignment	not modelled	10.2	12	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
45	c2ihnA_	Alignment	not modelled	8.9	12	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
46	d1pkxa2	Alignment	not modelled	7.8	15	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
47	c4djeE_	Alignment	not modelled	7.6	26	PDB header: transferase/vitamin-binding protein Chain: E: PDB Molecule: corrinoind/iron-sulfur protein large subunit; PDBTitle: crystal structure of folate-bound corrinoind iron-sulfur protein2 (cfesp) in complex with its methyltransferase (metr), co-crystallized3 with folate
48	d1g8ma2	Alignment	not modelled	7.3	15	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
49	d1zcza2	Alignment	not modelled	7.2	15	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
50	c1cmwA_	Alignment	not modelled	7.0	19	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain
51	c1qd1A_	Alignment	not modelled	6.9	22	PDB header: transferase Chain: A: PDB Molecule: formiminotransferase-cyclodeaminase; PDBTitle: the crystal structure of the formiminotransferase domain of2 formiminotransferase-cyclodeaminase.
52	c2h9aA_	Alignment	not modelled	6.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: carbon monoxide dehydrogenase corrinoind/iron-sulfur PDBTitle: corrinoind iron-sulfur protein
53	c3rqcB_	Alignment	not modelled	6.2	10	PDB header: transferase Chain: B: PDB Molecule: probable lipoamide acyltransferase; PDBTitle: crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum
54	c4pn7A_	Alignment	not modelled	6.1	19	PDB header: transcription Chain: A: PDB Molecule: putative transcription factor;

					PDBTitle: crystal structure of the tfiih p34 n-terminal domain
55	c2iswB_	Alignment 	not modelled	5.7	22
56	c1thzA_	Alignment 	not modelled	5.1	15

PDBTitle: crystal structure of the tfiih p34 n-terminal domain

PDB header:lyase

Chain: B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase;

PDBTitle: structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate

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