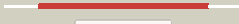



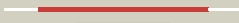


















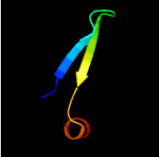




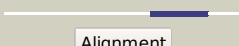

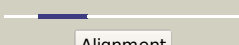
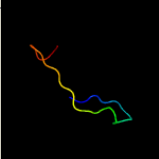
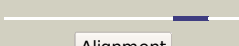
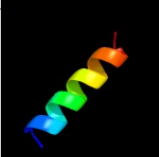
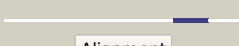


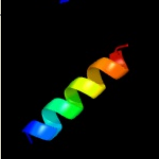

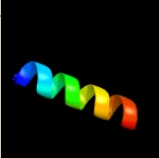
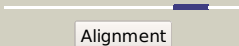
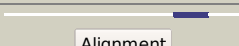
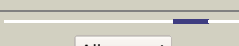
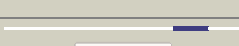
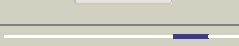
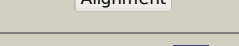
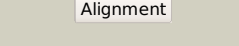




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1102c_(-)_1230665_1230976
Date	Wed Jul 31 22:05:18 BST 2019
Unique Job ID	b2be39055ee6cecf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ccaA_	 Alignment		100.0	98	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease mazf3; PDBTitle: crystal structure of mtb toxin
2	c4mzpC_	 Alignment		99.9	21	PDB header: hydrolase Chain: C: PDB Molecule: mazf mrna interferase; PDBTitle: mazf from s. aureus crystal form iii, c2221, 2.7 a
3	d1m1fa_	 Alignment		99.9	22	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
4	c5hjaz_	 Alignment		99.9	22	PDB header: hydrolase/rna Chain: A: PDB Molecule: endoribonuclease mazf9; PDBTitle: structure of m. tuberculosis mazf-mt1 (rv2801c) in complex with rna
5	d1ne8a_	 Alignment		99.9	24	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
6	d1ub4a_	 Alignment		99.9	18	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
7	c5wygC_	 Alignment		99.9	20	PDB header: hydrolase Chain: C: PDB Molecule: probable endoribonuclease mazf7; PDBTitle: the crystal structure of the apo form of mtb mazf
8	c5xe3B_	 Alignment		99.9	24	PDB header: hydrolase/antitoxin Chain: B: PDB Molecule: endoribonuclease mazf4; PDBTitle: endoribonuclease in complex with its cognate antitoxin from 2 mycobacterial species
9	c5hk3B_	 Alignment		99.9	26	PDB header: hydrolase/dna Chain: B: PDB Molecule: endoribonuclease mazf6; PDBTitle: crystal structure of m. tuberculosis mazf-mt3 t52d-f62d mutant in 2 complex with dna
10	c3jrza_	 Alignment		97.1	12	PDB header: toxin Chain: A: PDB Molecule: ccdb; PDBTitle: ccdbvfi-formii-ph5.6
11	d3vuba_	 Alignment		96.6	18	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: CcdB

12	c3d55A_			11.0	14	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
13	c6bwqB_			8.8	45	PDB header: metal binding protein Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometalase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
14	c3c19A_			8.8	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mk0293; PDBTitle: crystal structure of protein mk0293 from methanopyrus kandleri av19
15	d1rz4a1			8.3	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Eukaryotic translation initiation factor 3 subunit 12, eIF3k, C-terminal domain
16	c6n1bA_			7.8	13	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate-binding protein; PDBTitle: crystal structure of an n-acetylgalactosamine deacetylase from f.2 plautii in complex with blood group b trisaccharide
17	c4bxtD_			6.9	12	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
18	c5oiyG_			6.9	12	PDB header: viral protein Chain: G: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
19	c5oixA_			6.9	12	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
20	c5oiyE_			6.9	12	PDB header: viral protein Chain: E: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
21	c5oixE_		not modelled	6.9	12	PDB header: viral protein Chain: E: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
22	c5oiyC_		not modelled	6.9	12	PDB header: viral protein Chain: C: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
23	c5oixF_		not modelled	6.9	12	PDB header: viral protein Chain: F: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
24	c5oiyA_		not modelled	6.7	12	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
25	c5oiyB_		not modelled	6.7	12	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
26	c4bxtG_		not modelled	6.7	12	PDB header: viral protein Chain: G: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
27	c4bxtF_		not modelled	6.6	12	PDB header: viral protein Chain: F: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
28	c5oiyH_		not modelled	6.6	12	PDB header: viral protein Chain: H: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
29	c4bxtB_		not modelled	6.6	12	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein p;

29	c4uaxB_	Alignment	not modelled	6.6	12	PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
30	c5oixB_	Alignment	not modelled	6.6	12	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
31	c4bxtE_	Alignment	not modelled	6.6	12	PDB header: viral protein Chain: E: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
32	c5oixC_	Alignment	not modelled	6.6	12	PDB header: viral protein Chain: C: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
33	c3oeiB_	Alignment	not modelled	6.5	6	PDB header: toxin, protein binding Chain: B: PDB Molecule: relj (antitoxin rv3357); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
34	c5oixG_	Alignment	not modelled	6.5	12	PDB header: viral protein Chain: G: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
35	c4jhlA_	Alignment	not modelled	6.1	22	PDB header: hydrolase Chain: A: PDB Molecule: acetyl xylan esterase; PDBTitle: crystal structure of of axe2, an acetyl xylan esterase from geobacillus2 steaothermophilus
36	c5fmzB_	Alignment	not modelled	6.0	9	PDB header: transcription Chain: B: PDB Molecule: rna-directed rna polymerase catalytic subunit; PDBTitle: crystal structure of influenza b polymerase with bound 5' vrna
37	c4wsaB_	Alignment	not modelled	5.8	9	PDB header: transferase/rna Chain: B: PDB Molecule: rna-directed rna polymerase catalytic subunit; PDBTitle: crystal structure of influenza b polymerase bound to the vrna promoter2 (flub1 form)
38	c4q3kB_	Alignment	not modelled	5.3	11	PDB header: hydrolase Chain: B: PDB Molecule: mgs-m1; PDBTitle: crystal structure of mgs-m1, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library
39	c4bxtH_	Alignment	not modelled	5.2	12	PDB header: viral protein Chain: H: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
40	c5oixF_	Alignment	not modelled	5.2	12	PDB header: viral protein Chain: F: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
41	c2of3A_	Alignment	not modelled	5.2	12	PDB header: structural protein, cell cycle Chain: A: PDB Molecule: zyg-9; PDBTitle: tog domain structure from c.elegans zyg9
42	d2uubm1	Alignment	not modelled	5.1	20	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
43	c5oixD_	Alignment	not modelled	5.0	12	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
44	c5oixH_	Alignment	not modelled	5.0	12	PDB header: viral protein Chain: H: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
45	c5oixD_	Alignment	not modelled	5.0	12	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
46	c4bxtA_	Alignment	not modelled	5.0	12	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain