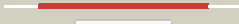



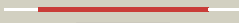

















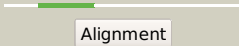

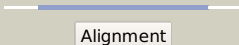

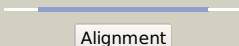

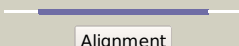
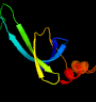
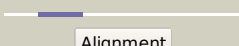

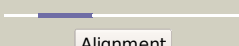

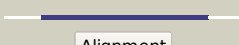




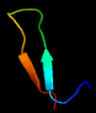

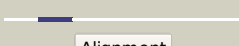

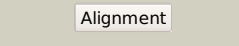
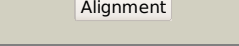
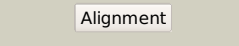



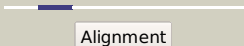
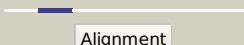
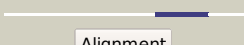


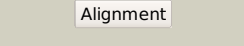


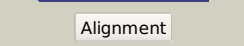
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1495 (-)_1686576_1686893
Date	Fri Aug 2 13:30:08 BST 2019
Unique Job ID	9e8a4081fdc06bfd

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xe3B_	 Alignment		100.0	97	PDB header: hydrolase/antitoxin Chain: B: PDB Molecule: endoribonuclease mazf4; PDBTitle: endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species
2	d1ub4a_	 Alignment		100.0	22	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
3	c5wygC_	 Alignment		100.0	26	PDB header: hydrolase Chain: C: PDB Molecule: probable endoribonuclease mazf7; PDBTitle: the crystal structure of the apo form of mtb mazf
4	d1m1fa_	 Alignment		100.0	33	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
5	d1ne8a_	 Alignment		100.0	24	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
6	c4mzpC_	 Alignment		100.0	29	PDB header: hydrolase Chain: C: PDB Molecule: mazf mrna interferase; PDBTitle: mazf from s. aureus crystal form iii, c2221, 2.7 a
7	c5hk3B_	 Alignment		99.9	31	PDB header: hydrolase/dna Chain: B: PDB Molecule: endoribonuclease mazf6; PDBTitle: crystal structure of m. tuberculosis mazf-mt3 t52d-f62d mutant in2 complex with dna
8	c5hjaz_	 Alignment		99.9	21	PDB header: hydrolase/rna Chain: A: PDB Molecule: endoribonuclease mazf9; PDBTitle: structure of m. tuberculosis mazf-mt1 (rv2801c) in complex with rna
9	c5ccaA_	 Alignment		99.9	26	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease mazf3; PDBTitle: crystal structure of mtb toxin
10	d3vuba_	 Alignment		95.9	11	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: CcdB
11	c3jrza_	 Alignment		95.9	11	PDB header: toxin Chain: A: PDB Molecule: ccdb; PDBTitle: ccdbvfi-formii-ph5.6

12	c5ikjA	 Alignment		57.9	28	PDB header: transcription Chain: A; PDB Molecule: cryptic loci regulator 2; PDBTitle: structure of clr2 bound to the clr1 c-terminus
13	c3llrA	 Alignment		25.2	22	PDB header: transferase Chain: A; PDB Molecule: dna (cytosine-5)-methyltransferase 3a; PDBTitle: crystal structure of the pwpp domain of human dna (cytosine-5-)-2 methyltransferase 3 alpha
14	d1h3za	 Alignment		21.6	12	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
15	c2l89A	 Alignment		19.4	16	PDB header: protein binding Chain: A; PDB Molecule: pwpp domain-containing protein 1; PDBTitle: solution structure of pdp1 pwpp domain reveals its unique binding2 sites for methylated h4k20 and dna
16	c4me8A	 Alignment		18.3	9	PDB header: hydrolase Chain: A; PDB Molecule: signal peptidase i; PDBTitle: crystal structure of a signal peptidase i (ef3073) from enterococcus2 faecalis v583 at 2.27 a resolution
17	c2z3tD	 Alignment		18.0	19	PDB header: oxidoreductase Chain: D; PDB Molecule: cytochrome p450; PDBTitle: crystal structure of substrate free cytochrome p450 stap2 (cyp245a1)
18	c4rmoA	 Alignment		9.8	12	PDB header: toxin/rna Chain: A; PDB Molecule: cptn toxin; PDBTitle: crystal structure of the cptn type iii toxin-antitoxin system from2 eubacterium rectale
19	c4z5qA	 Alignment		9.2	29	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450 hydroxylase; PDBTitle: crystal structure of the lnmz cytochrome p450 hydroxylase from the2 leinamycin biosynthetic pathway of streptomyces atroolivaceus s-1403 at 1.8 a resolution
20	c2dkkA	 Alignment		9.2	18	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450; PDBTitle: structure/function studies of cytochrome p450 158a1 from streptomyces2 coelicolor a3(2)
21	d1rz4a1	 Alignment	not modelled	7.9	11	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
22	c1pjtB	 Alignment	not modelled	7.9	31	PDB header: transferase/oxidoreductase/lyase Chain: B; PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelataze for3 siroheme synthesis
23	d1okja2	 Alignment	not modelled	7.4	30	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
24	c2of3A	 Alignment	not modelled	6.6	8	PDB header: structural protein, cell cycle Chain: A; PDB Molecule: zyg-9; PDBTitle: tog domain structure from c.elegans zyg9
25	c3zeyM	 Alignment	not modelled	6.6	22	PDB header: ribosome Chain: M; PDB Molecule: 40s ribosomal protein s18, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
26	c4xe3B	 Alignment	not modelled	6.6	27	PDB header: oxidoreductase Chain: B; PDB Molecule: cytochrome p-450; PDBTitle: olep, the cytochrome p450 epoxidase from streptomyces antibioticus2 involved in oleandomycin biosynthesis: functional analysis and3 crystallographic structure in complex with clotrimazole.
27	d1s1fa	 Alignment	not modelled	6.5	27	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
						PDB header: anti-hypertensive, anti-viral protein

28	c1bdsA_		Alignment	not modelled	6.1	43	Chain: A: PDB Molecule: bds-i; PDBTitle: determination of the three-dimensional solution structure of the2 antihypertensive and antiviral protein bds-i from the sea anemone3 anemonia sulcata. a study using nuclear magnetic resonance and hybrid4 distance geometry-dynamical simulated annealing
29	d1bdsa_		Alignment	not modelled	6.1	43	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
30	c2zkqm_		Alignment	not modelled	6.1	19	PDB header: ribosomal protein/rna Chain: M: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
31	c5zc2B_		Alignment	not modelled	6.0	8	PDB header: flavoprotein Chain: B: PDB Molecule: p-hydroxyphenylacetate 3-hydroxylase, reductase component; PDBTitle: acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
32	c1qp6B_		Alignment	not modelled	6.0	43	PDB header: de novo protein Chain: B: PDB Molecule: protein (alpha2d); PDBTitle: solution structure of alpha2d
33	d2daqal		Alignment	not modelled	5.8	9	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
34	c1cffB_		Alignment	not modelled	5.4	43	PDB header: calmodulin Chain: B: PDB Molecule: calcium pump; PDBTitle: nmr solution structure of a complex of calmodulin with a binding2 peptide of the ca2+-pump
35	c3iz6M_		Alignment	not modelled	5.4	15	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18 (s13p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
36	c2gfuA_		Alignment	not modelled	5.3	17	PDB header: dna binding protein Chain: A: PDB Molecule: dna mismatch repair protein msh6; PDBTitle: nmr solution structure of the pwwp domain of mismatch2 repair protein hmsh6