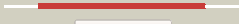



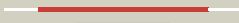

















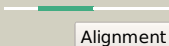
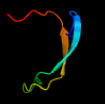
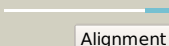
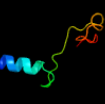
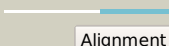
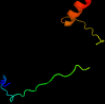


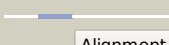

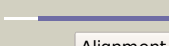

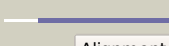

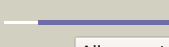



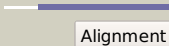
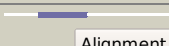
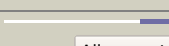

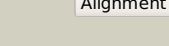

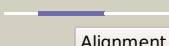



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2063A_(RVBD2063A)_2321065_2321475
Date	Mon Aug 5 13:25:17 BST 2019
Unique Job ID	3abb3586e299ebad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5wygC_	 Alignment		100.0	100	PDB header: hydrolase Chain: C: PDB Molecule: probable endoribonuclease mazf7; PDBTitle: the crystal structure of the apo form of mtb mazf
2	c4mzpC_	 Alignment		100.0	27	PDB header: hydrolase Chain: C: PDB Molecule: mazf mrna interferase; PDBTitle: mazf from s. aureus crystal form iii, c2221, 2.7 a
3	d1ne8a_	 Alignment		99.9	23	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
4	c5hjjA_	 Alignment		99.9	32	PDB header: hydrolase/rna Chain: A: PDB Molecule: endoribonuclease mazf9; PDBTitle: structure of m. tuberculosis mazf-mt1 (rv2801c) in complex with rna
5	c5xe3B_	 Alignment		99.9	26	PDB header: hydrolase/antitoxin Chain: B: PDB Molecule: endoribonuclease mazf4; PDBTitle: endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species
6	d1m1fa_	 Alignment		99.9	25	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
7	d1ub4a_	 Alignment		99.9	29	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
8	c5hk3B_	 Alignment		99.9	19	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
9	c5ccaA_	 Alignment		99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease mazf3; PDBTitle: crystal structure of mtb toxin
10	c3jrZA_	 Alignment		95.1	17	PDB header: toxin Chain: A: PDB Molecule: ccdb; PDBTitle: ccdbvfi-formii-ph5.6
11	d3vuba_	 Alignment		93.0	18	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: CcdB

12	c5ikjA	 Alignment		43.1	17	PDB header: transcription Chain: A; PDB Molecule: cryptic loci regulator 2; PDBTitle: structure of clr2 bound to the clr1 c-terminus
13	c4ijrA	 Alignment		37.6	11	PDB header: oxidoreductase Chain: A; PDB Molecule: d-arabinose dehydrogenase [nad(p)+] heavy chain; PDBTitle: crystal structure of saccharomyces cerevisiae arabinose dehydrogenase2 ara1 complexed with nadph
14	c4bedA	 Alignment		33.6	21	PDB header: oxygen transport Chain: A; PDB Molecule: hemocyanin klh1; PDBTitle: keyhole limpet hemocyanin (klh): 9a cryoem structure and molecular2 model of the klh1 didecamer reveal the interfaces and intricate3 topology of the 160 functional units
15	c2l89A	 Alignment		32.6	16	PDB header: protein binding Chain: A; PDB Molecule: ppwp domain-containing protein 1; PDBTitle: solution structure of pdp1 ppwp domain reveals its unique binding2 sites for methylated h4k20 and dna
16	c4me8A	 Alignment		23.0	20	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	c3llrA	 Alignment		15.0	17	PDB header: transferase Chain: A; PDB Molecule: dna (cytosine-5)-methyltransferase 3a; PDBTitle: crystal structure of the ppwp domain of human dna (cytosine-5-)-2 methyltransferase 3 alpha
18	c5vc8B	 Alignment		14.4	12	PDB header: dna binding protein Chain: B; PDB Molecule: histone-lysine n-methyltransferase nsd2; PDBTitle: crystal structure of the whsc1 ppwp1 domain
19	c2zkrt	 Alignment		13.8	21	PDB header: ribosomal protein/rna Chain: T; PDB Molecule: rna expansion segment es39 part iii; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
20	c3mxuA	 Alignment		12.5	24	PDB header: oxidoreductase Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from bartonella2 henselae
21	d1h3za	 Alignment	not modelled	12.1	14	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
22	d1okja2	 Alignment	not modelled	11.7	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
23	c4m8bR	 Alignment	not modelled	11.6	21	PDB header: transcription/dna Chain: R; PDB Molecule: yhr177w; PDBTitle: fungal protein
24	c4es2A	 Alignment	not modelled	10.8	12	PDB header: hydrolase Chain: A; PDB Molecule: bh0342 protein; PDBTitle: double-stranded endonuclease activity in b. halodurans clustered2 regularly interspaced short palindromic repeats (crispr)-associated3 cas2 protein
25	d1rz4a1	 Alignment	not modelled	10.6	22	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
26	c6n1bA	 Alignment	not modelled	10.6	14	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
27	d1pz1a	 Alignment	not modelled	10.5	31	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
28	c4qtkB	 Alignment	not modelled	10.1	57	PDB header: transcription/dna Chain: B; PDB Molecule: white-opaque regulator 1; PDBTitle: complex of wopr domain of wor1 in candida albicans with the 17bp dsdna

29	c3bcxA	Alignment	not modelled	9.0	14	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase
30	c2jysA	Alignment	not modelled	8.7	10	PDB header: hydrolase Chain: A: PDB Molecule: protease/reverse transcriptase; PDBTitle: solution structure of simian foamy virus (mac) protease
31	d1onla	Alignment	not modelled	8.4	22	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
32	d1zaka2	Alignment	not modelled	8.1	11	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
33	d1cxqa	Alignment	not modelled	8.1	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
34	d3e9va1	Alignment	not modelled	7.9	21	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
35	c2edgA	Alignment	not modelled	7.8	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: solution structure of the gcv_h domain from mouse glycine
36	c5zc2B	Alignment	not modelled	7.6	14	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)
37	d1b12a	Alignment	not modelled	7.2	21	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: Type 1 signal peptidase
38	c2gya3	Alignment	not modelled	7.2	13	PDB header: ribosome Chain: 3: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: structure of the 50s subunit of a pre-translocational e. coli ribosome2 obtained by fitting atomic models for rna and protein components into3 cryo-em map emd-1056
39	c2jnsA	Alignment	not modelled	6.7	8	PDB header: unknown function Chain: A: PDB Molecule: bromodomain-containing protein 4; PDBTitle: solution structure of the bromodomain-containing protein 42 et domain
40	c3iftA	Alignment	not modelled	5.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
41	d2daq1	Alignment	not modelled	5.9	17	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
42	d1coa	Alignment	not modelled	5.9	13	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
43	c5v1eA	Alignment	not modelled	5.8	50	PDB header: antimicrobial protein Chain: A: PDB Molecule: guavanin 2; PDBTitle: suboptimization of a glycine rich peptide allows the combinatorial2 space exploration for designing novel antimicrobial peptides
44	c3w1hB	Alignment	not modelled	5.7	14	PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) selenium transferase; PDBTitle: crystal structure of the selenocysteine synthase sela from aquifex2 aeolicus
45	c1zx4B	Alignment	not modelled	5.3	15	PDB header: cell cycle Chain: B: PDB Molecule: plasmid partition par b protein; PDBTitle: structure of parb bound to dna