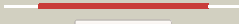
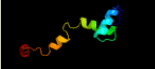

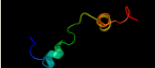

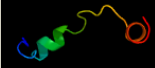







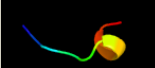








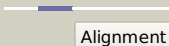
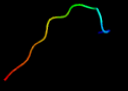
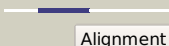

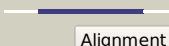



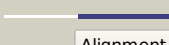
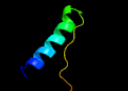
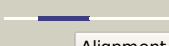


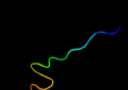
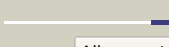


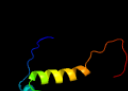
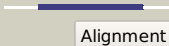
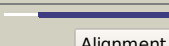


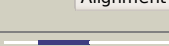
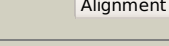
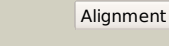
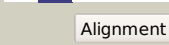
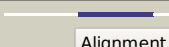


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2009_(-)_2258038_2258280
Date	Mon Aug 5 13:25:11 BST 2019
Unique Job ID	3323313d435efc23

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6a7vU_	 Alignment		99.6	56	PDB header: toxin/antitoxin Chain: U; PDB Molecule: antitoxin vappb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
2	c4chgJ_	 Alignment		99.5	100	PDB header: toxin/antitoxin Chain: J; PDB Molecule: antitoxin vappb15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
3	c4chgG_	 Alignment		99.0	100	PDB header: toxin/antitoxin Chain: G; PDB Molecule: antitoxin vappb15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
4	c5vgtA_	 Alignment		71.4	21	PDB header: viral protein Chain: A; PDB Molecule: gene 7 protein; PDBTitle: x-ray structure of bacteriophage sf6 tail adaptor protein gp7
5	c2m4hA_	 Alignment		54.5	19	PDB header: viral protein Chain: A; PDB Molecule: feline calicivirus vpg protein; PDBTitle: solution structure of the core domain (10-76) of the feline2 calicivirus vpg protein
6	c2mxdA_	 Alignment		45.7	20	PDB header: viral protein Chain: A; PDB Molecule: viral protein genome-linked; PDBTitle: solution structure of vpg of porcine sapovirus
7	c1xrxD_	 Alignment		24.1	60	PDB header: replication inhibitor Chain: D; PDB Molecule: seqa protein; PDBTitle: crystal structure of a dna-binding protein
8	d1xrx1	 Alignment		24.1	60	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like
9	c3fmtF_	 Alignment		21.2	60	PDB header: replication inhibitor/dna Chain: F; PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna
10	d2bj7a1	 Alignment		18.3	15	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
11	d1jcb2	 Alignment		15.6	18	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT

12	c5odlA_	 Alignment		11.3	23	PDB header: dna binding protein Chain: A; PDB Molecule: single-stranded dna-binding protein; PDBTitle: single-stranded dna-binding protein from bacteriophage enc34 in2 complex with ssdna
13	c4e0fB_	 Alignment		9.7	41	PDB header: transferase Chain: B; PDB Molecule: riboflavin synthase subunit alpha; PDBTitle: crystallographic structure of trimeric riboflavin synthase from2 brucella abortus in complex with riboflavin
14	d2hzab1	 Alignment		9.3	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
15	d2ieaa3	 Alignment		9.2	41	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
16	c5mu4A_	 Alignment		8.6	32	PDB header: viral protein Chain: A; PDB Molecule: tail tubular protein a; PDBTitle: tail tubular protein a of klebsiella pneumoniae bacteriophage kp32
17	c1i8dB_	 Alignment		8.2	47	PDB header: transferase Chain: B; PDB Molecule: riboflavin synthase; PDBTitle: crystal structure of riboflavin synthase
18	c1kzIA_	 Alignment		8.1	24	PDB header: transferase Chain: A; PDB Molecule: riboflavin synthase; PDBTitle: riboflavin synthase from s.pombe bound to2 carboxyethylumazine
19	c3i1IC_	 Alignment		8.1	33	PDB header: hydrolase Chain: C; PDB Molecule: hemagglutinin-esterase protein; PDBTitle: structure of porcine torovirus hemagglutinin-esterase in complex with2 its receptor
20	c1q5vB_	 Alignment		7.8	16	PDB header: transcription Chain: B; PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
21	d2hzaa1	 Alignment	not modelled	7.7	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
22	c6enoA_	 Alignment	not modelled	7.6	14	PDB header: oxidoreductase Chain: A; PDB Molecule: dehydratase family protein; PDBTitle: double cubane cluster oxidoreductase
23	c4kIkA_	 Alignment	not modelled	7.6	46	PDB header: unknown function Chain: A; PDB Molecule: phage-related protein duf2815; PDBTitle: phage-related protein duf2815 from enterococcus faecalis
24	c3dpgA_	 Alignment	not modelled	7.6	44	PDB header: hydrolase/dna Chain: A; PDB Molecule: sgrair restriction enzyme; PDBTitle: sgrai with noncognate dna bound
25	d1i8da2	 Alignment	not modelled	7.4	47	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Riboflavin synthase
26	c3l4gL_	 Alignment	not modelled	6.7	24	PDB header: ligase Chain: L; PDB Molecule: phenylalanyl-trna synthetase beta chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
27	c4jg2A_	 Alignment	not modelled	6.4	38	PDB header: unknown function Chain: A; PDB Molecule: phage-related protein; PDBTitle: structure of phage-related protein from bacillus cereus atcc 10987
28	c2vxzA_	 Alignment	not modelled	6.2	23	PDB header: viral protein Chain: A; PDB Molecule: pyrsv_gp04; PDBTitle: crystal structure of hypothetical protein pyrsv_gp04 from pyrobaculum2 spherical virus
						PDB header: transcription

29	c2bj3D_	Alignment	not modelled	5.8	15	Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nkr-apo
30	c5n6nC_	Alignment	not modelled	5.7	21	PDB header: signaling protein Chain: C: PDB Molecule: neutral trehalase; PDBTitle: crystal structure of the 14-3-3:neutral trehalase nth1 complex
31	d1uerc2	Alignment	not modelled	5.6	36	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
32	c5m4aA_	Alignment	not modelled	5.5	21	PDB header: hydrolase Chain: A: PDB Molecule: neutral trehalase; PDBTitle: neutral trehalase nth1 from saccharomyces cerevisiae in complex with2 trehalose
33	c2m1bA_	Alignment	not modelled	5.4	40	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulatory protein, c terminal family PDBTitle: solution structure of the chxr dna-binding domain
34	c2ns5A_	Alignment	not modelled	5.1	25	PDB header: signaling protein Chain: A: PDB Molecule: partitioning-defective 3 homolog; PDBTitle: the conserved n-terminal domain of par-3 adopts a novel pb1-2 like structure required for par-3 oligomerization and3 apical membrane localization
35	d1kzla2	Alignment	not modelled	5.1	24	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Riboflavin synthase
36	c1yx5A_	Alignment	not modelled	5.1	40	PDB header: hydrolase Chain: A: PDB Molecule: 26s proteasome non-atpase regulatory subunit 4; PDBTitle: solution structure of s5a uim-1/ubiquitin complex
37	d1ma1a2	Alignment	not modelled	5.1	44	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain