




















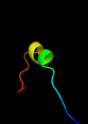

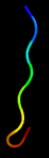




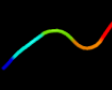
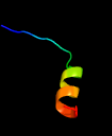



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2758c (-) _3070593_3070859
Date	Wed Aug 7 12:50:41 BST 2019
Unique Job ID	70581ac758872403

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6a7vU_	 Alignment		98.0	38	PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vappb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
2	c1ib8A_	 Alignment		37.7	30	PDB header: nucleic acid binding protein Chain: A: PDB Molecule: conserved protein sp14.3; PDBTitle: solution structure and function of a conserved protein2 sp14.3 encoded by an essential streptococcus pneumoniae3 gene
3	c3nctC_	 Alignment		24.3	50	PDB header: dna binding protein, chaperone Chain: C: PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
4	c3nvtA_	 Alignment		23.0	19	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
5	c5gl6A_	 Alignment		19.3	42	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome maturation factor rimp; PDBTitle: msmeg rimp
6	c4e6fB_	 Alignment		16.7	30	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4468 family protein (bacova_04320) from2 bacteroides ovatus atcc 8483 at 1.49 a resolution
7	c3f5hB_	 Alignment		14.2	42	PDB header: protein binding Chain: B: PDB Molecule: type i polyketide synthase pikaiii, type i polyketide PDBTitle: crystal structure of fused docking domains from pikaiii and pikaiv of2 the pikromycin polyketide synthase
8	c3lj4i_	 Alignment		13.8	58	PDB header: viral protein Chain: I: PDB Molecule: portal protein; PDBTitle: bacteriophage p22 portal protein bound to middle tail factor gp4. this2 file contain the first biological assembly
9	c2k5jB_	 Alignment		10.7	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
10	c2ehoL_	 Alignment		10.5	27	PDB header: replication Chain: L: PDB Molecule: gins complex subunit 3; PDBTitle: crystal structure of human gins complex
11	c2qs7D_	 Alignment		9.9	25	PDB header: oxidoreductase Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative oxidoreductase of the dsre/dsrf-like2 family (sso1126) from sulfobolus sulfataricus p2 at 2.09 a resolution

12	d2jfga1	Alignment		9.0	38	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
13	c5gqsA_	Alignment		7.9	44	PDB header: transport protein Chain: A: PDB Molecule: pts galactitol transporter subunit iib; PDBTitle: nmr based solution structure of pts system, galactitol-specific iib2 component from methicillin resistant staphylococcus aureus
14	d2e9xc2	Alignment		7.8	27	Fold: GINS/PriA/YqbF domain Superfamily: PriA/YqbF domain Family: PSF3 N-terminal domain-like
15	c2l2qa_	Alignment		7.2	38	PDB header: transferase Chain: A: PDB Molecule: pts system, cellobiose-specific iib component (cela); PDBTitle: solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
16	c6ajnF_	Alignment		6.8	13	PDB header: toxin Chain: F: PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atatr bound with accoa
17	d2bj7a1	Alignment		6.5	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
18	c6av8A_	Alignment		6.2	80	PDB header: toxin Chain: A: PDB Molecule: u5-theraphotoxin-hs1b 1; PDBTitle: exploring cystine dense peptide space to open a unique molecular2 toolbox
19	d1zbsa2	Alignment		6.0	28	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
20	c4nuxA_	Alignment		5.8	33	PDB header: immune system Chain: A: PDB Molecule: interleukin-17 receptor a; PDBTitle: structure of receptor a
21	d1zxoal	Alignment	not modelled	5.6	38	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
22	d1sqga1	Alignment	not modelled	5.4	21	Fold: NusB-like Superfamily: NusB-like Family: RmsB N-terminal domain-like
23	c4q69B_	Alignment	not modelled	5.4	26	PDB header: sugar binding protein Chain: B: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of a susd homolog (bt2259) from bacteroides2 thetaiotaomicron vpi-5482 at 2.50 a resolution
24	c5unkA_	Alignment	not modelled	5.3	19	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the red subdomain of the sleeping beauty transposase