















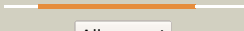


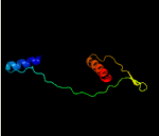

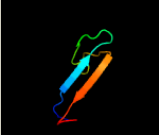

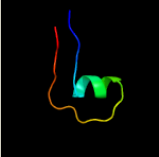
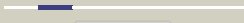
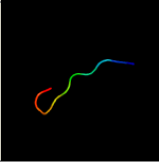


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3555c (-)_3995009_3995878
Date	Fri Aug 9 18:20:23 BST 2019
Unique Job ID	71d01f4c0d5d36ae

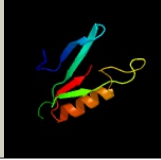
Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r3pB_	 Alignment		99.7	12	PDB header: hydrolase Chain: B: PDB Molecule: mobile intron protein; PDBTitle: homing endonuclease i-bth0305i catalytic domain
2	c3hrIA_	 Alignment		99.5	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: endonuclease-like protein; PDBTitle: crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
3	d1cw0a_	 Alignment		99.5	18	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
4	d1vsra_	 Alignment		98.4	19	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
5	c4oq2A_	 Alignment		97.5	20	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease pvurts1 i; PDBTitle: 5hmc specific restriction endonuclease pvurts1i
6	c4parC_	 Alignment		96.9	27	PDB header: dna binding protein/dna Chain: C: PDB Molecule: uncharacterized protein abasi; PDBTitle: the 5-hydroxymethylcytosine-specific restriction enzyme abasi in a2 complex with product-like dna
7	c6rdu2_	 Alignment		96.1	10	PDB header: proton transport Chain: 2: PDB Molecule: asa-2: polytomella f-atp synthase associated subunit 2; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
8	d1zela2	 Alignment		87.6	17	Fold: Rv2827c C-terminal domain-like Superfamily: Rv2827c C-terminal domain-like Family: Rv2827c C-terminal domain-like
9	c1zelaA_	 Alignment		82.2	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rv2827c; PDBTitle: crystal structure of rv2827c protein from mycobacterium tuberculosis
10	d1m0da_	 Alignment		48.2	15	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Endonuclease I (Holliday junction resolvase)
11	c4gqzB_	 Alignment		31.6	24	PDB header: metal binding protein Chain: B: PDB Molecule: putative periplasmic or exported protein; PDBTitle: crystal structure of s.cuep

12	d2fcla1  Alignment		27.2	27 Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: TM1012-like
13	c4ytkA  Alignment		9.1	27 PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow1-linker1 domain of transcription elongation2 factor spt5

14 [d2fuka1](#)

Alignment



6.6

15

Fold:alpha/beta-Hydrolases
Superfamily:alpha/beta-Hydrolases
Family:Atu1826-like