










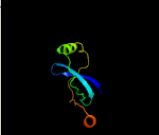





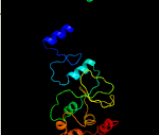

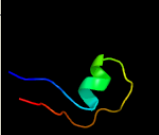




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3714c_(-)_4159109_4159999
Date	Fri Aug 9 18:20:41 BST 2019
Unique Job ID	35a036d60b87fec0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r3pB_	 Alignment		99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: mobile intron protein; PDBTitle: homing endonuclease i-bth0305i catalytic domain
2	c3hrIA_	 Alignment		99.4	25	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		99.3	23	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
4	d1vsra_	 Alignment		98.1	24	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
5	c4oq2A_	 Alignment		96.2	16	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease pvurts1 i; PDBTitle: 5hmc specific restriction endonuclease pvurts1i
6	c4parC_	 Alignment		96.2	21	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		95.3	14	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		90.7	19	Fold: Rv2827c C-terminal domain-like Superfamily: Rv2827c C-terminal domain-like Family: Rv2827c C-terminal domain-like
9	c1zelaA_	 Alignment		89.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rv2827c; PDBTitle: crystal structure of rv2827c protein from mycobacterium tuberculosis
10	d2fcla1	 Alignment		54.1	27	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: TM1012-like
11	d1m0da_	 Alignment		32.9	16	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Endonuclease I (Holliday junction resolvase)

12	c4gqzB_	Alignment		15.5	16	PDB header: metal binding protein Chain: B: PDB Molecule: putative periplasmic or exported protein; PDBTitle: crystal structure of s.cuep
13	c2m0nA_	Alignment		12.2	46	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c, seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
14	c5vrvA_	Alignment		11.6	17	PDB header: hydrolase,oxidoreductase Chain: A: PDB Molecule: protein regulated by acid ph; PDBTitle: 2.05 angstrom resolution crystal structure of c-terminal domain2 (duf2156) of putative lysylphosphatidylglycerol synthetase from3 agrobacterium fabrum.
15	c2lkyA_	Alignment		9.0	46	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysm.17112.b
16	d1jg5a_	Alignment		7.1	29	Fold: GTP cyclohydrolase I feedback regulatory protein, GFRP Superfamily: GTP cyclohydrolase I feedback regulatory protein, GFRP Family: GTP cyclohydrolase I feedback regulatory protein, GFRP
17	d1tfea_	Alignment		6.3	14	Fold: EF-Ts domain-like Superfamily: Elongation factor Ts (EF-Ts), dimerisation domain Family: Elongation factor Ts (EF-Ts), dimerisation domain
18	c4p6iB_	Alignment		6.0	18	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: crystal structure of the cas1-cas2 complex from escherichia coli
19	c2vldA_	Alignment		5.5	19	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease nucs; PDBTitle: crystal structure of a repair endonuclease from pyrococcus abyssii
20	d2csba2	Alignment		5.3	42	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
21	d1y5ea1	Alignment	not modelled	5.2	20	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
22	d1jsma_	Alignment	not modelled	5.0	22	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece