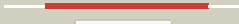
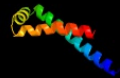











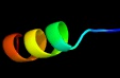



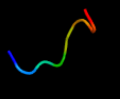

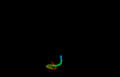

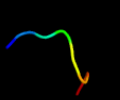


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1735Ac_(RVBD1735Ac)_1961894_1962136
 Date Fri Aug 2 13:30:34 BST 2019
 Unique Job ID 444d2b28b282485f

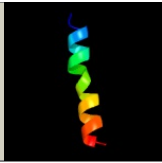
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3m7bA_	 Alignment		98.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein teha homolog; PDBTitle: crystal structure of plant slac1 homolog teha
2	c3m7eA_	 Alignment		98.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein teha homolog; PDBTitle: crystal structure of plant slac1 homolog teha
3	c5cofA_	 Alignment		12.9	27	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89
4	c6cfwB_	 Alignment		10.5	24	PDB header: membrane protein Chain: B: PDB Molecule: monovalent cation/h+ antiporter subunit f; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
5	d2a6aa1	 Alignment		9.8	43	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
6	c6n9aB_	 Alignment		9.4	38	PDB header: biosynthetic protein Chain: B: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsab; PDBTitle: crystal structure of thermotoga maritima threonylcarbamoyladenine2 biosynthesis complex tsab2d2e2 bound to atp and carboxy-amp
7	c6anrA_	 Alignment		8.8	27	PDB header: hydrolase Chain: A: PDB Molecule: colibactin self-protection protein clbs; PDBTitle: crystal structure of a self resistance protein clbs from colibactin2 biosynthetic gene cluster
8	c2lorA_	 Alignment		8.6	45	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane protein 141; PDBTitle: backbone structure of human membrane protein tmem141
9	c1okjB_	 Alignment		7.6	63	PDB header: hydrolase Chain: B: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsab; PDBTitle: crystal structure of the essential e. coli yeaz2 protein by mad method using the gadolinium complex3 "dotma"
10	d1okja1	 Alignment		7.4	71	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
11	c5br9C_	 Alignment		7.3	63	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein with similarity to2 peptidase yeaz from pseudomonas aeruginosa

12	c3r6mD_	Alignment		7.3	63	PDB header: hydrolase Chain: D: PDB Molecule: yeaz, resuscitation promoting factor; PDBTitle: crystal structure of vibrio parahaemolyticus yeaz
13	c2a6aB_	Alignment		6.6	38	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein tm0874; PDBTitle: crystal structure of glycoprotein endopeptidase (tm0874) from2 thermotoga maritima at 2.50 a resolution
14	c3dwwA_	Alignment		6.5	10	PDB header: isomerase Chain: A: PDB Molecule: prostaglandin e synthase; PDBTitle: electron crystallographic structure of human microsomal prostaglandin2 e synthase 1
15	c3leoA_	Alignment		6.4	23	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: structure of human leukotriene c4 synthase mutant r31q in complex with2 glutathione

16 [c3oh8A](#)

Alignment



5.9

24

PDB header:isomerase

Chain: A: **PDB Molecule:**nucleoside-diphosphate sugar epimerase (sua family);

PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91