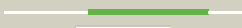

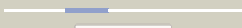
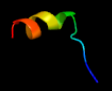





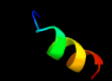





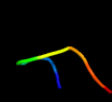



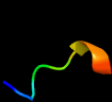




Phyre2

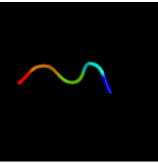
Email	mdejesus@rockefeller.edu
Description	RVBD0460 (-) _551752_551991
Date	Tue Jul 23 14:50:54 BST 2019
Unique Job ID	d514ba3bf023f668

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1o82a_	 Alignment		51.4	28	Fold: Saposin-like Superfamily: Bacteriocin AS-48 Family: Bacteriocin AS-48
2	c1cn3F_	 Alignment		20.1	31	PDB header: viral protein Chain: F; PDB Molecule: fragment of coat protein vp2; PDBTitle: interaction of polyomavirus internal protein vp2 with major2 capsid protein vp1 and implications for participation of 3 vp2 in viral entry
3	c6f34C_	 Alignment		19.3	75	PDB header: membrane protein Chain: C; PDB Molecule: mgmts; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue bound to arginine.
4	c5oqtC_	 Alignment		19.3	75	PDB header: transport protein Chain: C; PDB Molecule: uncharacterized protein ynem; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
5	c2x3mA_	 Alignment		12.7	50	PDB header: unknown function Chain: A; PDB Molecule: hypothetical protein orf239; PDBTitle: crystal structure of hypothetical protein orf239 from pyrobaculum2 spherical virus
6	c5faiA_	 Alignment		11.1	44	PDB header: transferase Chain: A; PDB Molecule: ribosomal rna small subunit methyltransferase nep1; PDBTitle: emg1 n1-specific pseudouridine methyltransferase
7	d3bbda1	 Alignment		6.6	56	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: EMG1/NEP1-like
8	c6cp9B_	 Alignment		6.1	88	PDB header: toxin/antitoxin Chain: B; PDB Molecule: cdii; PDBTitle: contact-dependent growth inhibition toxin - immunity protein complex2 from klebsiella pneumoniae 342
9	d1jqna_	 Alignment		5.9	45	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
10	d2v3ka1	 Alignment		5.7	44	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: EMG1/NEP1-like
11	c2lweA_	 Alignment		5.6	25	PDB header: signaling protein Chain: A; PDB Molecule: probable atp-dependent rna helicase ddx58; PDBTitle: solution structure of mutant (t170e) second card of human rig-i

12 [c1emxA](#)

Alignment



5.6

80

PDB header:toxin
Chain: A: **PDB Molecule:**heteropodatxin 2;
PDBTitle: solution structure of hptx2, a toxin from heteropoda2
venatoria spider venom that blocks kv4.2 potassium channel

13 [dljqoa_](#)

Alignment



5.4

45

Fold:TIM beta/alpha-barrel
Superfamily:Phosphoenolpyruvate/pyruvate domain
Family:Phosphoenolpyruvate carboxylase