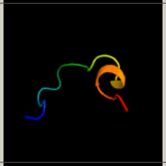
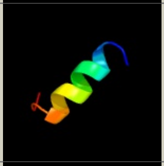
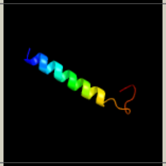
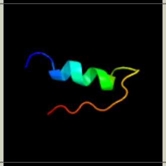
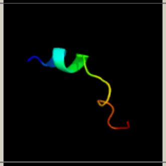
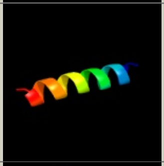
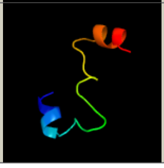
Phyre^2

Email	mdejesus@rockefeller.edu
Description	RVBD2078_(-)_2335067_2335381
Date	Mon Aug 5 13:25:19 BST 2019
Unique Job ID	8788678baacfbe7e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ypiF_	Alignment		12.6	58	**PDB header:**rna binding protein **Chain:** F: **PDB Molecule:**polymerase cofactor vp35; **PDBTitle:** structure of ebola virus nucleoprotein n-terminal fragment bound to a2 peptide derived from ebola vp35
2	c4ypiG_	Alignment		12.6	58	**PDB header:**rna binding protein **Chain:** G: **PDB Molecule:**polymerase cofactor vp35; **PDBTitle:** structure of ebola virus nucleoprotein n-terminal fragment bound to a2 peptide derived from ebola vp35
3	c2kk1A_	Alignment		11.7	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase abl2; **PDBTitle:** solution structure of c-terminal domain of tyrosine-protein2 kinase abl2 from homo sapiens, northeast structural3 genomics consortium (nesg) target hr5537a
4	c2m0eA_	Alignment		9.3	44	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 17; **PDBTitle:** solution structure of miz-1 zinc finger 6
5	c2r9iA_	Alignment		8.8	37	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative phage capsid protein; **PDBTitle:** crystal structure of putative phage capsid protein domain from2 corynebacterium diphtheriae
6	d3eeqa2	Alignment		7.7	30	**Fold:**CbiG N-terminal domain-like **Superfamily:**CbiG N-terminal domain-like **Family:**CbiG N-terminal domain-like
7	d1wf9a1	Alignment		7.6	41	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
8	c3h00A_	Alignment		6.6	20	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** structure of the c-terminal domain of a putative hiv-1 gp41 fusion2 intermediate
9	c1zzpA_	Alignment		6.3	62	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase abl1; **PDBTitle:** solution structure of the f-actin binding domain of bcr-2 abl/c-abl
10	c5ezbB_	Alignment		5.6	23	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chicken prestin stas domain,chicken prestin stas domain; **PDBTitle:** chicken prestin stas domain

11	c1g92A_	Alignment		5.4	44	**PDB header:**toxin **Chain:** A: **PDB Molecule:**poneratoxin; **PDBTitle:** solution structure of poneratoxin