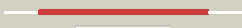





















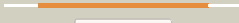

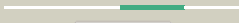
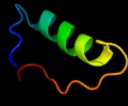





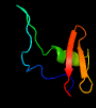






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1571 (-)_1778545_1779054
Date	Fri Aug 2 13:30:16 BST 2019
Unique Job ID	50a96b443793e2c2

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d4gA_	 Alignment		99.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein bsu11850; PDBTitle: structure of yjcg protein, a putative 2'-5' rna ligase from bacillus2 subtilis
2	d1jh6a_	 Alignment		99.9	16	Fold: LigT-like Superfamily: LigT-like Family: tRNA splicing product Appr>p cyclic nucleotide phosphodiesterase
3	c4qakA_	 Alignment		99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: 2'-5'-rna ligase; PDBTitle: crystal structure of phosphoesterase
4	c1vdxA_	 Alignment		99.9	12	PDB header: ligase Chain: A: PDB Molecule: hypothetical protein ph0099; PDBTitle: crystal structure of a pyrococcus horikoshii protein with2 similarities to 2'5' rna-ligase
5	c5h7eA_	 Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: rna 2',3'-cyclic phosphodiesterase; PDBTitle: crystal structure of native drcpdase
6	d1iuha_	 Alignment		99.9	14	Fold: LigT-like Superfamily: LigT-like Family: 2'-5' RNA ligase LigT
7	c2vfyA_	 Alignment		99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: akap18 delta; PDBTitle: akap18 delta central domain
8	c3j4rA_	 Alignment		99.8	13	PDB header: transferase Chain: A: PDB Molecule: a-kinase anchor protein 18; PDBTitle: pseudo-atomic model of the akap18-pka complex in a linear conformation2 derived from electron microscopy
9	c4h7wA_	 Alignment		99.7	14	PDB header: unknown function Chain: A: PDB Molecule: upf0406 protein c16orf57; PDBTitle: crystal structure of human c16orf57
10	c4z5vA_	 Alignment		97.9	20	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 2a; PDBTitle: crystal structure of mhv ns2 pde domain
11	d2fsqa1	 Alignment		93.7	18	Fold: LigT-like Superfamily: LigT-like Family: Atu0111-like

12	c5uqjA_	 Alignment		87.5	15	PDB header: hydrolase Chain: A: PDB Molecule: u6 snrna phosphodiesterase; PDBTitle: structure of yeast usb1
13	d1em8a_	 Alignment		48.9	15	Fold: DNA polymerase III chi subunit Superfamily: DNA polymerase III chi subunit Family: DNA polymerase III chi subunit
14	c3gr1A_	 Alignment		35.3	10	PDB header: membrane protein Chain: A: PDB Molecule: protein prgh; PDBTitle: periplasmic domain of the t3ss inner membrane protein prgh from <i>S. typhimurium</i> (fragment 170-392)
15	c3ce8A_	 Alignment		34.2	13	PDB header: unknown function Chain: A: PDB Molecule: putative pii-like nitrogen regulatory protein; PDBTitle: crystal structure of a duf3240 family protein (sba1_0098) from <i>S. shewanella baltica</i> os155 at 2.40 Å resolution
16	c2i3eA_	 Alignment		25.5	14	PDB header: hydrolase Chain: A: PDB Molecule: g-rich; PDBTitle: solution structure of catalytic domain of goldfish rich2 protein
17	c5af2C_	 Alignment		21.2	17	PDB header: hydrolase Chain: C: PDB Molecule: vp3; PDBTitle: crystal structure of the c-terminal 2',5'-phosphodiesterase2 domain of group A rotavirus protein vp3
18	d2ilxa1	 Alignment		20.5	22	Fold: LigT-like Superfamily: LigT-like Family: 2',3'-cyclic nucleotide 3'-phosphodiesterase, catalytic domain

19 [c2n9zA_](#)

Alignment



6.1

20

PDB header: toxin
Chain: A: **PDB Molecule:** tau-theraphotoxin-hs1a;
PDBTitle: solution structure of k1 lobe of double-knot toxin