

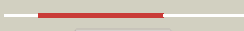








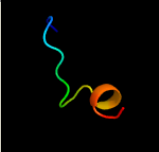

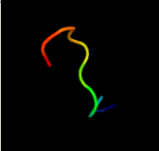

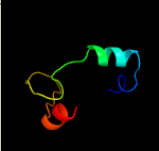

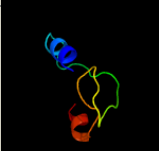




# Phyre2

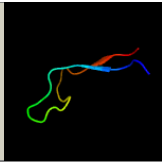
Email	mdejesus@rockefeller.edu
Description	RVBD2181_(-)_2443310_2444593
Date	Mon Aug 5 13:25:30 BST 2019
Unique Job ID	13734e150594f76f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5f15A_</a>	 Alignment		98.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; <b>PDBTitle:</b> crystal structure of arnt from cupriavidus metallidurans bound to 2 undecaprenyl phosphate
2	<a href="#">c6p25A_</a>	 Alignment		98.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dolichyl-phosphate-mannose--protein mannosyltransferase 1; <b>PDBTitle:</b> structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor
3	<a href="#">c6p2rB_</a>	 Alignment		98.2	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dolichyl-phosphate-mannose--protein mannosyltransferase 2; <b>PDBTitle:</b> structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
4	<a href="#">c3wajA_</a>	 Alignment		44.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane oligosaccharyl transferase; <b>PDBTitle:</b> crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
5	<a href="#">c5c77B_</a>	 Alignment		25.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein arginine n-methyltransferase sfm1; <b>PDBTitle:</b> a novel protein arginine methyltransferase
6	<a href="#">c2zkry_</a>	 Alignment		9.0	38	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> Y: <b>PDB Molecule:</b> 5s ribosomal rna; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an 3.8.7 a cryo-em map
7	<a href="#">c5d6hB_</a>	 Alignment		7.5	45	<b>PDB header:</b> chaperone/protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> csua/b; <b>PDBTitle:</b> crystal structure of csuc-csua/b chaperone-major subunit pre-assembly2 complex from csu biofilm-mediating pili of acinetobacter baumannii
8	<a href="#">c3dwqD_</a>	 Alignment		7.0	34	<b>PDB header:</b> toxin <b>Chain:</b> D: <b>PDB Molecule:</b> subtilase cytotoxin, subunit b; <b>PDBTitle:</b> crystal structure of the a-subunit of the ab5 toxin from e.2 coli with neu5gc-2,3gal-1,3glcnac
9	<a href="#">c4k6IC_</a>	 Alignment		5.7	22	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> putative pertussis-like toxin subunit; <b>PDBTitle:</b> structure of typhoid toxin
10	<a href="#">c5whvF_</a>	 Alignment		5.6	25	<b>PDB header:</b> toxin <b>Chain:</b> F: <b>PDB Molecule:</b> artb protein; <b>PDBTitle:</b> crystal structure of artb

11 [d2f69a1](#)

Alignment



5.6

28

**Fold:**open-sided beta-meander

**Superfamily:**Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain

**Family:**Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain