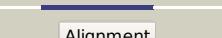
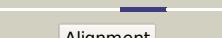
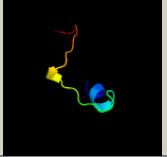


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD2654c_(-)_2976999_2977244
Date	Wed Aug 7 12:50:30 BST 2019
Unique Job ID	be3d128706050dfd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1yt3a2</a>	 Alignment		10.1	37	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> RNase D C-terminal domains
2	<a href="#">d1xrsb1</a>	 Alignment		7.8	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
3	<a href="#">c2jv8A_</a>	 Alignment		6.4	47	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ne1242; <b>PDBTitle:</b> solution structure of protein ne1242 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net4
4	<a href="#">c4jgiB_</a>	 Alignment		6.2	24	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfobacterium hafniense dcb-2
5	<a href="#">d1mylb_</a>	 Alignment		5.6	70	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors

6	<a href="#">c3zvmA</a>		<a href="#">Alignment</a>		5.6	26	<b>PDB header:</b> hydrolase/transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional polynucleotide phosphatase/kinase; <b>PDBTitle:</b> the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
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