


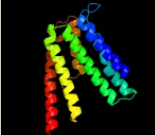



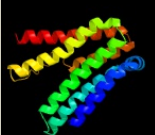





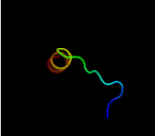







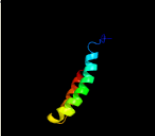


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2746c_(pgsA3)_3058612_3059241
Date	Wed Aug 7 12:50:40 BST 2019
Unique Job ID	37b8664d7f17267d

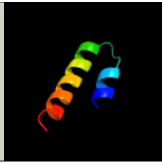
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6h59B_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cdp-diacylglycerol--inositol 3-phosphatidyltransferase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis phosphatidylinositol2 phosphate synthase (pgsa1) with cdp-dag bound
2	<a href="#">c5d92B_</a>	 Alignment		99.9	18	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> af2299 protein,phosphatidylinositol synthase; <b>PDBTitle:</b> structure of a phosphatidylinositolphosphate (pip) synthase from2 renibacterium salmoninarum
3	<a href="#">c4o6mA_</a>	 Alignment		99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> af2299, a cdp-alcohol phosphotransferase; <b>PDBTitle:</b> structure of af2299, a cdp-alcohol phosphotransferase (cmp-bound)
4	<a href="#">c4mndA_</a>	 Alignment		99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp l-myo-inositol-1-phosphate cytidyltransferase/cdp-l- <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
5	<a href="#">c2voyG_</a>	 Alignment		32.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium atpase 1; <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
6	<a href="#">c4i0xJ_</a>	 Alignment		24.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> J: <b>PDB Molecule:</b> esat-6-like protein mab_3113; <b>PDBTitle:</b> crystal structure of the mycobacterum abscessus esexf (mab_3112-2 mab_3113) complex
7	<a href="#">c6mjbC_</a>	 Alignment		23.3	17	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> kinetochore-associated protein dsn1; <b>PDBTitle:</b> structure of candida glabrata csm1:dsn1(14-72) complex
8	<a href="#">c2rkhA_</a>	 Alignment		21.9	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative apha-like transcription factor; <b>PDBTitle:</b> crystal structure of a putative apha-like transcription factor2 (zp_00208345.1) from magnetospirillum magnetotacticum ms-1 at 2.00 a3 resolution
9	<a href="#">c2le7A_</a>	 Alignment		13.4	36	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily h member 2; <b>PDBTitle:</b> solution nmr structure of the s4s5 linker of herg potassium channel
10	<a href="#">c2mpnB_</a>	 Alignment		8.2	8	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> inner membrane protein ygap; <b>PDBTitle:</b> 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
11	<a href="#">c2mpnA_</a>	 Alignment		8.2	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> inner membrane protein ygap; <b>PDBTitle:</b> 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli

12	<a href="#">c4n3xD_</a>	Alignment		7.0	45	<b>PDB header:</b> endocytosis <b>Chain:</b> D: <b>PDB Molecule:</b> rab5 gdp/gtp exchange factor; <b>PDBTitle:</b> crystal structure of rabex-5 cc domain
13	<a href="#">c6mjeB_</a>	Alignment		5.9	18	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> dsn1p; <b>PDBTitle:</b> structure of candida glabrata csm1: s. cerevisiae dsn1 complex
14	<a href="#">c6mjeH_</a>	Alignment		5.9	18	<b>PDB header:</b> cell cycle <b>Chain:</b> H: <b>PDB Molecule:</b> dsn1p; <b>PDBTitle:</b> structure of candida glabrata csm1: s. cerevisiae dsn1 complex
15	<a href="#">c6mjeF_</a>	Alignment		5.9	18	<b>PDB header:</b> cell cycle <b>Chain:</b> F: <b>PDB Molecule:</b> dsn1p; <b>PDBTitle:</b> structure of candida glabrata csm1: s. cerevisiae dsn1 complex
16	<a href="#">c6mjeD_</a>	Alignment		5.9	18	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> dsn1p; <b>PDBTitle:</b> structure of candida glabrata csm1: s. cerevisiae dsn1 complex
17	<a href="#">d2cx6a1</a>	Alignment		5.8	17	<b>Fold:</b> Barstar-like <b>Superfamily:</b> Barstar-related <b>Family:</b> Barstar-related

18 [c4arpB\\_](#)

Alignment



5.3

13

**PDB header:**hydrolase  
**Chain:** B: **PDB Molecule:**pesticin;  
**PDBTitle:** structure of the inactive pesticin e178a mutant