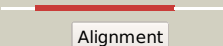



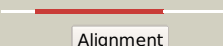

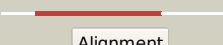

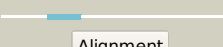

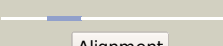



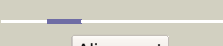
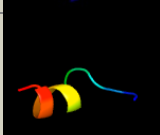

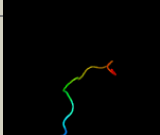

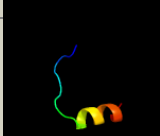

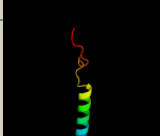
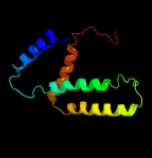

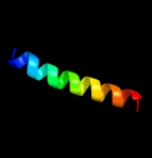

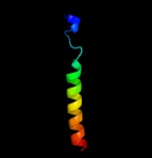
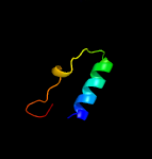


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0436c\_(pssA)\_524533\_525393  
 Date Tue Jul 23 14:50:51 BST 2019  
 Unique Job ID 758f89878081033d

Detailed template information

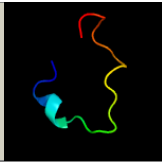
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6h59B_</a>	 Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cdp-diacylglycerol--inositol 3-phosphatidyltransferase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis phosphatidylinositol2 phosphate synthase (pgsa1) with cdp-dag bound
2	<a href="#">c5d92B_</a>	 Alignment		99.9	17	<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	17	<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	15	<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="#">d2cx6a1</a>	 Alignment		32.7	17	<b>Fold:</b> Barstar-like <b>Superfamily:</b> Barstar-related <b>Family:</b> Barstar-related
6	<a href="#">d1ay7b_</a>	 Alignment		28.4	21	<b>Fold:</b> Barstar-like <b>Superfamily:</b> Barstar-related <b>Family:</b> Barstar-related
7	<a href="#">c4i0xl_</a>	 Alignment		21.2	17	<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 mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
8	<a href="#">c2le7A_</a>	 Alignment		11.0	64	<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
9	<a href="#">c2kt5B_</a>	 Alignment		10.8	40	<b>PDB header:</b> rna binding protein / viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> icp27; <b>PDBTitle:</b> rrm domain of mrna export adaptor ref2-i bound to hsv-1 icp27 peptide
10	<a href="#">c6mjbC_</a>	 Alignment		10.0	26	<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
11	<a href="#">c1w8xP_</a>	 Alignment		9.5	15	<b>PDB header:</b> virus <b>Chain:</b> P: <b>PDB Molecule:</b> protein p16; <b>PDBTitle:</b> structural analysis of prd1

12	<a href="#">c3lrcC_</a>	Alignment		8.2	15	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> arginine/agmatine antiporter; <b>PDBTitle:</b> structure of e. coli adic (p1)
13	<a href="#">c1gl2D_</a>	Alignment		6.4	29	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> syntaxin 8; <b>PDBTitle:</b> crystal structure of an endosomal snare core complex
14	<a href="#">c3b5nL_</a>	Alignment		6.0	29	<b>PDB header:</b> membrane protein <b>Chain:</b> L: <b>PDB Molecule:</b> protein transport protein sec9; <b>PDBTitle:</b> structure of the yeast plasma membrane snare complex
15	<a href="#">c2ov2O_</a>	Alignment		5.7	17	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> O: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 4; <b>PDBTitle:</b> the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)
16	<a href="#">c6h2eP_</a>	Alignment		5.6	23	<b>PDB header:</b> toxin <b>Chain:</b> P: <b>PDB Molecule:</b> ahlc; <b>PDBTitle:</b> structure of the soluble ahlc of the tripartite alpha-pore forming2 toxin, ahl, from aeromonas hydrophila.
17	<a href="#">d1y0ka1</a>	Alignment		5.1	13	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> PA4535-like

18 [c2amwA\\_](#)



Alignment



5.1

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**PDB header:** structural genomics, unknown function  
**Chain:** A: **PDB Molecule:** hypothetical protein ne2163;  
**PDBTitle:** solution nmr structure of protein ne2163 from nitrosomonas europaea.2 northeast structural genomics consortium target net1.