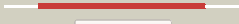
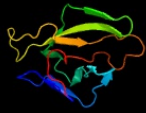
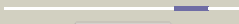


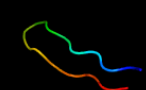



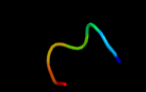



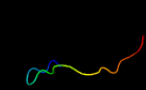

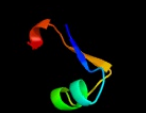





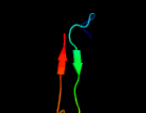


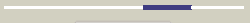
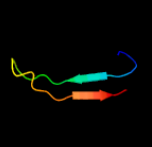


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1670_(-)_1896127_1896474
Date	Fri Aug 2 13:30:26 BST 2019
Unique Job ID	64ffd6a7d52b18c0

Detailed template information

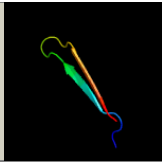
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3djmA_</a>	 Alignment		100.0	28	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein duf427; <b>PDBTitle:</b> crystal structure of a protein of unknown function from duf427 family2 (rsph17029_0682) from rhodobacter sphaeroides 2.4.1 at 2.51 a3 resolution
2	<a href="#">d1sxja1</a>	 Alignment		16.1	50	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
3	<a href="#">d1yuaa2</a>	 Alignment		15.7	38	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Prokaryotic DNA topoisomerase I, a C-terminal fragment
4	<a href="#">c4b1qP_</a>	 Alignment		13.0	33	<b>PDB header:</b> toxin <b>Chain:</b> P; <b>PDB Molecule:</b> conotoxin cctx; <b>PDBTitle:</b> nmr structure of the glycosylated conotoxin cctx from conus consors
5	<a href="#">c2mjca_</a>	 Alignment		12.0	57	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit g; <b>PDBTitle:</b> zn-binding domain of eukaryotic translation initiation factor 3,2 subunit g
6	<a href="#">d1d6za4</a>	 Alignment		9.5	18	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> Copper amine oxidase, domain N <b>Family:</b> Copper amine oxidase, domain N
7	<a href="#">c4mkqA_</a>	 Alignment		8.5	17	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> monalysin; <b>PDBTitle:</b> crystal structure of the pore-forming toxin monalysin mutant deleted2 of the membrane-spanning domain
8	<a href="#">c6fhtB_</a>	 Alignment		8.3	38	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> bacteriophytochrome,adenylate cyclase; <b>PDBTitle:</b> crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form
9	<a href="#">c3zh6B_</a>	 Alignment		7.2	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> protein e; <b>PDBTitle:</b> the structure of haemophilus influenzae se_met form of protein e
10	<a href="#">c4joiD_</a>	 Alignment		7.1	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> cst complex subunit ten1; <b>PDBTitle:</b> crystal structure of the human telomeric stn1-ten1 complex
11	<a href="#">c4cawA_</a>	 Alignment		6.5	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> glycylpeptide n-tetradecanoyltransferase; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus n-myristoyl2 transferase in complex with myristoyl coa and a pyrazole3 sulphonamide ligand

12 <a href="#">d1m9sa4</a>	 Alignment		6.1	19 <b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Prokaryotic SH3-related domain <b>Family:</b> GW domain
13 <a href="#">d1rxta2</a>	 Alignment		5.4	4 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-myristoyl transferase, NMT

14

[dliica2](#)

Alignment



5.3

17

**Fold:** Acyl-CoA N-acyltransferases (Nat)  
**Superfamily:** Acyl-CoA N-acyltransferases (Nat)  
**Family:** N-myristoyl transferase, NMT