






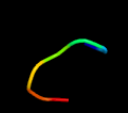



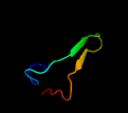
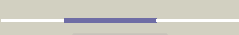
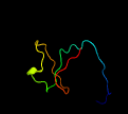

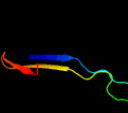

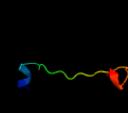



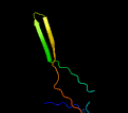




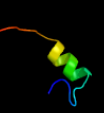
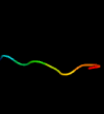

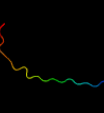



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0140 (-) _166908_167288
Date	Tue Jul 23 14:50:18 BST 2019
Unique Job ID	5643f9ae58f13a67

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3djmA_</a>	 Alignment		100.0	35	<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="#">c4azzB_</a>	 Alignment		19.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> levanase; <b>PDBTitle:</b> carbohydrate binding module cbm66 from bacillus subtilis
3	<a href="#">c4b1qP_</a>	 Alignment		13.1	25	<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
4	<a href="#">c2mjcA_</a>	 Alignment		12.9	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
5	<a href="#">c5hj0C_</a>	 Alignment		12.5	15	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> kinetochore protein mis18; <b>PDBTitle:</b> crystal structure of mis18 'yippe-like' domain
6	<a href="#">d2bf2a1</a>	 Alignment		11.9	20	<b>Fold:</b> Monooxygenase (hydroxylase) regulatory protein <b>Superfamily:</b> Monooxygenase (hydroxylase) regulatory protein <b>Family:</b> Monooxygenase (hydroxylase) regulatory protein
7	<a href="#">d1w66a1</a>	 Alignment		11.9	23	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> LpIA-like
8	<a href="#">c4qhzC_</a>	 Alignment		10.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> putative glycosyl hydrolase; <b>PDBTitle:</b> crystal structure of a putative glycosyl hydrolase (bdj_3914) from2 parabacteroides distasonis atcc 8503 at 2.13 a resolution
9	<a href="#">c4e6nB_</a>	 Alignment		9.7	25	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> methyltransferase type 12; <b>PDBTitle:</b> crystal structure of bacterial pnkp-c/hen1-n heterodimer
10	<a href="#">d2bf5a1</a>	 Alignment		9.4	20	<b>Fold:</b> Monooxygenase (hydroxylase) regulatory protein <b>Superfamily:</b> Monooxygenase (hydroxylase) regulatory protein <b>Family:</b> Monooxygenase (hydroxylase) regulatory protein
11	<a href="#">c4u62D_</a>	 Alignment		8.2	17	<b>PDB header:</b> viral protein <b>Chain:</b> D; <b>PDB Molecule:</b> structural protein vp1; <b>PDBTitle:</b> trichodysplasia spinulosa-associated polyomavirus (tspyv) vp1 in2 complex with 3'-sialyllactose

12	<a href="#">d2gu3a2</a>	Alignment		8.2	21	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Cystatin/monellin <b>Family:</b> PepSY-like
13	<a href="#">c3zr6A_</a>	Alignment		7.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> galactocerebrosidase; <b>PDBTitle:</b> structure of galactocerebrosidase from mouse in complex with galactose
14	<a href="#">c6m9yD_</a>	Alignment		7.6	3	<b>PDB header:</b> fluorescent protein <b>Chain:</b> D: <b>PDB Molecule:</b> fluorescent protein lanfp6a; <b>PDBTitle:</b> x-ray structure of branchiostoma floridae fluorescent protein lanfp6a
15	<a href="#">c2kl4A_</a>	Alignment		7.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh2032 protein; <b>PDBTitle:</b> nmr structure of the protein nb7804a
16	<a href="#">c5xyiL_</a>	Alignment		6.6	39	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
17	<a href="#">d1yuaa2</a>	Alignment		6.4	40	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Prokaryotic DNA topoisomerase I, a C-terminal fragment
18	<a href="#">c6fhtB_</a>	Alignment		6.1	27	<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
19	<a href="#">c4mbyB_</a>	Alignment		5.9	32	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> major capsid protein vp1; <b>PDBTitle:</b> structure of b-lymphotropic polyomavirus vp1 in complex with 3'-2 sialyllactose
20	<a href="#">c3pt1A_</a>	Alignment		5.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> upf0364 protein ymr027w; <b>PDBTitle:</b> structure of duf89 from saccharomyces cerevisiae co-crystallized with2 f6p.
21	<a href="#">d2cu2a1</a>	Alignment	not modelled	5.7	31	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Guanosine diphospho-D-mannose pyrophosphorylase/mannose-6-phosphate isomerase linker domain <b>Family:</b> Guanosine diphospho-D-mannose pyrophosphorylase/mannose-6-phosphate isomerase linker domain
22	<a href="#">c2xznQ_</a>	Alignment	not modelled	5.3	30	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> ribosomal protein s17 containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
23	<a href="#">c3iysA_</a>	Alignment	not modelled	5.2	21	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> major capsid protein vp1; <b>PDBTitle:</b> homology model of avian polyomavirus asymmetric unit
24	<a href="#">d1rxta2</a>	Alignment	not modelled	5.1	8	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-myristoyl transferase, NMT