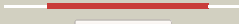



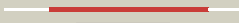








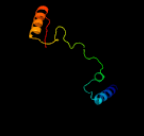



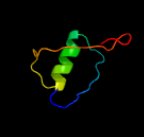



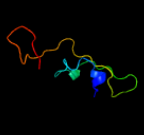


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1368\_(lprF)\_1541026\_1541811  
 Date Wed Jul 31 22:05:47 BST 2019  
 Unique Job ID 6c817173eddf1a9f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4qa8A_</a>	 Alignment		100.0	100	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein lprf; <b>PDBTitle:</b> crystal structure of lprf from mycobacterium bovis
2	<a href="#">c3mhaB_</a>	 Alignment		100.0	31	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein lprg; <b>PDBTitle:</b> crystal structure of lprg from mycobacterium tuberculosis bound to pim
3	<a href="#">d2byoa1</a>	 Alignment		100.0	29	<b>Fold:</b> LolA-like prokaryotic lipoproteins and lipoprotein localization factors <b>Superfamily:</b> Prokaryotic lipoproteins and lipoprotein localization factors <b>Family:</b> LppX-like
4	<a href="#">c3buuB_</a>	 Alignment		97.5	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized lola superfamily protein ne2245; <b>PDBTitle:</b> crystal structure of lola superfamily protein ne2245 from2 nitrosomonas europaea
5	<a href="#">c2v43A_</a>	 Alignment		92.3	14	<b>PDB header:</b> regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sigma-e factor regulatory protein rseb; <b>PDBTitle:</b> crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
6	<a href="#">c4mxtA_</a>	 Alignment		92.2	14	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an outer-membrane lipoprotein carrier protein2 (bacuni_04723) from bacteroides uniformis atcc 8492 at 1.40 a3 resolution
7	<a href="#">c3woaA_</a>	 Alignment		62.4	11	<b>PDB header:</b> dna binding protein, sugar binding prote <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein ci, maltose-binding periplasmic protein; <b>PDBTitle:</b> crystal structure of lambda repressor (1-45) fused with maltose-2 binding protein
8	<a href="#">c4z48B_</a>	 Alignment		57.5	17	<b>PDB header:</b> structural biology, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf1329 family protein (despig_00262) from2 desulfovibrio piger atcc 29098 at 1.75 a resolution
9	<a href="#">c4mjsQ_</a>	 Alignment		29.4	16	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> Q: <b>PDB Molecule:</b> protein kinase c zeta type; <b>PDBTitle:</b> crystal structure of a pb1 complex
10	<a href="#">c3bk5A_</a>	 Alignment		8.9	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative outer membrane lipoprotein-sorting protein; <b>PDBTitle:</b> crystal structure of putative outer membrane lipoprotein-sorting2 protein domain from vibrio parahaemolyticus
11	<a href="#">c3a5zD_</a>	 Alignment		8.8	20	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> elongation factor p; <b>PDBTitle:</b> crystal structure of escherichia coli genx in complex with elongation2 factor p

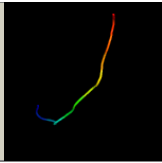
12	<a href="#">d1wmxa_</a>	Alignment		8.8	50	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Family 30 carbohydrate binding module, CBM30 (PKD repeat)
13	<a href="#">c3ks6A_</a>	Alignment		7.8	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (17743486) from agrobacterium tumefaciens str. c583 (dupont) at 1.80 a resolution
14	<a href="#">c5cw9A_</a>	Alignment		6.6	13	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed ferredoxin-ferredoxin domain insertion <b>PDBTitle:</b> crystal structure of de novo designed ferredoxin-ferredoxin domain2 insertion protein
15	<a href="#">c2o55A_</a>	Alignment		6.4	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycerophosphodiester phosphodiesterase; <b>PDBTitle:</b> crystal structure of a putative glycerophosphodiester2 phosphodiesterase from galdieria sulphuraria
16	<a href="#">c4oecD_</a>	Alignment		5.6	6	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of glycerophosphodiester phosphodiesterase from2 thermococcus kodakarensis kod1
17	<a href="#">c3qvqB_</a>	Alignment		5.4	6	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphodiesterase olei02445; <b>PDBTitle:</b> the structure of an oleispira antarctica phosphodiesterase olei024452 in complex with the product sn-glycerol-3-phosphate
18	<a href="#">c3n3fB_</a>	Alignment		5.4	11	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-1(xv) chain; <b>PDBTitle:</b> crystal structure of the human collagen xv trimerization domain: a2 potent trimerizing unit common to multiplexin collagens
19	<a href="#">c2hcuA_</a>	Alignment		5.2	27	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-isopropylmalate dehydratase small subunit; <b>PDBTitle:</b> crystal structure of smu.1381 (or leud) from streptococcus mutans

20

[d1k81a\\_](#)



Alignment



5.2

50

**Fold:**Zinc-binding domain of translation initiation factor 2 beta  
**Superfamily:**Zinc-binding domain of translation initiation factor 2 beta  
**Family:**Zinc-binding domain of translation initiation factor 2 beta