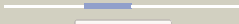


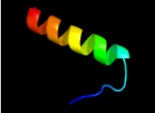









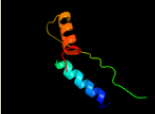










# Phyre2

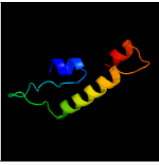
Email mdejesus@rockefeller.edu  
 Description RVBD1690\_(lprj)\_1915534\_1915917  
 Date Fri Aug 2 13:30:29 BST 2019  
 Unique Job ID 5f2e1a9df581aac2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2csua3</a>	 Alignment		27.4	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
2	<a href="#">d1mkea1</a>	 Alignment		19.6	4	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
3	<a href="#">c5uqdA_</a>	 Alignment		14.3	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dumpy; shorter than wild-type; <b>PDBTitle:</b> dpy-21 in complex with fe(ii) and alpha-ketoglutarate
4	<a href="#">c2ifsA_</a>	 Alignment		13.3	4	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> wiskott-aldrich syndrome protien interacting protein and <b>PDBTitle:</b> structure of the n-wasp evh1 domain in complex with an extended wip2 peptide
5	<a href="#">c6c3rB_</a>	 Alignment		11.3	10	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> cricket paralysis virus 1a protein; <b>PDBTitle:</b> cricket paralysis virus rnai suppressor protein crpv-1a
6	<a href="#">d1xoda1</a>	 Alignment		8.4	23	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
7	<a href="#">d1nyed_</a>	 Alignment		8.2	16	<b>Fold:</b> OsmC-like <b>Superfamily:</b> OsmC-like <b>Family:</b> Ohr/OsmC resistance proteins
8	<a href="#">c3ss4C_</a>	 Alignment		6.7	38	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> glutaminase c; <b>PDBTitle:</b> crystal structure of mouse glutaminase c, phosphate-bound form
9	<a href="#">d1eucb1</a>	 Alignment		6.6	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
10	<a href="#">c5dggB_</a>	 Alignment		6.1	23	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> central domain of uncharacterized lpg1148 protein from legionella2 pneumophila
11	<a href="#">c2lweA_</a>	 Alignment		6.1	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx58; <b>PDBTitle:</b> solution structure of mutant (t170e) second card of human rig-i

12 [c5h75B\\_](#)

Alignment



6.0

11

**PDB header:** lyase  
**Chain:** B: **PDB Molecule:** mersacidin decarboxylase, immunoglobulin g-binding protein  
**PDBTitle:** crystal structure of the mrsd-protein a fusion protein

13 [clvjqB\\_](#)

Alignment



6.0

42

**PDB header:** structural genomics, de novo protein  
**Chain:** B: **PDB Molecule:** designed protein;  
**PDBTitle:** designed protein based on backbone conformation of 2  
procarboxypeptidase-a (1aye) with sidechains chosen for maximal 3  
predicted stability.