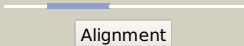

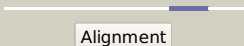
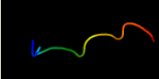
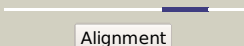

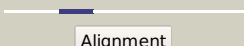

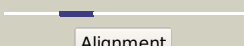

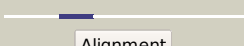
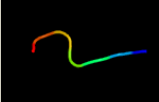
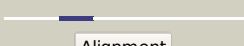
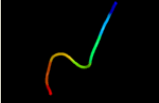
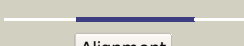
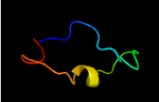



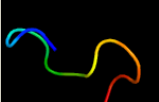




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2304c (-) _2575026_2575235
Date	Mon Aug 5 13:25:44 BST 2019
Unique Job ID	228f133a71dcc482

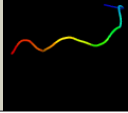
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2elrA_</a>	 Alignment		29.9	37	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> zinc finger protein 406; <b>PDBTitle:</b> solution structure of the 15th c2h2 zinc finger of human2 zinc finger protein 406
2	<a href="#">c1tx6J_</a>	 Alignment		11.9	62	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> J; <b>PDB Molecule:</b> bowman-birk type trypsin inhibitor; <b>PDBTitle:</b> trypsin:bbi complex
3	<a href="#">c3c97A_</a>	 Alignment		8.4	27	<b>PDB header:</b> signaling protein, transferase <b>Chain:</b> A; <b>PDB Molecule:</b> signal transduction histidine kinase; <b>PDBTitle:</b> crystal structure of the response regulator receiver domain of a2 signal transduction histidine kinase from aspergillus oryzae
4	<a href="#">c3jtcC_</a>	 Alignment		8.4	57	<b>PDB header:</b> blood clotting <b>Chain:</b> C; <b>PDB Molecule:</b> vitamin k-dependent protein c; <b>PDBTitle:</b> importance of mg2+ in the ca2+-dependent folding of the gamma-2 carboxylglutamic acid domains of vitamin k-dependent clotting and3 anticlotting proteins
5	<a href="#">c3jtcD_</a>	 Alignment		8.4	57	<b>PDB header:</b> blood clotting <b>Chain:</b> D; <b>PDB Molecule:</b> vitamin k-dependent protein c; <b>PDBTitle:</b> importance of mg2+ in the ca2+-dependent folding of the gamma-2 carboxylglutamic acid domains of vitamin k-dependent clotting and3 anticlotting proteins
6	<a href="#">c1lqvC_</a>	 Alignment		8.4	57	<b>PDB header:</b> blood clotting <b>Chain:</b> C; <b>PDB Molecule:</b> vitamin-k dependent protein c; <b>PDBTitle:</b> crystal structure of the endothelial protein c receptor with2 phospholipid in the groove in complex with gla domain of protein c.
7	<a href="#">c1lqvD_</a>	 Alignment		8.4	57	<b>PDB header:</b> blood clotting <b>Chain:</b> D; <b>PDB Molecule:</b> vitamin-k dependent protein c; <b>PDBTitle:</b> crystal structure of the endothelial protein c receptor with2 phospholipid in the groove in complex with gla domain of protein c.
8	<a href="#">c3g3lA_</a>	 Alignment		8.0	47	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized membrane-associated protein; <b>PDBTitle:</b> crystal structure of putative membrane-associated protein of unknown2 function (yp_211325.1) from bacteroides fragilis nctc 9343 at 2.20 a3 resolution
9	<a href="#">c6re80_</a>	 Alignment		7.9	32	<b>PDB header:</b> proton transport <b>Chain:</b> 0; <b>PDB Molecule:</b> asa-10: polytomella f-atp synthase associated subunit 10; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 2d,2 composite map
10	<a href="#">c3a9kC_</a>	 Alignment		7.2	38	<b>PDB header:</b> signaling protein/metal binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> mitogen-activated protein kinase kinase kinase 7- <b>PDBTitle:</b> crystal structure of the mouse tab3-nzf in complex with2 lys63-linked di-ubiquitin
11	<a href="#">c2i7fB_</a>	 Alignment		7.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> ferredoxin component of dioxygenase; <b>PDBTitle:</b> sphingomonas yanoikuyae b1 ferredoxin

12	<a href="#">c4o1iA_</a>	Alignment		6.4	31	<p><b>PDB header:</b>transcription regulator</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>transcriptional regulatory protein;</p> <p><b>PDBTitle:</b> crystal structure of the regulatory domain of mtbglr</p>
13	<a href="#">c2ayxA_</a>	Alignment		6.0	33	<p><b>PDB header:</b>transferase</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>sensor kinase protein rcsc;</p> <p><b>PDBTitle:</b> solution structure of the e.coli rcsc c-terminus (residues2700-949) containing linker region and phosphoreceiver3 domain</p>
14	<a href="#">c6dzpy_</a>	Alignment		5.4	38	<p><b>PDB header:</b>ribosome</p> <p><b>Chain:</b> Y: <b>PDB Molecule:</b></p> <p><b>PDBTitle:</b> cryo-em structure of mycobacterium smegmatis c(minus)50s ribosomal2 subunit</p>
15	<a href="#">c2js3B_</a>	Alignment		5.3	54	<p><b>PDB header:</b>structural genomics, unknown function</p> <p><b>Chain:</b> B: <b>PDB Molecule:</b>uncharacterized protein;</p> <p><b>PDBTitle:</b> nmr structure of protein q6n9a4_hopa. northeast structural genomics2 consortium target rpt8</p>
16	<a href="#">d2ae8a2</a>	Alignment		5.2	41	<p><b>Fold:</b>Ribosomal protein S5 domain 2-like</p> <p><b>Superfamily:</b>Ribosomal protein S5 domain 2-like</p> <p><b>Family:</b>Imidazole glycerol phosphate dehydratase</p>
17	<a href="#">d1m9sa2</a>	Alignment		5.1	31	<p><b>Fold:</b>SH3-like barrel</p> <p><b>Superfamily:</b>Prokaryotic SH3-related domain</p> <p><b>Family:</b>GW domain</p>
18	<a href="#">c6ddgl_</a>	Alignment		5.0	38	<p><b>PDB header:</b>ribosome/antibiotic</p> <p><b>Chain:</b> J: <b>PDB Molecule:</b>50s ribosomal protein l28;</p> <p><b>PDBTitle:</b> structure of the 50s ribosomal subunit from methicillin resistant2 staphylococcus aureus in complex with the oxazolidinone antibiotic3 lzd-6</p>

19 [c2qn5B](#)

Alignment



5.0

33

**PDB header:**hydrolase inhibitor/hydrolase  
**Chain:** B: **PDB Molecule:**bowman-birk type bran trypsin inhibitor;  
**PDBTitle:** crystal structure and functional study of the bowman-birk2 inhibitor from rice bran in complex with bovine trypsin