






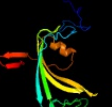









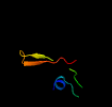

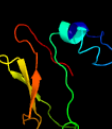


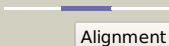
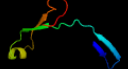
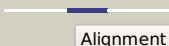
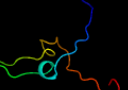
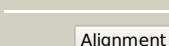



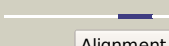

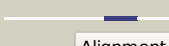
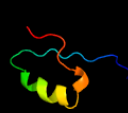

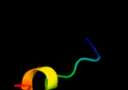
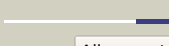
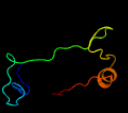


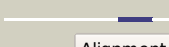


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1927_(- )_2179680_2180453
Date	Fri Aug 2 13:30:54 BST 2019
Unique Job ID	7e15273f3f21dcb5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3bgtD_</a>	 Alignment		99.7	16	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> probable acetoacetate decarboxylase; <b>PDBTitle:</b> structural studies of acetoacetate decarboxylase
2	<a href="#">c3bh2C_</a>	 Alignment		99.6	12	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> acetoacetate decarboxylase; <b>PDBTitle:</b> structural studies of acetoacetate decarboxylase
3	<a href="#">c4jmeA_</a>	 Alignment		99.4	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein mppr; <b>PDBTitle:</b> enduracididine biosynthesis enzyme mppr complexed with 2-keto-2 enduracididine
4	<a href="#">d3c8wa1</a>	 Alignment		99.0	13	<b>Fold:</b> Acetoacetate decarboxylase-like <b>Superfamily:</b> Acetoacetate decarboxylase-like <b>Family:</b> Acetoacetate decarboxylase-like
5	<a href="#">c4zbtB_</a>	 Alignment		99.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> acetoacetate decarboxylase; <b>PDBTitle:</b> streptomyces bingchenggensis aldolase-dehydratase in schiff base2 complex with pyruvate
6	<a href="#">c5upbA_</a>	 Alignment		98.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> acetoacetate decarboxylase; <b>PDBTitle:</b> swit_4259, an acetoacetate decarboxylase-like enzyme from sphingomonas2 wittichii rw1
7	<a href="#">d3cmba1</a>	 Alignment		98.6	13	<b>Fold:</b> Acetoacetate decarboxylase-like <b>Superfamily:</b> Acetoacetate decarboxylase-like <b>Family:</b> Acetoacetate decarboxylase-like
8	<a href="#">c5jxpA_</a>	 Alignment		19.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
9	<a href="#">d1s1da_</a>	 Alignment		14.0	31	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Apyrase <b>Family:</b> Apyrase
10	<a href="#">c2yueA_</a>	 Alignment		12.6	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein neuralized; <b>PDBTitle:</b> solution structure of the neuz (nhr) domain in neuralized2 from drosophila melanogaster
11	<a href="#">d1ttza_</a>	 Alignment		10.7	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase

12	<a href="#">c3wo1B_</a>	 Alignment		10.3	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> dipeptidyl aminopeptidase bii; <b>PDBTitle:</b> crystal structure of the dap bii dipeptide complex i
13	<a href="#">c5w61A_</a>	 Alignment		9.5	12	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> rtx repeat-containing cytotoxin; <b>PDBTitle:</b> crystal structure of rrsp, a martx toxin effector domain from vibrio2 vulnificus cmcp6
14	<a href="#">c3jb9K_</a>	 Alignment		7.5	40	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> K; <b>PDB Molecule:</b> pre-mrna-splicing factor prp5; <b>PDBTitle:</b> cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
15	<a href="#">c2j58G_</a>	 Alignment		7.3	13	<b>PDB header:</b> membrane protein <b>Chain:</b> G; <b>PDB Molecule:</b> outer membrane lipoprotein wza; <b>PDBTitle:</b> the structure of wza
16	<a href="#">c5ij1A_</a>	 Alignment		6.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> dna polymerase ii large subunit; <b>PDBTitle:</b> d-family dna polymerase - dp2 subunit (catalytic subunit)
17	<a href="#">c3fxtB_</a>	 Alignment		5.7	16	<b>PDB header:</b> gene regulation <b>Chain:</b> B; <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 6; <b>PDBTitle:</b> crystal structure of the n-terminal domain of human nudt6
18	<a href="#">d2b5dx1</a>	 Alignment		5.7	50	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Families 57/38 glycoside transferase middle domain <b>Family:</b> AmyC C-terminal domain-like
19	<a href="#">c6gzfB_</a>	 Alignment		5.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> xi class gst from natrialba magadii
20	<a href="#">c3bsuF_</a>	 Alignment		5.4	21	<b>PDB header:</b> hydrolase/rna/dna <b>Chain:</b> F; <b>PDB Molecule:</b> ribonuclease h1; <b>PDBTitle:</b> hybrid-binding domain of human rnase h1 in complex with 12-2 mer rna/dna
21	<a href="#">c6hmsB_</a>	 Alignment	not modelled	5.4	19	<b>PDB header:</b> replication <b>Chain:</b> B; <b>PDB Molecule:</b> dna polymerase ii large subunit,dna polymerase ii large <b>PDBTitle:</b> cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna