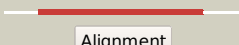



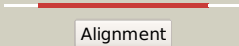







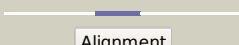
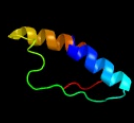
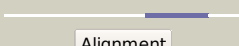

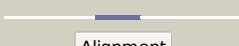

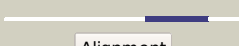


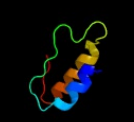

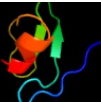


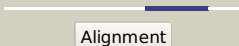





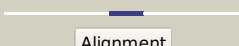
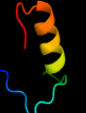
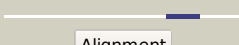
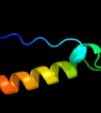
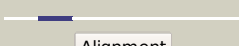







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3815c_(-)_4280211_4280966
Date	Fri Aug 9 18:20:52 BST 2019
Unique Job ID	64dd44de0de5389c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5kymA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-acyl-sn-glycerol-3-phosphate acyltransferase; <b>PDBTitle:</b> crystal structure of the 1-acyl-sn-glycerophosphate (lpa)2 acyltransferase, plsc, from thermotoga maritima
2	<a href="#">c5f34A_</a>	 Alignment		99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol mannoside acyltransferase; <b>PDBTitle:</b> crystal structure of membrane associated pata from mycobacterium2 smegmatis in complex with s-hexadecyl coenzyme a - p21 space group
3	<a href="#">c5knkB_</a>	 Alignment		99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipid a biosynthesis lauroyl acyltransferase; <b>PDBTitle:</b> lipid a secondary acyltransferase lpxm from acinetobacter baumannii2 with catalytic residue substitution (e127a)
4	<a href="#">d1iuga_</a>	 Alignment		99.0	17	<b>Fold:</b> Glycerol-3-phosphate (1)-acyltransferase <b>Superfamily:</b> Glycerol-3-phosphate (1)-acyltransferase <b>Family:</b> Glycerol-3-phosphate (1)-acyltransferase
5	<a href="#">c4cyyA_</a>	 Alignment		18.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pantetheinase; <b>PDBTitle:</b> the structure of vanin-1: defining the link between metabolic disease,2 oxidative stress and inflammation
6	<a href="#">d1l8na1</a>	 Alignment		13.0	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> alpha-D-glucuronidase/Hyaluronidase catalytic domain
7	<a href="#">c5khaA_</a>	 Alignment		11.6	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-dependent nad+ synthetase; <b>PDBTitle:</b> structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
8	<a href="#">d1h41a1</a>	 Alignment		11.5	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> alpha-D-glucuronidase/Hyaluronidase catalytic domain
9	<a href="#">c3hkxA_</a>	 Alignment		10.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidase; <b>PDBTitle:</b> crystal structure analysis of an amidase from nesterenkonia sp.
10	<a href="#">c1mqrA_</a>	 Alignment		9.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-d-glucuronidase; <b>PDBTitle:</b> the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 steartothermophilus t-6
11	<a href="#">c5vrhA_</a>	 Alignment		9.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein n-acyltransferase; <b>PDBTitle:</b> apolipoprotein n-acyltransferase c387s active site mutant

12	<a href="#">c1wx4B_</a>			8.8	22	<b>PDB header:</b> oxidoreductase/metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> melc; <b>PDBTitle:</b> crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a cddie protein3 prepared by the addition of dithiothreitol
13	<a href="#">c1emsB_</a>			8.8	8	<b>PDB header:</b> antitumor protein <b>Chain:</b> B: <b>PDB Molecule:</b> nit-fragile histidine triad fusion protein; <b>PDBTitle:</b> crystal structure of the c. elegans nitfhit protein
14	<a href="#">c1gqkB_</a>			8.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-d-glucuronidase; <b>PDBTitle:</b> structure of pseudomonas cellulosa alpha-d-glucuronidase complexed2 with glucuronic acid
15	<a href="#">d1uf5a_</a>			7.8	16	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Carbamilase
16	<a href="#">d1o59a2</a>			7.5	18	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Allantoicase repeat
17	<a href="#">d1aopa2</a>			7.3	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
18	<a href="#">d2q8za1</a>			6.9	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Decarboxylase
19	<a href="#">c6ehrD_</a>			6.9	44	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> ragulator complex protein lamtor4; <b>PDBTitle:</b> the crystal structure of the human lamtor-raga ctd-ragc ctd complex
20	<a href="#">d1o59a1</a>			5.9	33	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Allantoicase repeat
21	<a href="#">d1jcua_</a>		not modelled	5.9	14	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> YrdC-like
22	<a href="#">c3wuyA_</a>		not modelled	5.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrilase; <b>PDBTitle:</b> crystal structure of nit6803