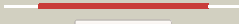



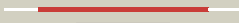

















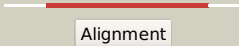

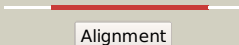

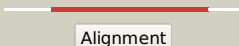



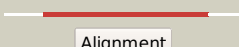

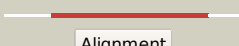
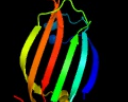
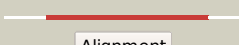






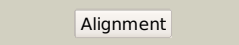

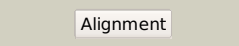

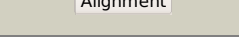


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2949c_(-)_3299981_3300580
Date	Thu Aug 8 16:20:10 BST 2019
Unique Job ID	842334267951e928

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2nwia1</a>	 Alignment		100.0	25	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> AF1396-like
2	<a href="#">d1tt8a_</a>	 Alignment		100.0	19	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> Chorismate lyase
3	<a href="#">c3f8lC_</a>	 Alignment		98.5	13	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> hth-type transcriptional repressor phnf; <b>PDBTitle:</b> crystal structure of the effector domain of phnf from mycobacterium2 smegmatis
4	<a href="#">d3cnva1</a>	 Alignment		98.3	14	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
5	<a href="#">d2p19a1</a>	 Alignment		98.2	12	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
6	<a href="#">c4zsiA_</a>	 Alignment		98.0	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor dasr; <b>PDBTitle:</b> crystal structure of the effector-binding domain of dasr (dasr-ebd) in2 complex with glucosamine-6-phosphate
7	<a href="#">c2ra5A_</a>	 Alignment		97.9	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative transcriptional regulator2 from streptomyces coelicolor
8	<a href="#">d2ra5a1</a>	 Alignment		97.9	9	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
9	<a href="#">d3bwqa2</a>	 Alignment		97.9	10	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
10	<a href="#">d2ogga1</a>	 Alignment		97.8	9	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
11	<a href="#">c3hfiA_</a>	 Alignment		97.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative regulator; <b>PDBTitle:</b> the crystal structure of the putative regulator from escherichia coli2 cft073

12	<a href="#">d2fa1a1</a>	 Alignment		97.7	7	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
13	<a href="#">d2ikka1</a>	 Alignment		97.6	11	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
14	<a href="#">d2pkha1</a>	 Alignment		97.4	13	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
15	<a href="#">d2ooia1</a>	 Alignment		97.3	8	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
16	<a href="#">c3lheA</a>	 Alignment		96.9	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> gntR family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of a gntR2 family transcriptional regulator from bacillus anthracis3 str. sterne
17	<a href="#">d3ddva1</a>	 Alignment		96.3	13	<b>Fold:</b> Chorismate lyase-like <b>Superfamily:</b> Chorismate lyase-like <b>Family:</b> UTRA domain
18	<a href="#">c3f8mA</a>	 Alignment		92.1	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gntR-family protein transcriptional regulator; <b>PDBTitle:</b> crystal structure of phnF from mycobacterium smegmatis
19	<a href="#">c4zs8A</a>	 Alignment		91.9	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor dasR; <b>PDBTitle:</b> crystal structure of ligand-free, full length dasR
20	<a href="#">c3edpB</a>	 Alignment		88.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lin2111 protein; <b>PDBTitle:</b> the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
21	<a href="#">c3eetA</a>	 Alignment	not modelled	85.2	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative gntR-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative gntR-family transcriptional2 regulator
22	<a href="#">c2wv0H</a>	 Alignment	not modelled	65.4	17	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> hth-type transcriptional repressor yvoa; <b>PDBTitle:</b> crystal structure of the gntR-hutC family member yvoa from2 bacillus subtilis
23	<a href="#">c3bwgA</a>	 Alignment	not modelled	60.4	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator yydk; <b>PDBTitle:</b> the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
24	<a href="#">d2pnwa1</a>	 Alignment	not modelled	15.7	21	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> Barwin-like endoglucanases <b>Family:</b> MLTA-like
25	<a href="#">c6oitG</a>	 Alignment	not modelled	7.8	27	<b>PDB header:</b> plant protein <b>Chain:</b> G: <b>PDB Molecule:</b> protein chromatin remodeling 35; <b>PDBTitle:</b> cryoem structure of arabidopsis dd' complex (drd1 peptide-dms3-rdm1)
26	<a href="#">c1wr1B</a>	 Alignment	not modelled	5.9	20	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like protein dsk2; <b>PDBTitle:</b> the complex structure of dsk2p uba with ubiquitin