




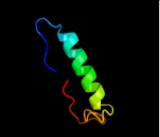

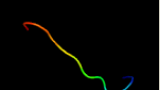

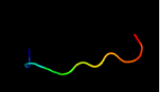

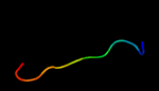



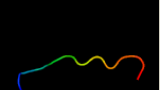

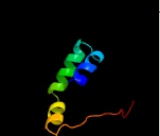




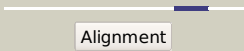
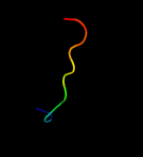
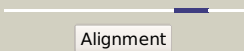

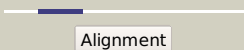







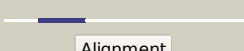

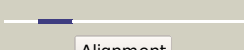
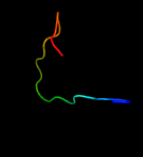

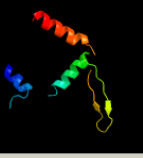



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1035c_(-)_1159379_1160065
Date	Wed Jul 31 22:05:11 BST 2019
Unique Job ID	6cc9d0ad1a1cf11a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3iwfA_</a>	 Alignment		26.1	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator rpir family; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
2	<a href="#">c4furD_</a>	 Alignment		15.0	50	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> urease subunit gamma 2; <b>PDBTitle:</b> crystal structure of urease subunit gamma 2 from brucella melitensis2 biovar abortus 2308
3	<a href="#">c4zmmB_</a>	 Alignment		14.8	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> ggdef domain of dcsbis complexed with c-di-gmp
4	<a href="#">c2fvhB_</a>	 Alignment		14.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> urease gamma subunit; <b>PDBTitle:</b> crystal structure of rv1848, a urease gamma subunit urea (urea2 amidohydrolase), from mycobacterium tuberculosis
5	<a href="#">d1e9ya2</a>	 Alignment		14.3	17	<b>Fold:</b> Urease, gamma-subunit <b>Superfamily:</b> Urease, gamma-subunit <b>Family:</b> Urease, gamma-subunit
6	<a href="#">d4ubpa_</a>	 Alignment		14.1	17	<b>Fold:</b> Urease, gamma-subunit <b>Superfamily:</b> Urease, gamma-subunit <b>Family:</b> Urease, gamma-subunit
7	<a href="#">c4z42A_</a>	 Alignment		12.4	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> urease subunit gamma; <b>PDBTitle:</b> crystal structure of urease from yersinia enterocolitica
8	<a href="#">d1ejxa_</a>	 Alignment		10.0	25	<b>Fold:</b> Urease, gamma-subunit <b>Superfamily:</b> Urease, gamma-subunit <b>Family:</b> Urease, gamma-subunit
9	<a href="#">c3wz4F_</a>	 Alignment		9.6	13	<b>PDB header:</b> unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> doti; <b>PDBTitle:</b> structure of the periplasmic domain of doti (crystal form i)
10	<a href="#">c2mxfA_</a>	 Alignment		9.6	21	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> mvat; <b>PDBTitle:</b> structure of the dna complex of the c-terminal domain of mvat
11	<a href="#">c3qgaD_</a>	 Alignment		9.6	8	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> fusion of urease beta and gamma subunits; <b>PDBTitle:</b> 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae

12	<a href="#">c1e9zA_</a>	 Alignment		9.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> urease subunit alpha; <b>PDBTitle:</b> crystal structure of helicobacter pylori urease
13	<a href="#">c4ntqB_</a>	 Alignment		8.4	22	<b>PDB header:</b> toxin <b>Chain:</b> B; <b>PDB Molecule:</b> ecl cdii; <b>PDBTitle:</b> cdia-ct/cdii toxin and immunity complex from enterobacter cloacae
14	<a href="#">c5cn1A_</a>	 Alignment		8.4	11	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> icml-like; <b>PDBTitle:</b> crystal structure of an icml-like type iv secretion system protein2 (lpg0120) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 at 2.65 a resolution
15	<a href="#">d1t9ba1</a>	 Alignment		7.9	8	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
16	<a href="#">c1p9cA_</a>	 Alignment		5.7	11	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> 26s proteasome non-atpase regulatory subunit 4; <b>PDBTitle:</b> nmr solution structure of the c-terminal ubiquitin-2 interacting motif of the proteasome subunit s5a
17	<a href="#">c2zihC_</a>	 Alignment		5.5	17	<b>PDB header:</b> protein transport <b>Chain:</b> C; <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 74; <b>PDBTitle:</b> crystal structure of yeast vps74
18	<a href="#">c3wz3A_</a>	 Alignment		5.5	15	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> tram protein; <b>PDBTitle:</b> structure of a periplasmic fragment of tram
19	<a href="#">d3ebya1</a>	 Alignment		5.4	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
20	<a href="#">c2ziiA_</a>	 Alignment		5.3	17	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 74; <b>PDBTitle:</b> crystal structure of yeast vps74-n-term truncation variant
21	<a href="#">c3hefB_</a>	 Alignment	not modelled	5.3	30	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> gene 1 protein; <b>PDBTitle:</b> crystal structure of the bacteriophage sf6 terminase small subunit