







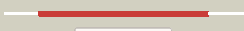













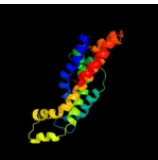
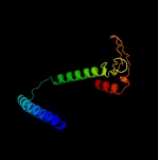




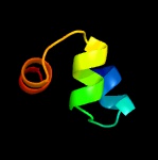




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2399c_cysT_2695806_2696657
Date	Mon Aug 5 13:25:56 BST 2019
Unique Job ID	1a0b8ed79fe00484

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4tqv1_</a>	 Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> I; <b>PDB Molecule:</b> algm1; <b>PDBTitle:</b> crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
2	<a href="#">c3fh6F_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> F; <b>PDB Molecule:</b> maltose transport system permease protein malF; <b>PDBTitle:</b> crystal structure of the resting state maltose transporter from e.2 coli
3	<a href="#">c3d31D_</a>	 Alignment		100.0	28	<b>PDB header:</b> transport protein <b>Chain:</b> D; <b>PDB Molecule:</b> sulfate/molybdate abc transporter, permease protein; <b>PDBTitle:</b> modbc from methanosarcina acetivorans
4	<a href="#">d3d31c1</a>	 Alignment		100.0	28	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
5	<a href="#">c2onkC_</a>	 Alignment		100.0	27	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> molybdate/tungstate abc transporter, permease <b>PDBTitle:</b> abc transporter modbc in complex with its binding protein2 moda
6	<a href="#">d2onkc1</a>	 Alignment		100.0	27	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
7	<a href="#">d2r6gg1</a>	 Alignment		100.0	19	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
8	<a href="#">c2r6gF_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> F; <b>PDB Molecule:</b> maltose transport system permease protein malF; <b>PDBTitle:</b> the crystal structure of the e. coli maltose transporter
9	<a href="#">c4tqv1_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> J; <b>PDB Molecule:</b> algm2; <b>PDBTitle:</b> crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
10	<a href="#">d2r6gf2</a>	 Alignment		100.0	20	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
11	<a href="#">c4ymuC_</a>	 Alignment		100.0	19	<b>PDB header:</b> protein binding/transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> abc-type amino acid transport system, permease component; <b>PDBTitle:</b> crystal structure of an amino acid abc transporter complex with2 arginines and atps

12	<a href="#">d3dhwa1</a>	Alignment		100.0	19	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
13	<a href="#">c5kbuA</a>	Alignment		85.5	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate receptor 2,voltage-dependent calcium channel <b>PDBTitle:</b> cryo-em structure of glua2-2xstz complex at 7.8 angstrom resolution
14	<a href="#">d2r6gf1</a>	Alignment		77.4	18	<b>Fold:</b> MalF N-terminal region-like <b>Superfamily:</b> MalF N-terminal region-like <b>Family:</b> MalF N-terminal region-like
15	<a href="#">c2m8gX</a>	Alignment		39.9	16	<b>PDB header:</b> transcription <b>Chain:</b> X: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> structure, function, and tethering of dna-binding domains in 542 transcriptional activators
16	<a href="#">c4l5eA</a>	Alignment		35.3	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of a. aeolicus ntrc1 dna binding domain
17	<a href="#">c1umqA</a>	Alignment		29.7	19	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein; <b>PDBTitle:</b> solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
18	<a href="#">d1umqa</a>	Alignment		29.7	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
19	<a href="#">d1ntca</a>	Alignment		29.3	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
20	<a href="#">c2jwaA</a>	Alignment		22.1	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-2; <b>PDBTitle:</b> erbB2 transmembrane segment dimer spatial structure
21	<a href="#">c2ks1A</a>	Alignment	not modelled	22.1	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-2; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbB1 and erbB2 receptors enabling kinase activation
22	<a href="#">c2n2aA</a>	Alignment	not modelled	21.7	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-2; <b>PDBTitle:</b> spatial structure of her2/erbB2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
23	<a href="#">d1fipa</a>	Alignment	not modelled	20.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
24	<a href="#">c3e7ID</a>	Alignment	not modelled	18.0	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4's dna binding2 domain
25	<a href="#">d1etob</a>	Alignment	not modelled	17.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
26	<a href="#">d1etxa</a>	Alignment	not modelled	12.8	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
27	<a href="#">c2hx6A</a>	Alignment	not modelled	12.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease; <b>PDBTitle:</b> solution structure analysis of the phage t42 endoribonuclease regB
28	<a href="#">c6agfB</a>	Alignment	not modelled	10.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> sodium channel subunit beta-1; <b>PDBTitle:</b> structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1 <b>PDB header:</b> transcription

29	<a href="#">c1g2hA_</a>	Alignment	not modelled	8.6	20	<b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein tyrr homolog; <b>PDBTitle:</b> solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
30	<a href="#">d1g2ha_</a>	Alignment	not modelled	8.6	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
31	<a href="#">c2momC_</a>	Alignment	not modelled	8.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> lysosome-associated membrane glycoprotein 2; <b>PDBTitle:</b> structural insights of tm domain of lamp-2a in dpc micelles
32	<a href="#">c2momB_</a>	Alignment	not modelled	8.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> lysosome-associated membrane glycoprotein 2; <b>PDBTitle:</b> structural insights of tm domain of lamp-2a in dpc micelles
33	<a href="#">d2oara1</a>	Alignment	not modelled	8.0	13	<b>Fold:</b> Gated mechanosensitive channel <b>Superfamily:</b> Gated mechanosensitive channel <b>Family:</b> Gated mechanosensitive channel
34	<a href="#">c1p7bB_</a>	Alignment	not modelled	7.0	13	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> integral membrane channel and cytosolic domains; <b>PDBTitle:</b> crystal structure of an inward rectifier potassium channel
35	<a href="#">c3rkoF_</a>	Alignment	not modelled	6.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
36	<a href="#">c5m7nA_</a>	Alignment	not modelled	6.1	6	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen assimilation regulatory protein; <b>PDBTitle:</b> crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
37	<a href="#">c1ojlD_</a>	Alignment	not modelled	5.5	19	<b>PDB header:</b> response regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulatory protein zrar; <b>PDBTitle:</b> crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
38	<a href="#">c2lcxB_</a>	Alignment	not modelled	5.5	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-4; <b>PDBTitle:</b> spatial structure of the erbb4 dimeric tm domain