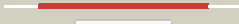



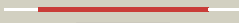



















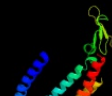








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2039c_(- )_2284807_2285649
Date	Mon Aug 5 13:25:15 BST 2019
Unique Job ID	1c1a48e6e3e0fa90

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2r6gg1</a>	 Alignment		100.0	27	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
2	<a href="#">c4tqvj_</a>	 Alignment		100.0	25	<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
3	<a href="#">c3fh6F_</a>	 Alignment		100.0	19	<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
4	<a href="#">c4tqvj_</a>	 Alignment		100.0	17	<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
5	<a href="#">c2r6gF_</a>	 Alignment		100.0	22	<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
6	<a href="#">d2onkc1</a>	 Alignment		100.0	16	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
7	<a href="#">c2onkC_</a>	 Alignment		100.0	16	<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
8	<a href="#">c3d31D_</a>	 Alignment		100.0	15	<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
9	<a href="#">d3d31c1</a>	 Alignment		100.0	15	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
10	<a href="#">d2r6gf2</a>	 Alignment		100.0	22	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
11	<a href="#">c4ymuC_</a>	 Alignment		100.0	9	<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		99.8	13	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
13	<a href="#">d2r6gf1</a>	Alignment		84.0	19	<b>Fold:</b> MalF N-terminal region-like <b>Superfamily:</b> MalF N-terminal region-like <b>Family:</b> MalF N-terminal region-like
14	<a href="#">c5kbuA</a>	Alignment		57.5	9	<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
15	<a href="#">c2hx6A</a>	Alignment		28.7	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
16	<a href="#">c3hd7A</a>	Alignment		19.5	22	<b>PDB header:</b> exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
17	<a href="#">c2m8gX</a>	Alignment		18.3	17	<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
18	<a href="#">c4l5eA</a>	Alignment		18.0	13	<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
19	<a href="#">d1umqa</a>	Alignment		15.3	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
20	<a href="#">c1umqA</a>	Alignment		15.3	6	<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
21	<a href="#">c2kogA</a>	Alignment	not modelled	13.6	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> lipid-bound synaptobrevin solution nmr structure
22	<a href="#">c3ipdB</a>	Alignment	not modelled	12.4	6	<b>PDB header:</b> exocytosis <b>Chain:</b> B: <b>PDB Molecule:</b> syntaxin-1a; <b>PDBTitle:</b> helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
23	<a href="#">c3e7lD</a>	Alignment	not modelled	12.0	23	<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
24	<a href="#">d1ntca</a>	Alignment	not modelled	11.6	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
25	<a href="#">c6gcs6</a>	Alignment	not modelled	10.1	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> 6: <b>PDB Molecule:</b> nd6 subunit (nu6m); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
26	<a href="#">d1etob</a>	Alignment	not modelled	9.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
27	<a href="#">c1g2hA</a>	Alignment	not modelled	8.9	20	<b>PDB header:</b> transcription <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
28	<a href="#">d1g2ha</a>	Alignment	not modelled	8.9	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like

29	<a href="#">d1fipa_</a>	Alignment	not modelled	8.3	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
30	<a href="#">d1etxa_</a>	Alignment	not modelled	7.8	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
31	<a href="#">c1ojlD_</a>	Alignment	not modelled	6.1	13	<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
32	<a href="#">d1cf7a_</a>	Alignment	not modelled	5.7	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Cell cycle transcription factor e2f-dp
33	<a href="#">c5m7nA_</a>	Alignment	not modelled	5.5	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
34	<a href="#">d2diia1</a>	Alignment	not modelled	5.4	28	<b>Fold:</b> BSD domain-like <b>Superfamily:</b> BSD domain-like <b>Family:</b> BSD domain
35	<a href="#">d1brwa3</a>	Alignment	not modelled	5.3	24	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Pyrimidine nucleoside phosphorylase C-terminal domain <b>Family:</b> Pyrimidine nucleoside phosphorylase C-terminal domain
36	<a href="#">c2jwaA_</a>	Alignment	not modelled	5.2	18	<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
37	<a href="#">c2ks1A_</a>	Alignment	not modelled	5.2	18	<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
38	<a href="#">d2tpta3</a>	Alignment	not modelled	5.1	24	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Pyrimidine nucleoside phosphorylase C-terminal domain <b>Family:</b> Pyrimidine nucleoside phosphorylase C-terminal domain
39	<a href="#">c2diia_</a>	Alignment	not modelled	5.0	28	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> tffiH basal transcription factor complex p62 <b>PDBTitle:</b> solution structure of the bsd domain of human tffiH basal2 transcription factor complex p62 subunit