



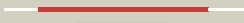

















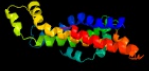
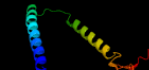
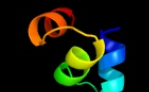








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0930_(pstA1)_1037015_1037917
Date	Fri Jul 26 01:50:52 BST 2019
Unique Job ID	f20fd079b7784170

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	15	<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="#">c4tqv1_</a>	 Alignment		100.0	12	<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
4	<a href="#">c2r6gF_</a>	 Alignment		100.0	16	<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
5	<a href="#">d2r6gg1</a>	 Alignment		100.0	13	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
6	<a href="#">d2r6gf2</a>	 Alignment		100.0	16	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
7	<a href="#">d2onkc1</a>	 Alignment		100.0	19	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
8	<a href="#">c2onkC_</a>	 Alignment		100.0	19	<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
9	<a href="#">d3d31c1</a>	 Alignment		100.0	22	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
10	<a href="#">c3d31D_</a>	 Alignment		100.0	22	<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
11	<a href="#">c4ymuC_</a>	 Alignment		100.0	15	<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	21	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
13	<a href="#">c5kbuA</a>	Alignment		87.6	15	<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="#">c2m8gX</a>	Alignment		38.7	23	<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
15	<a href="#">c2hx6A</a>	Alignment		36.9	42	<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="#">c1umqA</a>	Alignment		28.1	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
17	<a href="#">d1umqa</a>	Alignment		28.1	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
18	<a href="#">d1ntca</a>	Alignment		27.7	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
19	<a href="#">c4l5eA</a>	Alignment		26.2	25	<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
20	<a href="#">d1fipa</a>	Alignment		21.1	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
21	<a href="#">d1etob</a>	Alignment	not modelled	17.7	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
22	<a href="#">d2r6gf1</a>	Alignment	not modelled	16.1	12	<b>Fold:</b> MalF N-terminal region-like <b>Superfamily:</b> MalF N-terminal region-like <b>Family:</b> MalF N-terminal region-like
23	<a href="#">c3e7lD</a>	Alignment	not modelled	14.9	22	<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="#">d1etxa</a>	Alignment	not modelled	13.9	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
25	<a href="#">c2ks1A</a>	Alignment	not modelled	13.4	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
26	<a href="#">c2jwaA</a>	Alignment	not modelled	13.4	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
27	<a href="#">c2n2aA</a>	Alignment	not modelled	12.9	18	<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 jxtamembrane domains <b>PDB header:</b> signaling protein
28	<a href="#">c6c0aB</a>	Alignment	not modelled	11.3	19	<b>Chain:</b> B: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel subunit alpha-1c; <b>PDBTitle:</b> actinin-1 ef-hand bound to the cav1.2 iq motif <b>PDB header:</b> calcium binding protein/membrane protein

29	<a href="#">c6dadD_</a>	Alignment	not modelled	11.1	19	<b>Chain:</b> D; <b>PDB Molecule:</b> voltage-dependent l-type calcium channel subunit alpha-1c; <b>PDBTitle:</b> 1.65 angstrom crystal structure of the n97i ca/cam:cav1.2 iq domain2 complex
30	<a href="#">c6daeD_</a>	Alignment	not modelled	11.1	18	<b>PDB header:</b> calcium binding protein/membrane protein <b>Chain:</b> D; <b>PDB Molecule:</b> voltage-dependent l-type calcium channel subunit alpha-1c; <b>PDBTitle:</b> 2.0 angstrom crystal structure of the d95v ca/cam:cav1.2 iq domain2 complex
31	<a href="#">c1g2hA_</a>	Alignment	not modelled	9.8	17	<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
32	<a href="#">d1g2ha_</a>	Alignment	not modelled	9.8	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
33	<a href="#">c2be6D_</a>	Alignment	not modelled	9.7	19	<b>PDB header:</b> membrane protein <b>Chain:</b> D; <b>PDB Molecule:</b> voltage-dependent l-type calcium channel alpha-1c subunit; <b>PDBTitle:</b> 2.0 a crystal structure of the cav1.2 iq domain-ca/cam complex
34	<a href="#">c6dafD_</a>	Alignment	not modelled	9.0	19	<b>PDB header:</b> calcium binding protein/membrane protein <b>Chain:</b> D; <b>PDB Molecule:</b> voltage-dependent l-type calcium channel subunit alpha-1c; <b>PDBTitle:</b> 2.4 angstrom crystal structure of the f141l ca/cam:cav1.2 iq domain2 complex
35	<a href="#">c6iiuA_</a>	Alignment	not modelled	8.6	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> soluble cytochrome b562,thromboxane a2 receptor,rubredoxin, <b>PDBTitle:</b> crystal structure of the human thromboxane a2 receptor bound to2 ramatroban
36	<a href="#">c2be6F_</a>	Alignment	not modelled	8.4	19	<b>PDB header:</b> membrane protein <b>Chain:</b> F; <b>PDB Molecule:</b> voltage-dependent l-type calcium channel alpha-1c subunit; <b>PDBTitle:</b> 2.0 a crystal structure of the cav1.2 iq domain-ca/cam complex
37	<a href="#">c6dadC_</a>	Alignment	not modelled	8.0	19	<b>PDB header:</b> calcium binding protein/membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> voltage-dependent l-type calcium channel subunit alpha-1c; <b>PDBTitle:</b> 1.65 angstrom crystal structure of the n97i ca/cam:cav1.2 iq domain2 complex
38	<a href="#">c2m20B_</a>	Alignment	not modelled	7.6	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> epidermal growth factor receptor; <b>PDBTitle:</b> egfr transmembrane - jxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
39	<a href="#">c1ojlD_</a>	Alignment	not modelled	7.3	16	<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
40	<a href="#">c5lq3F_</a>	Alignment	not modelled	6.6	17	<b>PDB header:</b> transport protein <b>Chain:</b> F; <b>PDB Molecule:</b> cmeb; <b>PDBTitle:</b> structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb