








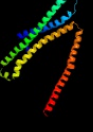



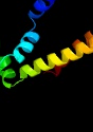

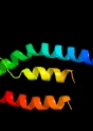


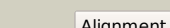

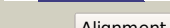
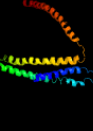
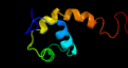
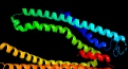
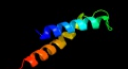
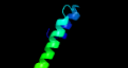



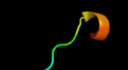
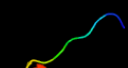


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1101c_(-)_1229396_1230553
Date	Wed Jul 31 22:05:18 BST 2019
Unique Job ID	d6e731e3e228c78c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1kkxa_</a>	 Alignment		55.4	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> ARID-like <b>Family:</b> ARID domain
2	<a href="#">d3b60a2</a>	 Alignment		44.1	11	<b>Fold:</b> ABC transporter transmembrane region <b>Superfamily:</b> ABC transporter transmembrane region <b>Family:</b> ABC transporter transmembrane region
3	<a href="#">c3qf4B_</a>	 Alignment		40.6	6	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized abc transporter atp-binding protein <b>PDBTitle:</b> crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
4	<a href="#">c5u1dB_</a>	 Alignment		24.6	10	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> antigen peptide transporter 2; <b>PDBTitle:</b> cryo-em structure of the human tap atp-binding cassette transporter
5	<a href="#">c5c76D_</a>	 Alignment		17.2	11	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> wlab protein; <b>PDBTitle:</b> atp-driven lipid-linked oligosaccharide flippase pglk in apo-inward2 facing state (2)
6	<a href="#">c4pl0B_</a>	 Alignment		17.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> microcin-j25 export atp-binding/permease protein mcjd; <b>PDBTitle:</b> crystal structure of the antibacterial peptide abc transporter mcjd in2 an outward occluded state
7	<a href="#">c4yzfA_</a>	 Alignment		16.9	15	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> band 3 anion transport protein; <b>PDBTitle:</b> crystal structure of the anion exchanger domain of human erythrocyte2 band 3
8	<a href="#">c5jqnA_</a>	 Alignment		15.3	15	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> phospho-n-acetylmuramoyl-pentapeptide-transferase; <b>PDBTitle:</b> mray tunicamycin complex
9	<a href="#">d1ryua_</a>	 Alignment		11.8	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> ARID-like <b>Family:</b> ARID domain
10	<a href="#">c3rlbA_</a>	 Alignment		11.1	13	<b>PDB header:</b> thiamine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> thit; <b>PDBTitle:</b> crystal structure at 2.0 a of the s-component for thiamin from an ecf-2 type abc transporter
11	<a href="#">c3b5wE_</a>	 Alignment		8.7	10	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> lipid a export atp-binding/permease protein msba; <b>PDBTitle:</b> crystal structure of eschericia coli msba

12	<a href="#">d1ig6a_</a>	Alignment		8.5	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> ARID-like <b>Family:</b> ARID domain
13	<a href="#">c3qf4A_</a>	Alignment		8.3	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, atp-binding protein; <b>PDBTitle:</b> crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
14	<a href="#">c4p6vB_</a>	Alignment		8.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> na(+)-translocating nadh-quinone reductase subunit b; <b>PDBTitle:</b> crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
15	<a href="#">c2b6pA_</a>	Alignment		8.1	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lens fiber major intrinsic protein; <b>PDBTitle:</b> x-ray structure of lens aquaporin-0 (aqp0) (lens mip) in an open pore2 state
16	<a href="#">c5nf2A_</a>	Alignment		8.1	10	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> minor fimbrium subunit mfa1; <b>PDBTitle:</b> the fimbrial shaft protein mfa1 from porphyromonas gingivalis
17	<a href="#">c3j2wE_</a>	Alignment		8.1	26	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> glycoprotein e1; <b>PDBTitle:</b> electron cryo-microscopy of chikungunya virus
18	<a href="#">c3j2wH_</a>	Alignment		8.1	26	<b>PDB header:</b> virus <b>Chain:</b> H: <b>PDB Molecule:</b> glycoprotein e1; <b>PDBTitle:</b> electron cryo-microscopy of chikungunya virus
19	<a href="#">c3j7kF_</a>	Alignment		7.9	25	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit f; <b>PDBTitle:</b> model of the human eif3 pci-mpn octamer docked into the 43s em map
20	<a href="#">c3j7jF_</a>	Alignment		7.9	25	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit f; <b>PDBTitle:</b> model of the human eif3 pci-mpn octamer docked into the 43s-hcv ires2 em map
21	<a href="#">c3j8bF_</a>	Alignment	not modelled	7.9	25	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit f; <b>PDBTitle:</b> model of the human eif3 pci-mpn octamer docked into the 43s-hcv ires2 em map
22	<a href="#">c3j8cF_</a>	Alignment	not modelled	7.9	25	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit f; <b>PDBTitle:</b> model of the human eif3 pci-mpn octamer docked into the 43s em map
23	<a href="#">c4j72B_</a>	Alignment	not modelled	7.6	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phospho-n-acetylmuramoyl-pentapeptide-transferase; <b>PDBTitle:</b> crystal structure of polyprenyl-phosphate n-acetyl hexosamine 1-2 phosphate transferase
24	<a href="#">c4tkrB_</a>	Alignment	not modelled	7.6	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> thiamine transporter thia; <b>PDBTitle:</b> native-sad phasing for thit from listeria monocytogenes serovar.
25	<a href="#">c2eqyA_</a>	Alignment	not modelled	7.6	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> jumonji, at rich interactive domain 1b; <b>PDBTitle:</b> solution structure of the arid domain of jarid1b protein
26	<a href="#">c2mfrA_</a>	Alignment	not modelled	7.4	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> insulin receptor; <b>PDBTitle:</b> solution structure of the transmembrane domain of the insulin receptor2 in micelles
27	<a href="#">c6ithA_</a>	Alignment	not modelled	6.8	29	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> syndecan-2; <b>PDBTitle:</b> structure of the transmembrane domain of syndecan 2 in micelles
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane oligosaccharyl

28	<a href="#">c3wajA_</a>	Alignment	not modelled	6.7	11	transferase; <b>PDBTitle:</b> crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
29	<a href="#">c6hu9t_</a>	Alignment	not modelled	6.7	15	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> T; <b>PDB Molecule:</b> cytochrome b-c1 complex subunit 9; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
30	<a href="#">c6caaA_</a>	Alignment	not modelled	6.6	21	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> electrogenic sodium bicarbonate cotransporter 1; <b>PDBTitle:</b> cryoem structure of human slc4a4 sodium-coupled acid-base transporter2 nbce1
31	<a href="#">c6navl_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> structural protein <b>Chain:</b> I; <b>PDB Molecule:</b> m9ud72; <b>PDBTitle:</b> cryo-em reconstruction of sulfolobus islandicus la14/1 pilus
32	<a href="#">c3rlbB_</a>	Alignment	not modelled	6.3	13	<b>PDB header:</b> thiamine-binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> thit; <b>PDBTitle:</b> crystal structure at 2.0 a of the s-component for thiamin from an ecf-2 type abc transporter
33	<a href="#">c2jwaA_</a>	Alignment	not modelled	6.0	19	<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
34	<a href="#">c2ks1A_</a>	Alignment	not modelled	6.0	19	<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 erbb22 receptors enabling kinase activation
35	<a href="#">c4wpmA_</a>	Alignment	not modelled	5.9	6	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> mrna export protein; <b>PDBTitle:</b> structure of the chaetomium thermophilum mex67:mtr2 complex
36	<a href="#">c2lm1A_</a>	Alignment	not modelled	5.5	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> lysine-specific demethylase lid; <b>PDBTitle:</b> solution nmr structure of lysine-specific demethylase lid from2 drosophila melanogaster, northeast structural genomics consortium3 target fr824d
37	<a href="#">c3dl8C_</a>	Alignment	not modelled	5.5	15	<b>PDB header:</b> protein transport <b>Chain:</b> C; <b>PDB Molecule:</b> sece; <b>PDBTitle:</b> structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
38	<a href="#">c3dl8D_</a>	Alignment	not modelled	5.5	15	<b>PDB header:</b> protein transport <b>Chain:</b> D; <b>PDB Molecule:</b> sece; <b>PDBTitle:</b> structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
39	<a href="#">d2hyda2</a>	Alignment	not modelled	5.4	9	<b>Fold:</b> ABC transporter transmembrane region <b>Superfamily:</b> ABC transporter transmembrane region <b>Family:</b> ABC transporter transmembrane region