

# Annotation of *Campylobacter jejuni* at Locus Tags CJ0236c, CJ0468, CJ1161c, CJ0001, and CJ0991c

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## Abstract

A group of genes from the microorganism *Campylobacter jejuni* were annotated using the collaborative genome annotation website GENI-ACT. The Genbank proposed gene product name for each gene was assessed in terms of the general genomic information, amino acid sequence-based similarity data, structure-based evidence from the amino acid sequence, and cellular localization data. The Genbank proposed gene product name did not differ significantly from the proposed gene annotation for each of the genes in the group and as such, the genes appear to be correctly annotated by the computer database.

## Introduction

*Campylobacter jejuni* is a common foodborne pathogen associated with foodborne illness and food poisoning. In fact, it is currently the leading cause of bacterial food poisoning in the United States. The bacteria can enter and infect an organism by the consumption of contaminated food, most often uncooked/raw poultry, or water. Upon entering an organism, the bacteria penetrates the gastrointestinal mucus that is supposed to serve as a barrier for the intestines to protect them. After doing so, several toxins are secreted that attack the small and large intestines, causing symptoms such as bloody diarrhea, fever, and nausea. Diseases that result from *Campylobacter jejuni*, such as gastroenteritis or campylobacter enteritis, are not often long lasting and can be treated with antibiotics, or even go away untreated. Most recoveries from a bacterial infection of this type are quick. Instances of serious diseases such as arthritis, however, have resulted after long-term infection in some cases. Death is also possible. *Campylobacter jejuni* has developed antibiotic resistance to ampicillin and penicillin, but the antibiotic known as erythromycin has shown to be effective. Erythromycin resistance has been present in some cases, but a very low and currently insignificant amount (less than five percent). Also, the bacteria is sensitive to certain temperatures, acidities, and oxygen levels, so the control of this bacteria is rather easy and a reason why it often is eliminated from the body without proper treatment.

Scanning electron micrograph of *Campylobacter jejuni*. Credit: De Wood, Pooley, USDA's Agricultural Research Service.medicalxpress.com



## Methods

Modules of the GENI-ACT (<http://www.geni-act.org/>) were used to complete *Campylobacter jejuni* genome annotation. The modules are described below:

Modules	Activities	Questions Investigated
Module 1- Basic Information Module	DNA Coordinates and Sequence, Protein Sequence	What is the sequence of my gene and protein? Where is it located in the genome?
Module 2- Sequence-Based Similarity Data	Blast, CDD, T-Coffee, WebLogo	Is my sequence similar to other sequences in Genbank?
Module 3- Structure-Based Evidence	TIGRFam, Pfam, PDB	Are there functional domains in my protein?
Module 4- Cellular Localization Data	Gram Stain, TMHMM, SignalP, PSORT, Phobius	Is my protein in the cytoplasm, secreted or embedded in the membrane?

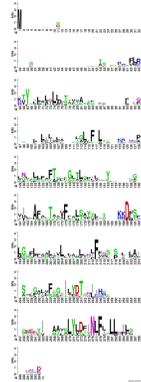
## Results

Gene Locus: CJ0236c		
Basic Information	DNA Coordinates	218523..219218
	DNA Length	696 nt
	Amino Acid Sequence Length	231 aa
Sequence-based Similarity	COGS	YbhL- Integral membrane protein, interacts with FtsH [General function prediction only]; sporadically conserved at the middle to end
	T-Coffee	Not well conserved from amino acid 1 to 52. Well conserved from 65-81. Sporadically conserved from the middle to the end. Many hydrophobic and polar amino acids.
	Web-Logo	
Structure-based Evidence	TIGRFAMs	none
	PFAMs	Inhibitor of apoptosis-promoting Bax1
	HMM Logo Key Residues	Y8, G81, F144, F200
	PDB	Entity 1 containing Chain A Crystal structure of YelJ from Bacillus Subtilis at pH 6 by Pt-SAD
Cellular Localization	Transmembrane Helices	no result given
	Signal Peptide	none
	PSORTb Final Prediction	cytoplasmic

### *Campylobacter jejuni* CJ0236c:

COG and PFAM data predict CJ0236c to be an inhibitor of apoptosis. Apoptosis is the process of programmed cell death in multicellular organisms. Due to the many orthologs seen in this research, it may be inferred that it is a common protein that many different bacteria species may have that help contribute to cell death. Although TMHMM data was inconclusive, the PSORTb final prediction was the protein resides in the cytoplasmic membrane.

Figure 1 – WebLogo data for *Campylobacter jejuni* CJ0236c showing conservation in the middle of the protein with many hydrophobic and polar amino acids.



Gene Locus: CJ0468		
Basic Information	DNA Coordinates	432356..433012
	DNA Length	657 nt
	Amino Acid Sequence Length	218 aa
Sequence-based Similarity	COGS	COG0765: HisM-ABC-type amino acid transport system, permease component [Amino acid transport and metabolism]
	T-Coffee	not conserved well at all until approximately halfway through, where it is well conserved from then on
	Web-Logo	not conserved well at all until approximately halfway through, where it is well conserved from then on
	TIGRFAMs	ectoine/hydroxyectoine ABC transporter, permease protein EhuD
Structure-based Evidence	PFAMs	Binding-protein-dependent transport system inner membrane component
	HMM Logo Key Residues	N/A
	PDB	Crystal structure of an amino acid ABC transporter
	Transmembrane Helices	5
Cellular Localization	Signal Peptide	None
	PSORTb Final Prediction	Cytoplasmic membrane

### *Campylobacter jejuni* CJ0468:

COG, TIGRFAM and PFAM data predict CJ0468 to be a transport protein, specifically permease. The protein is supported to transport amino acids into and out of the cell by the use of ATP, making it an ABC transport protein (ATP-binding cassette transporter). Due to the many orthologs seen in this research, it may be inferred that it is a common protein to many different species of bacteria. Cellular localization data predicts that this protein resides within the cytoplasmic membrane with 5 transmembrane helices.

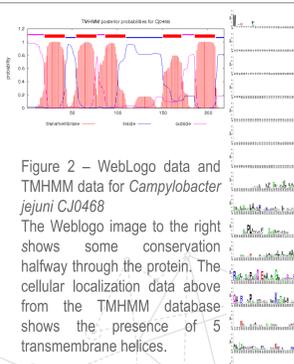


Figure 2 – WebLogo data and TMHMM data for *Campylobacter jejuni* CJ0468. The Weblogo image to the right shows some conservation halfway through the protein. The cellular localization data above from the TMHMM database shows the presence of 5 transmembrane helices.

Gene Locus: CJ1161c		
Basic Information	DNA Coordinates	complement(1091795..1093894)
	DNA Length	2,100 nt
	Amino Acid Sequence Length	699 aa
Sequence-based Similarity	COGS	No significant COG hit
	T-Coffee	Sporadically conserved in the middle
	Web-Logo	Sporadically conserved in the middle
Structure-based Evidence	TIGRFAMs	TIGR01511 ATPase_P-type, and ATPase-IB_Cu-P-type heavy metal-transporting ATPase
	PFAMs	pfam00122 E1-E2_ATPase
	HMM Logo Key Residues	G26, D27, D40, T56, G57, P160, L163
Cellular Localization	PDB	High resolution helical reconstruction of the bacterial p-type ATPase copper transporter CopA
	Transmembrane Helices	8
	Signal Peptide	No signal Peptide
	PSORTb Final Prediction	Cytoplasmic membrane

### *Campylobacter jejuni* CJ1161c:

Data from the PFAM, TIGRFAM, and TMHMM databases supports CJ1161c to be a membrane protein with 8 transmembrane helices, whose function is to pump metals across the membrane, specifically copper. Due to the numerous orthologs, it can be inferred that many species of bacteria contain similar proteins with similar functions.

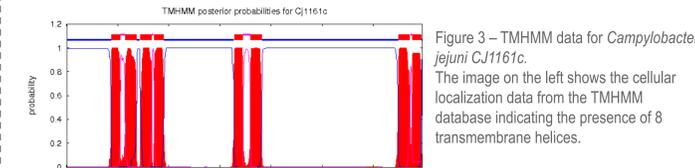


Figure 3 – TMHMM data for *Campylobacter jejuni* CJ1161c. The image on the left shows the cellular localization data from the TMHMM database indicating the presence of 8 transmembrane helices.

Gene Locus: CJ0001		
Basic Information	DNA Coordinates	1..1323
	DNA Length	1323nt
	Amino Acid Sequence Length	440aa
Sequence-based Similarity	COGS	DnaA-Chromosomal replication initiation ATPase DnaA [Replication, recombination and repair]
	T-Coffee	Well conserved throughout
	Web-Logo	Well conserved from 1-103,121-480. Not well conserved at the end.
Structure-based Evidence	TIGRFAMs	DnaA
	PFAMs	Bac_DnaA
	HMM Logo Key Residues	F7, F10, G13, N16, P36, G44, G44, H49, Y69, F75, D99, D104, D105, D138, P141, G158, R203
	PDB	Crystal structure of domain III from the <i>Thermotoga maritima</i> replication initiation protein DnaA
Cellular Localization	Transmembrane Helices	None
	Signal Peptide	None
	PSORTb Final Prediction	Cytoplasmic

### *Campylobacter jejuni* CJ0001:

COG, TIGRFAM, PFAM, and PDB data predict that CJ0001 contains an initiator protein to replicate, repair, and recombine chromosomes found in the cytoplasm. It allows the bacteria to make new DNA or repair it when more cells are made. Due to presence of many orthologs, the data supports the conclusion that this protein is common in many different species of bacteria. Cellular localization data predicts that this protein resides within the cytoplasm.

Figure 4 – WebLogo data for *Campylobacter jejuni* CJ0001 showing areas of conservation in the middle with less conservation at the C and N terminals.



Gene Locus: CJ0991c		
Basic Information	DNA Coordinates	complement(922155..923420)
	DNA Length	1266 nt
	Amino Acid Sequence Length	421 aa
Sequence-based Similarity	COGS	COG0247-GlpC Fe-S oxidoreductase [Energy production and conversion]
	T-Coffee	well conserved
	Web-Logo	well conserved middle to end
Structure-based Evidence	TIGRFAMs	TIGR03379- glycerol3P_GlpC: glycerol-3-phosphate dehydrogenase
	PFAMs	PF02754- CCG: Cysteine-rich domain
	HMM Logo Key Residues	C7, C40, C41, C80
	PDB	no results
Cellular Localization	Transmembrane Helices	none
	Signal Peptide	none
	PSORTb Final Prediction	Cytoplasmic membrane

### *Campylobacter jejuni* CJ0991c:

Data from the COG, PFAM, and TIGRFAM, databases supports CJ0991c to be an iron-sulfur glycolate oxidase enzyme. It helps to transfer a hydrogen atom from glycolate to an oxygen molecule forming either water or hydrogen peroxide. Cellular localization data predicts this protein to reside in the membrane, with no transmembrane helices.

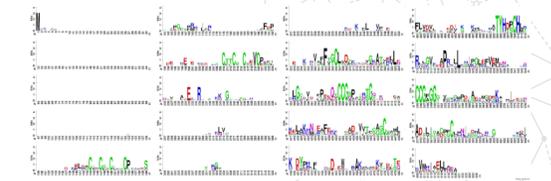


Figure 5 – WebLogo data for *Campylobacter jejuni* CJ0991c showing areas of conservation in the middle and at the C terminus with less conservation at the N terminus.

## Conclusion

The GENI-ACT proposed gene product did not differ significantly from the proposed gene annotation for each of the genes in the group and as such, the genes appear to be correctly annotated by the computer database.

Gene Locus	Geni-Act Gene Products	Proposed Annotation
CJ0236c	Inhibitor of apoptosis	Inhibitor of apoptosis
CJ0468	ABC-type amino acid transport system	ABC-type amino acid transport system
CJ1161c	Heavy metal-transporting ATPase	Heavy metal-transporting ATPase
CJ0001	Replication initiation protein DnaA	Replication initiation protein DnaA
CJ0991c	GlpC Fe-S oxidoreductase	GlpC Fe-S oxidoreductase

## References

Altekruse, S. F., Stern, N. J., Field, P. I., & Swerdlow, D. L. (2010, December 10). *Campylobacter jejuni*-An Emerging Foodborne Pathogen - Volume 5, Number 1-February 1999 - Emerging Infectious Disease journal - CDC. Retrieved from [https://wwwnc.cdc.gov/eid/article/5/1/99-0104\\_article](https://wwwnc.cdc.gov/eid/article/5/1/99-0104_article)

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