

# Annotation of the *Helicobacter pylori* 83 Genomes from DNA Coordinates 60073 to 60789 and 65824 to 66522

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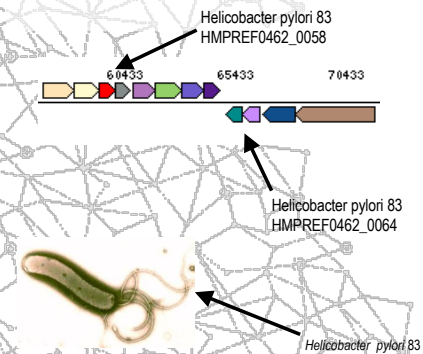
## Abstract

Our group annotated 2 genes from *Helicobacter pylori* 83 using the modules given by GENI-ACT. Following the instructions given in our GENI-ACT manual, we went to many different sites that aided us in annotating our genes. These included BLAST, CDD, T-coffee, WebLogo, Gram Stain, TMHMM, SignalP, Psort, Phobius, IMG EDU, TIGRfam, Pfam, PDB, KEGG, MetaCyc and Rfam. We recorded these findings on the online GENI-ACT lab notebook. Our results were established using both student annotations. Finally, as you can see, we are presenting our results on this trifold poster. We added pictures and diagrams to help show what our genes do. In the end, most of the proposed annotations for the sequenced genomes were the same. The purpose of our research was to annotate specific genes then compare the results to those already given by GENI-ACT and see if the data proposed annotations were either correct or incorrect.

## Introduction

The gram negative *Helicobacter pylori* 83 bacterium can alter the human regulatory mechanisms for gastric acid production. During initial, *Helicobacter pylori* 83 can decrease acid secretion levels in the stomach. This can result in ulcers in the stomach, and even in the duodenum. For many years, people believed that smoking, stress, spicy food, and other lifestyle caused stomach ulcers. It was later found that *Helicobacter pylori* 83 was ingested through unclean food. The pylorus is the sphincter muscles between the duodenum and the stomach. This research is very important because it will help us learn new ways to fight diseases and bacteria, such as *Helicobacter pylori* 83.

Our bioinformatics group has been working to analyze and annotate eight different genomes, that make up *Helicobacter pylori* 83. We split into two groups of four, who each annotated parts of the genome. We used websites such as Pfam, Tigrfam, Kegg, T-Coffee, to discover what our genes do, and what purpose they serve a in *Helicobacter pylori* 83.



## Methods

Modules of the GENI-ACT (<http://www.geni-act.org/>) were used to complete *Helicobacter pylori* 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- Cellular Localization Data            | Gram Stain, TMHMM, SignalP, PSORT, Phobius     | Is my protein in the cytoplasm, secreted or embedded in the membrane?            |
| Module 4- Alternative Open Reading Frame        | IMG Sequence Viewer For Alternate ORF Search   | Has the amino acid sequence of my protein been called correctly by the computer? |
| Module 5- Structure-Based Evidence              | TIGRfam, Pfam, PDB                             | Are there functional domains in my protein?                                      |
| Module 6- Enzymatic Function                    | KEGG, MetaCyc, E.C. Number.                    | In what process does my protein take part?                                       |
| Module 7- Gene Duplication/ Gene Degradation    | Paralog, Pseudogene                            | Are there other forms of my gene in the bacterium? Is my gene functional?        |
| Module 8- Evidence for Horizontal Gene Transfer | Phylogenetic Tree.                             | Has my gene co-evolved with other genes in the genome?                           |
| Module 9- RNA                                   | RFAM   | Does my gene encode a functional RNA?  |

## Results

### Helicobacter pylori 83 HMPREF0462 0058:

The initial proposed product of the gene by GENI-ACT was a Acyltransferase and our research supports this conclusion. Furthermore, it is most likely a transmembrane helix that resides within the cytoplasmic membrane. Its function is most likely to transfer acyl through the cell membrane.

### Helicobacter pylori 83 HMPREF0462 0064:

The original gene proposed was DNA Methyltransferase. This evidence was supported by a swissprot BLAST search, CDD results, and T-Coffee results. This search later remained a DNA Methyltransferase, supported by Pfam results, TIGRFAM results, and also, PDB results.

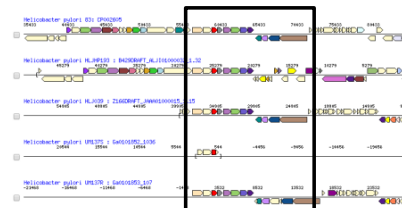


Figure 1 - the above picture is a snippet from the ortholog gene neighborhood of *Helicobacter pylori* 83, HMPREF0462\_0058 and HMPREF0462\_0064 showing very similar organisms meaning there is no horizontal gene transfer.



Figure 2: This is a picture of a WEBLogo from HMPREF0462\_0044. It shows well conserved amino acids in other closely related species. This lends credibility to the conclusion that this gene is imperative to the function of *Helicobacter pylori* 83

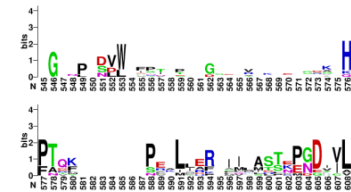


Figure 3: This is a picture of a WEBLogo from HMPREF0462\_0064. It shows not very well conserved amino acids in other closely related species. This shows that the this gene is not very important to the function of the *Helicobacter pylori* 83.

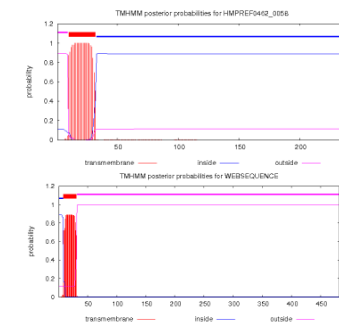


Figure 3: This is the Transmembrane topology graph from TMHMM. This shows that both the genes are transmembrane proteins, but one appears to have the majority of the protein in the cytoplasm, where as the other is mostly on the outside of the cell..

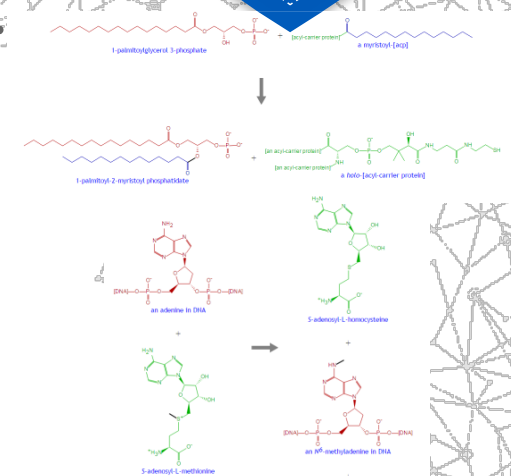


Figure 4: This is a MetaCyc diagram that depicts the function of our gene sequences within *Helicobacter pylori*. the HMPREF0462\_0058 diagram shows how it connects to and transfers its acyl group. the HMPREF0462\_0064 diagram shows how it receives a methyl group from the S-adenosyl-L-methionine

## Conclusion

| Locus Tag Numbers | Proposed annotation | Most likely annotation   |
|-------------------|---------------------|--|
| HMPREF0462_0058:  | Acyltransferase     | Transmembrane helix<br>Acyltransferase<br>through the<br>cytoplasmic<br>membrane |
| HMPREF0462_0064:  | Methylase.          | DNA<br>Methyltransferase<br>through the<br>membrane.                             |

## References

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Geni-act.org

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