

Annotation of the *Pseudomonas aeruginosa* Genome PA01

Locus Tags PA0009 to PA0011

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Abstract

A group of 3 consecutive genes from the microorganism *Pseudomonas aeruginosa* (PA0009 – PA0011) were annotated using the collaborative genome annotation website GENI-ACT. The Genbank proposed gene product name did not differ significantly from the proposed gene annotation. These genes can be used for medical research and have a clinical significance. These genes can be used to create new drugs that can prevent infections caused by *Pseudomonas aeruginosa*.

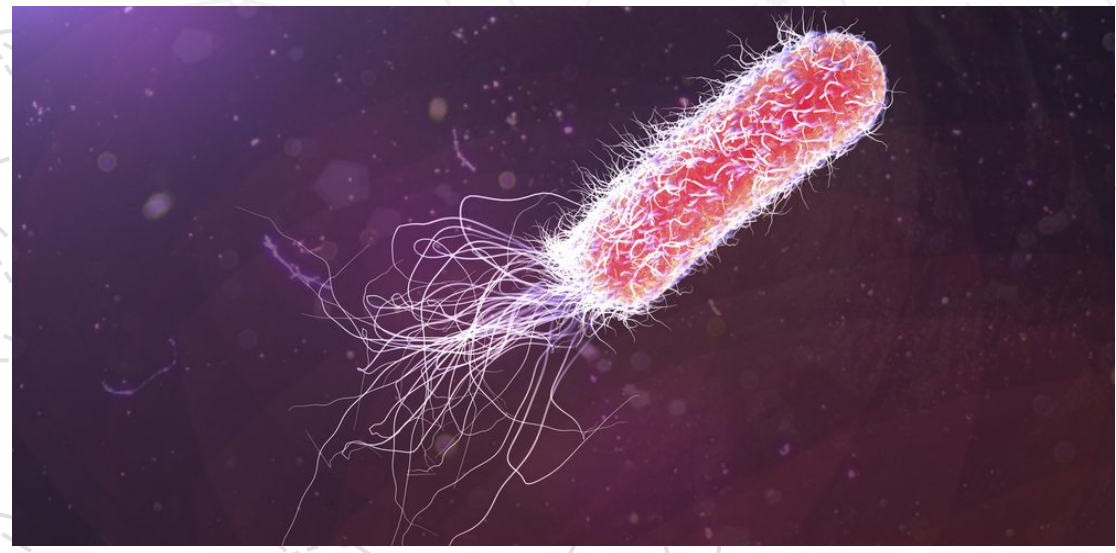


Figure 1 - An animated depiction of *Pseudomonas aeruginosa*

Introduction

Pseudomonas aeruginosa PA01 is a gram-negative, rode-shaped, asporogenous, monoflagellated bacteria. This bacteria can causes an infection in every part of the body, but rarely affects people who are relatively healthy. It is a moderately virulent pathogen that causes acute and chronic infections. *Pseudomonas* thrives in a wide variety of environments. It has a broad host range including humans. French chemist Carle Gessard first discovered *Pseudomonas aeruginosa* through an experiment that identifies the microbe by its water soluble pigments that turn blue-green when exposed to ultra violet light. This bacteria thrives on moist surfaces which allows it to effectively colonize in the lungs, kidneys, and urinary tract. It has been known to develop in patients with cystic fibrosis. *Pseudomonas aeruginosa* has a large resistance island of over fifty resistance genes within its genome. It has chromosomally encoded antibiotic resistant genes which causes it to have a low antibiotic susceptibility. This makes it a bacterium of interest for scientists to understand so it can be treated effectively.

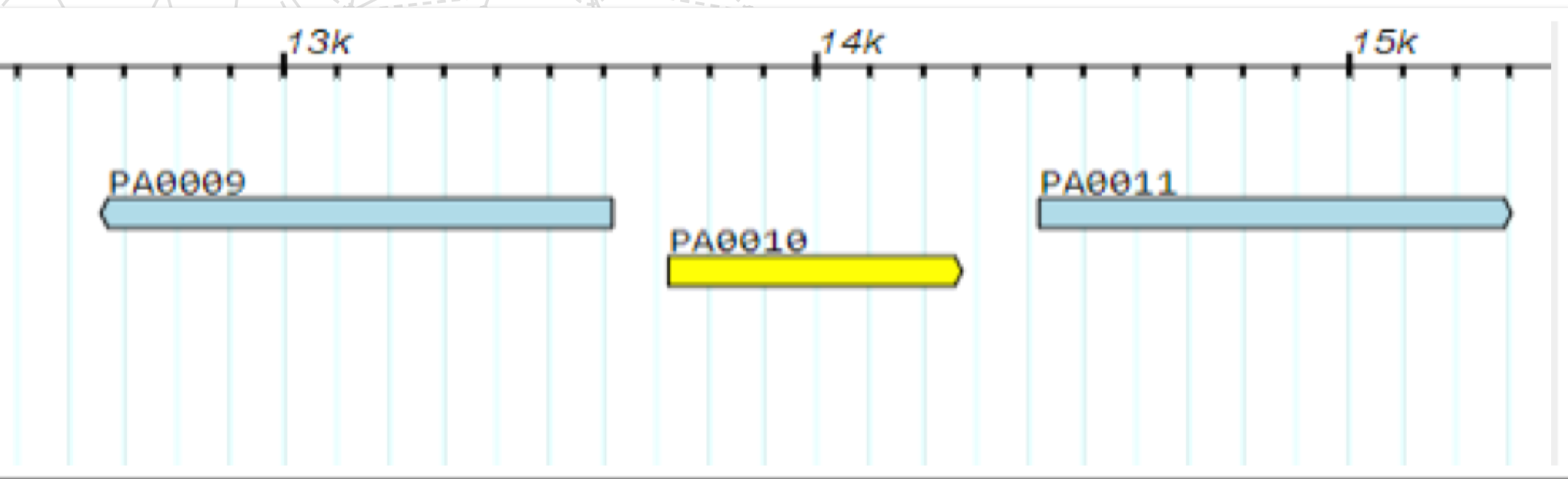


Figure 2 - The locus tags and relative position of the genes under investigation in this research. This includes the segments of PA0009 (Steffey, Stewart), PA0010 (Peters, Sirianni), and PA0011 (Wade).

Methods

Modules of the GENI-ACT (<http://www.geni-act.org/>) were used to complete *Pseudomonas aeruginosa* 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

PA0009: The initial proposed gene by GENI - ACT was glycine- - tRNA ligase subunit alpha. This gene product proposal was supported by the top BLAST hits for the amino acid sequence.

PA0010: The initial proposed gene by GENI - ACT was DNA – 3 – methyladenine glycosidase I. This gene product proposal was supported by the top BLAST hits for the amino acid sequence, it was also supported by the Pfam results as well as the t-coffee results.

PA0011: The initial proposed gene by GENI - ACT was lipid A biosynthesis lauroyl acyltransferase. This gene product proposal was supported by the top BLAST hits for the amino acid sequence, and the swissprot COG.

Phylogenetic Tree



Figure 3 - This diagram represents a phylogenetic tree of the Locus tag PA0009, this follows the evolutionary similarities between *Pseudomonas aeruginosa* and other similar organisms with the same genetic strand.

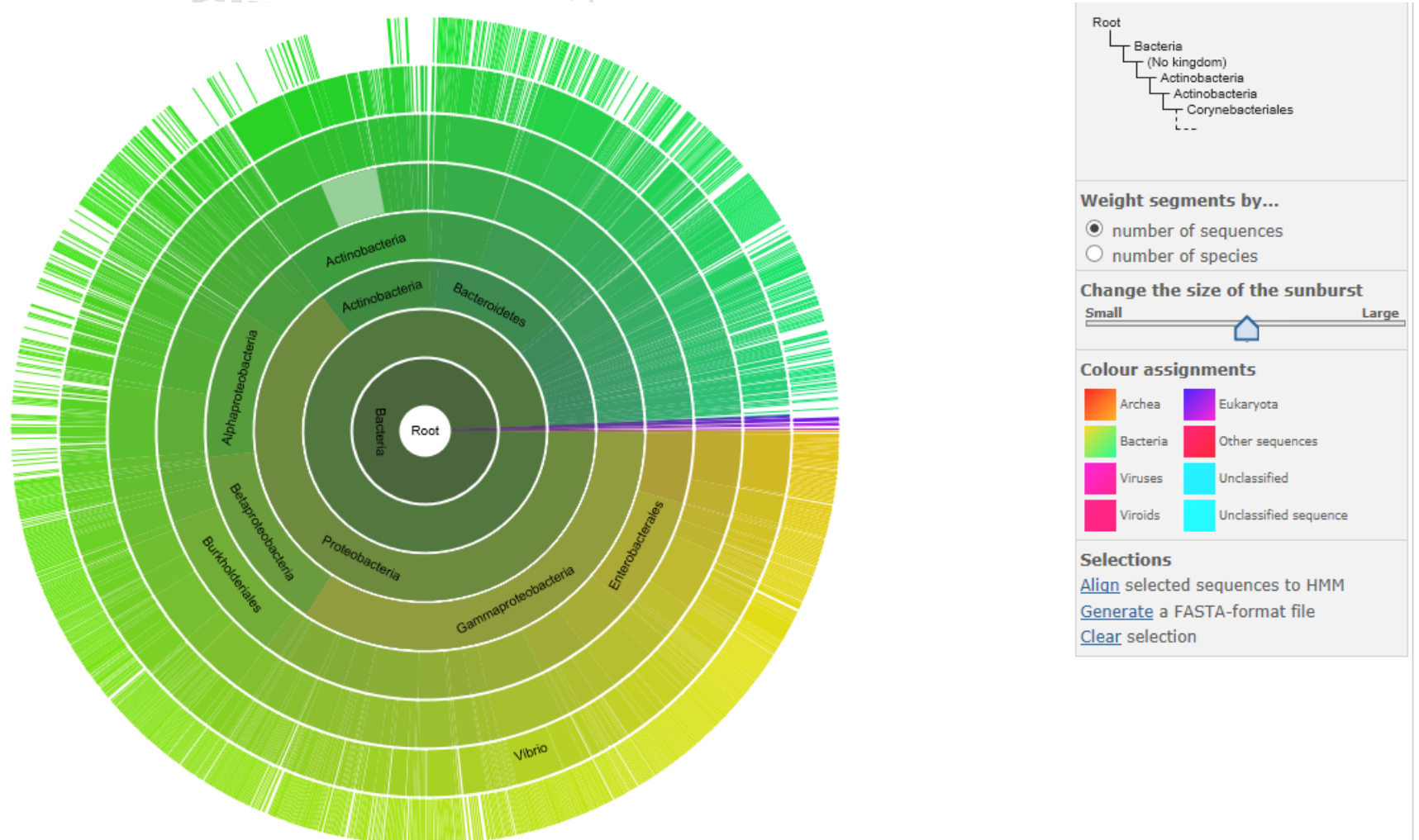


Figure 4 – This represents the evolutionary history of *Pseudomonas aeruginosa* through the locus tag of PA0011.

PFAM

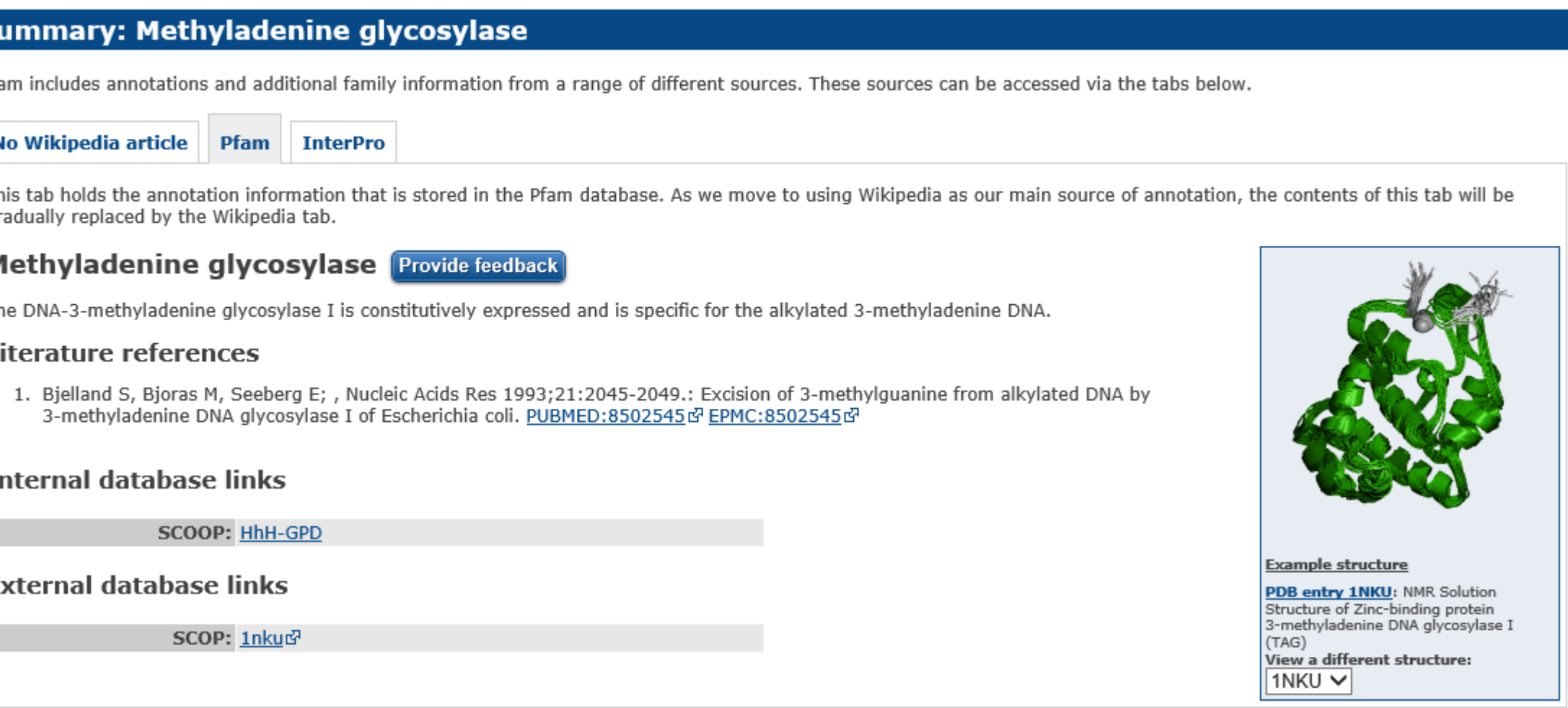


Figure 5 – Pfam results of PA0010 showing that this codes for DNA – 3 – methyladenine glycosidase I.

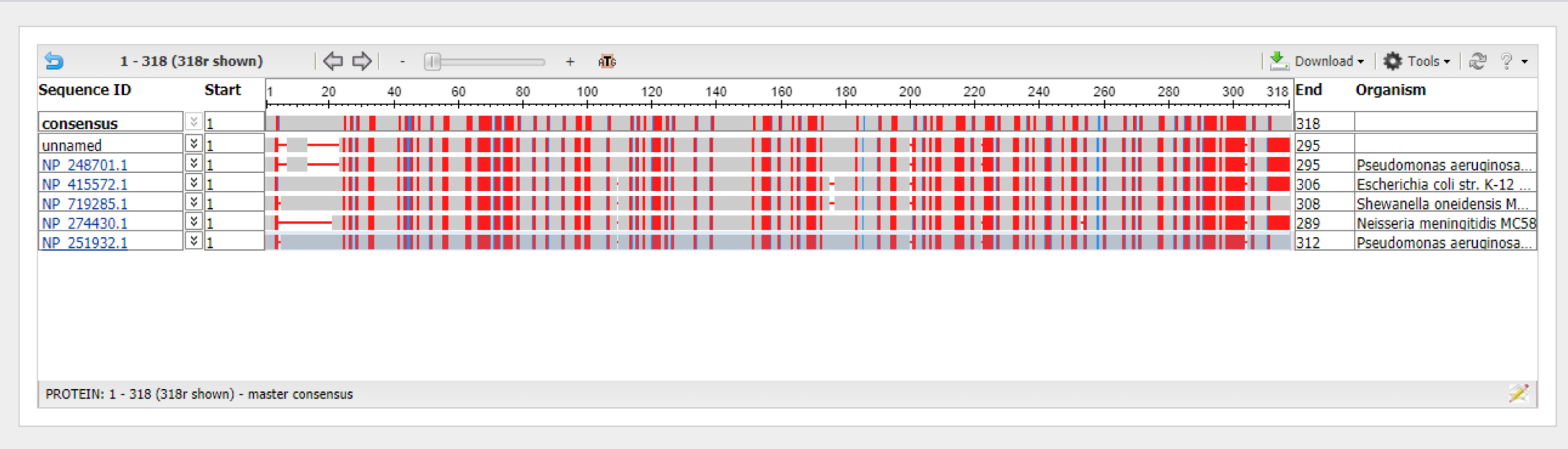


Figure 6 – This diagram is a smart blast from the locus tag PA0011 showing the top hits to the organism *Pseudomonas aeruginosa*.

Correct class	Predicted class				
	SPaseI	SPaseII	Cytoplasmic	TMH	Total
SPaseI	309	2	14	3	328
SPaseII	2	61	0	0	63
Cytoplasmic	5	1	382	0	388
TMH	8	0	21	142	171

Figure 7 – This chart shows a prediction chart of the locus tag PA0010 which shows the a predicted Signal peptidase I cleavage site.

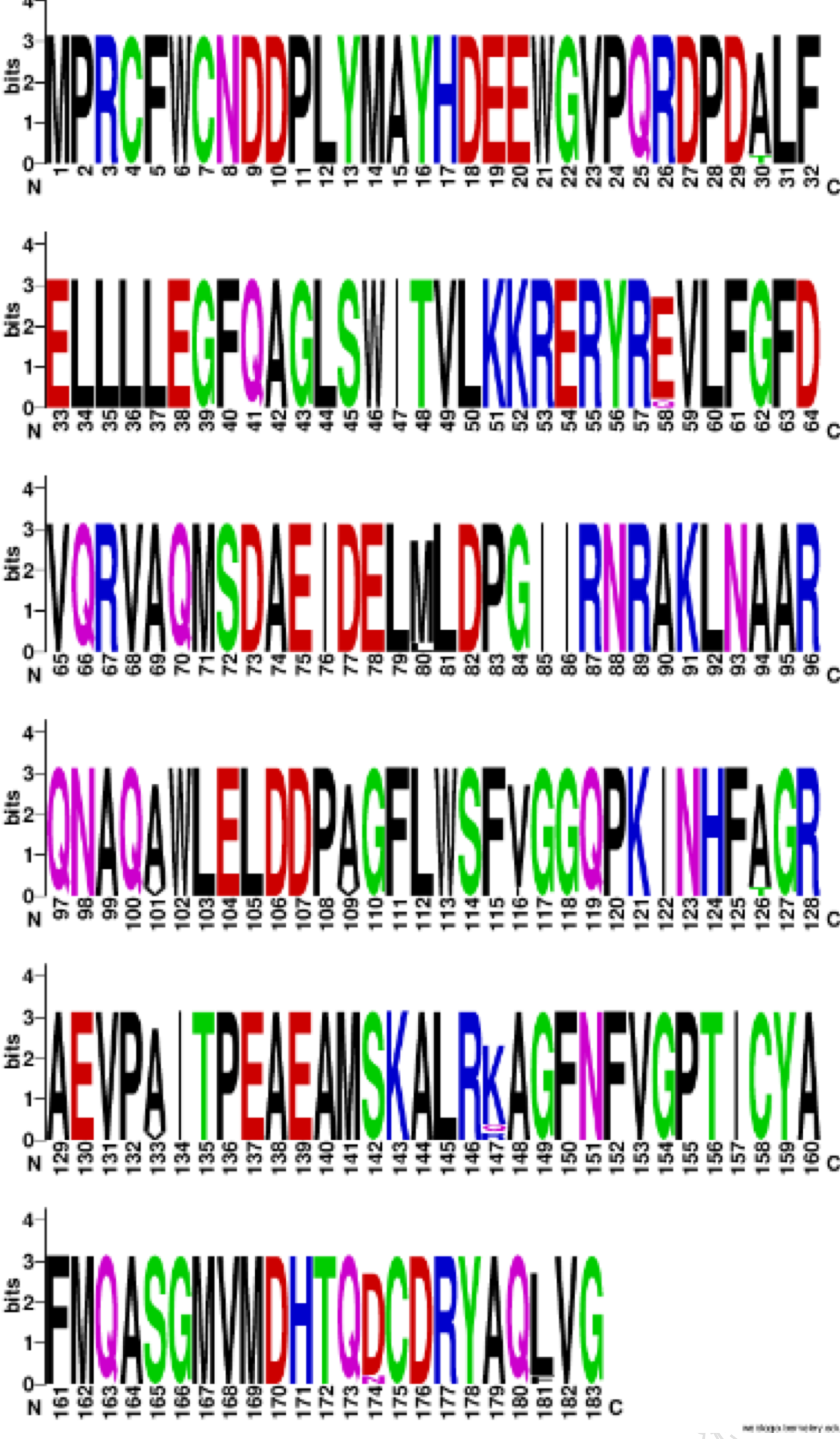


Figure 8 – This represents a weblogo showing from PA0010 which contains a depiction of significant features of the locus tag's alignment.

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
PA0009	DNA – 3 – methyladenine glycosidase I	DNA – 3 – methyladenine glycosidase I
PA0010	DNA – 3 – methyladenine glycosidase I	DNA – 3 – methyladenine glycosidase I
PA0011	lipid A biosynthesis lauroyl acyltransferase	lipid A biosynthesis lauroyl acyltransferase

References

https://microbewiki.kenyon.edu/index.php/Pseudomonas_aeruginosa
<http://www.pseudomonas.com/feature/show/?id=134032&view=functions>.

Acknowledgments

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