Annotation of the *Kytococcus sedentarius* Genome from DNA Coordinates 679771 to 682339

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**Abstract**

A group of 3 conserved genes from the microorganism *Kytococcus sedentarius* (Ksed_06870 – Ksed_06880) were annotated using the collaborative genome annotation website GENI-Act. The Genbank proposed gene product name for each gene was used in terms of the general genomic information, amino acid sequence-based similarity data, structure-based evidence from the amino acid sequence, cellular localization data, potential alternative open reading frames, enzymatic function, presence or absence of gene duplication and degradation, the possibility of horizontal gene transfer, and the production of an RNA product. 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 database.

**Methods and Materials**

Modules of the GENI-Act (http://www.geni-act.org) were used to complete *Kytococcus sedentarius* genome annotation. The modules are described below:

**Results**

*Kytococcus Sedentarius* 06870

We determined that this gene most likely codes for a membrane protein. We decided this because of the TMHMM (Transmembrane Helices; Hidden Markov Model) results showing evidence of multiple helices, or folds in the protein that cross the cellular membrane. This concludes that ksed_06870 has the highest probability of being a membrane protein.

*Kytococcus Sedentarius* 06880

Through extensive research, we found out that this portion of the genome binds adenosine triphosphate. This gene is known as an ABC transporter. It does not have any transmembrane helices, and it is a cytoplasmic protein. We found this out by doing the TMHMM test, which showed results that were very well conserved.

Eye-appealing WebLogo biological illustrations showing significant conservation of sequences.

**Foot affected by pitted keratolysis caused by *Kytococcus sedentarius***

**References**


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