

# Annotation of the *Kytococcus sedentarius* Genome from Locus Tags Ksed\_08500 to Ksed\_08570

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## Abstract

A group of four genes from the microorganism *Kytococcus sedentarius* (Ksed\_08500 – Ksed\_08570) were annotated using the collaborative genome annotation website GENI-ACT. The proposed gene product name for each gene was determined 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 proposed gene product name did not differ significantly from the proposed gene annotation for each of the genes, however some genes had little information on properties, such as the location of the gene. In general, the genes have been annotated correctly.

## Introduction

*Kytococcus sedentarius* (formerly known as *Micrococcus nishinomiyaensis*) is an aerobic gram positive bacteria that can be found in a marine environment, and on human skin. It does not move utilizing its own power and is usually found in tetrad formation. Particular amino acids present within an ionic salt such as 10% NaCl solution is a satisfactory environment for *Kytococcus sedentarius* to develop.

The interest in *Kytococcus sedentarius* has come from the rarity of study of the actinobacterial suborder *Micrococinae*, in which *Kytococcus sedentarius* is a member. *K. sedentarius* has been found to be a main contributor to pitted keratolysis (Sims et al., 2009). Pitted keratolysis is a condition where either the hands or feet of an individual become laden with small, dark pits. This condition is usually non-hurtful to the person, although an offensive odor can be caused because of it. *K. sedentarius* has also been linked to cases of pneumonia. However, *K. sedentarius* has proven to be useful in its capacity to create oligopeptide antibiotics.

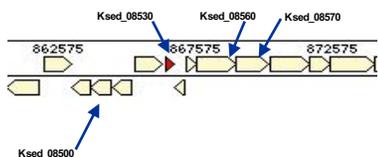


Fig. 1- Gene neighborhood of the four *Kytococcus sedentarius* genes annotated

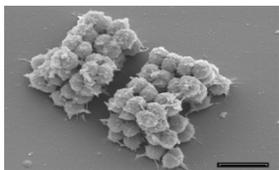


Fig II- Picture of the *Kytococcus sedentarius* micro-organism. [http://www.genome.jgi.doe.gov/kyse/kyse\\_home.html](http://www.genome.jgi.doe.gov/kyse/kyse_home.html)

## Methods and Materials

GENI-ACT (<http://www.geni-act.org/>) modules were completed to annotate the *Kytococcus sedentarius* genome. The module descriptions are 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

### *Kytococcus sedentarius*08500:

The proposed product name for Ksed\_08500 by GENI-ACT was 3-oxoacid CoA-transferase, A subunit. This prediction was based on BLAST, COG, Pfam hits for this gene's amino acid sequence. It was also identified that the gene is responsible for pseudouridine synthase TruB family. Although some databases gave minimal information it was still determined that the gene was a regulator.

### *Kytococcus sedentarius*08530:

The proposed product name for Ksed\_08530 by GENI-ACT was a transcription factor WhiB. The prediction was based on the BLAST and CDD hits for this gene's amino acid sequence. It was also identified that the gene is responsible as a regulatory protein, and sensing redox. Although some databases gave minimal information it was still determined that the gene was a regulator.

### *Kytococcus sedentarius*08560:

The Ksed\_08560 gene is suggested to be a phosphomannomutase, with the possibility to be a phosphoglucomutase. Most databases concluded the gene to be a phosphomannomutase, with the exception of KOG. In either case the gene is involved in carbohydrate transport and metabolism. In detail, this gene creates an enzyme that attaches long chain sugar molecules to proteins in order for the protein to work properly.

### *Kytococcus sedentarius*08570:

The proposed product name for Ksed\_08570 by GENI-ACT was a phosphosugar isomerase. This prediction was based on the BLAST and CDD hits for this gene's amino acid sequence. It was also identified that the gene is responsible for regulating DNA-binding transcription. Although some databases gave minimal information it was still determined that the gene was a regulator.

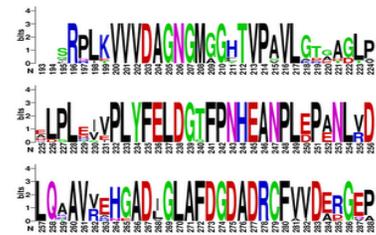


Figure III – A portion of the WebLogo for Ksed\_08560. A conserved region is necessary to the life of the organism, and are noted where there is only one large letter in a section.

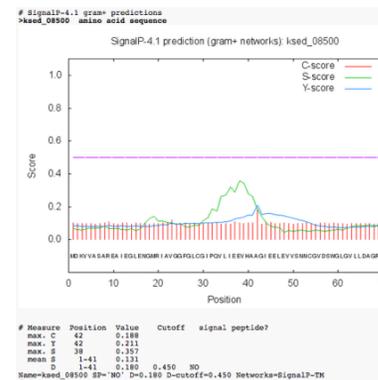


Figure IV – SignalP output for Ksed\_08500 indicating that it does not have a signal peptide.

RecName: Full=Transcriptional regulator WhiB  
 Sequence ID: [sp|Q7AKN0|WHIB\\_STRCQ](#) Length: 87 Number of Matches: 1

Range	Score	Expect	Method	Identities	Positives	Gaps
1:19 to 87	128 bits(321)	2e-39	Compositional matrix adjust.	59/69(86%)	65/69(94%)	0/69(0%)

Query 17 MQRALCAQDFEAFPPKGGSTREARVTCGVSRSECLVALENERDFIINGLSEKE 76  
 MQRALCAQDFEAFPPKGGSTREARVTCGVSRSECLVALENERDFIINGLSEKE  
 Sbjct 19 MQRALCAQDFEAFPPKGGSTREARVTCGVSRSECLVALENERDFIINGLSEKE 78

Query 77 SEELKREAV 87  
 SEELKREAV 87  
 Sbjct 79 SEELKREAV 87

Figure V – The top Swiss-Prot database BLAST hit for Ksed\_08530. This indicates that it should be annotated as a transcriptional regulator WhiB.

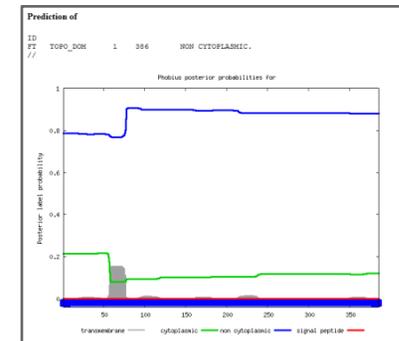


Figure V - Phobius graph of Ksed\_08570 indicating that it does not have transmembrane helices or a signal peptide.

## 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 Product	Proposed Annotation
Ksed_08500	3-oxoacid CoA-transferase, A subunit	3-oxoacid CoA-transferase, A subunit
Ksed_08530	Transcription factor WhiB	Transcription factor WhiB
Ksed_08560	phosphomannomutase	phosphomannomutase
Ksed_08570	Phosphosugar isomerase	Phosphosugar isomerase

## References

Sims et al. (2009). Complete genome sequence of *Kytococcus sedentarius* type strain (541T). *Standards in Genomic Sciences*, 12-20.

## Acknowledgments

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