**Gene Annotation of Ksed_2300, a Putative Protein Tyrosine Phosphatase (PTP) in Kytococcus sendentarius**

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**Abstract**

*Kytococcus sendentarius* is a Gram-positive coccus. A section of the bacteria’s genome was annotated to verify information and look for possible functions for the gene product. Eight GENI-ACT modules were used to gather this information. The results show a protein found in the cytoplasm. This is thought to be signal transduction protein tyrosine phosphatase. They play a very important role in cellular signaling.

**Introduction**

*Kytococcus sendentarius* is a Gram positive bacterium that is arranged in packets if eight in a cubical shape. It is coccolid or a spherical shaped bacterium that can live on the skin. The genome of *Kytococcus sendentarius* 541 2,785,024 bp long and codes for 2,703 genes. Of the 2,703 genes predicted, 2,639 were protein-coding genes. 72.1% of these genes were assigned with a predicted function while the remaining ones were annotated as hypothetical proteins.

The gene that we investigated, Ksed_2300 had the DNA coordinates of 227593..228096 containing 504 base pairs. This section codes for 167 amino acids. The purpose of this was to help learn more about *Kytococcus sendentarius* because it is not a well known type of bacteria. The information from GENI-ACT helps us in understanding the gene better.

**Methods and Materials**

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

- **Module 1: Basic Information Module**
  - **Activities**: Gene Coordinates and Sequences, Protein Sequence
  - **Questions Investigated**: What is the sequence of my gene and protein? Where is it located in the genome?

- **Module 2: Sequence-Based Similarity Search**
  - **Activities**: Blast, CGG, T-Coffee, HsScan
  - **Questions Investigated**: Is my sequence similar to other sequences in GenBank?

- **Module 3: Gene Localisation Diag**
  - **Activities**: GenomEAT, TIGRMM, SignPath, PSORT, Phind
  - **Questions Investigated**: Is my protein in the nucleus, cytoplasm, periplasm or extracellularly?

- **Module 4: Alternative Open Reading Frames**
  - **Activities**: RIO Sequence Viewer For Alternative ORF Search
  - **Questions Investigated**: Has the amino acid sequence of my protein been called correctly by the computer?

- **Module 5: Structure-Based Evidence**
  - **Activities**: TIGRMs, Pfam, PS4
  - **Questions Investigated**: Are there functional domains in my protein?

- **Module 6: Enzyme Annotation**
  - **Activities**: KEGG, MetaCyc, E.C.
  - **Questions Investigated**: Are there known functions in my gene family?

- **Module 7: Gene Description**
  - **Activities**: Pfam, Phanogene
  - **Questions Investigated**: Are there other forms of my gene in the database? Are my gene functions?

- **Module 8: Evidence for Horizontal Gene Transfer**
  - **Activities**: Phylogenetic Tree, KyleMarkovTree
  - **Questions Investigated**: Gene codon evolution with other genes is the gene evolution?

**Results**

**protein tyrosine phosphatase (Sericoccus marinus)**

**Sequence:** Ksed_2300

**Function:** Phosphatase activity

**Module:** 1

**Summary:**

1. **Score:** 0.766918
2. **expect:** 4.51
3. **bit score:** 57.62
4. **E-value:** 6.62E-50

**Query:**

- **Ksed_2300**
- **Ksed_2300**
- **Ksed_2300**
- **Ksed_2300**

**Subject:**

- **Ksed_2300**
- **Ksed_2300**
- **Ksed_2300**
- **Ksed_2300**

**Identification:**

- **KO0012**
- **KO0012**
- **KO0012**
- **KO0012**

**Annotation:**

- **PTP**
- **PTP**
- **PTP**
- **PTP**

**Conclusion**

Protein tyrosine phosphorylation is the putative gene product, the protein is a fundamental regulatory mechanism controlling cell proliferation, differentiation, communication, and adhesion. Disruption of this key regulatory mechanism contributes to a variety of human diseases including cancer, diabetes, and autoimmune diseases.

Protein Tyrosine Phosphatases (PTPs) represent a large family of enzymes. They play a very important role in cellular signaling within and between cells. PTPs work with Protein Tyrosine Kinases (PTKs) to regulate signal transduction in a cell. PTKs phosphorylate tyrosine residues on a substrate protein and PTPs remove these phosphates from substrate tyrosines (dephosphorylation). Since the phosphorylation status of a protein can modulate its function, PTKs and PTPs work together to regulate protein function in response to a variety of signals, including hormones, mitogens, and oncogenes.

Protein tyrosine phosphatases (PTPs) are a group of enzymes that catalyze the removal of phosphate groups from tyrosine residues by the hydrolysis of phosphoric acid monoesters. They directly oppose the actions of kinase and phosphatase enzymes.

**References**


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