Annotation of genes responsible for synthesis of uroporphyrinogen III from L-glutamate, the first half of the pathway of heme biosynthetic pathway, in *Kytococcus sedentarius*.

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**Abstract**

Genome annotation is a set of algorithmic software tools that allows complete sequencing of an organism's genome. The objective of this study was to annotate the genome of *Kytococcus sedentarius*. A common side organism in the *Kytococcus* genus has been associated with genital incontinence, and at times fatal pneumonia in immunocompromised patients (Chaudhary and Finkle, 2010). Formerly known as *S. schottii* and *S. sedentarius*, the genome was sequenced by the Joint Genome Institute (2001). The newly sequenced genome was used to analyze the metabolic pathway responsible for the production of uroporphyrinogen III. The E.C. number and enzymes responsible for each step are mentioned in Table 1.

**Results**

The results obtained from the PSORT-B (http://www.psort.org/psortb) were used to annotate the localization of the protein, based on specific cellular component scores.

**Alternative open reading frame**

The open reading frame for the homologous gene in *K. sedentarius* was used to identify protein-protein interactions. The protein identification was performed using the TMHMM server (http://www.cbs.dtu.dk/services/TMHMM/). The results obtained from the PSORT-B (http://www.psort.org/psortb) were used to annotate the localization of the protein, based on specific cellular component scores.

**Structural evidence module**

The results obtained from the TMHMM server (http://www.cbs.dtu.dk/services/TMHMM/) were used to identify protein-protein interactions. The protein identification was performed using the TMHMM server (http://www.cbs.dtu.dk/services/TMHMM/). The results obtained from the PSORT-B (http://www.psort.org/psortb) were used to annotate the localization of the protein, based on specific cellular component scores.

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**Materials and Methods**

**Reference**


2. Chaudhary, D. and S. N. Finkle (2010). "Peritoneal dialysis-associated peritonitis due to *Kytococcus sedentarius* (Ertam, Aytimur et al., 2005; Sims, Brettin et al., 2009). A common side organism in the *Kytococcus* genus has been associated with genital incontinence, and at times fatal pneumonia in immunocompromised patients (Chaudhary and Finkle, 2010). Formerly known as *S. schottii* and *S. sedentarius*, the genome was sequenced by the Joint Genome Institute (2001). The newly sequenced genome was used to analyze the metabolic pathway responsible for the production of uroporphyrinogen III. The E.C. number and enzymes responsible for each step are mentioned in Table 1.