

## Web alert

# Bacterial genome annotation tools

## An annotated selection of World Wide Web sites relevant to the topics in *Environmental Microbiology*

### MANATEE

<http://manatee.sourceforge.net/>

MANATEE is a genome annotation tool that allows users to quickly identify genes and make high quality functional assignments. It is very useful for prokaryotic genomes.

### PIRATE

<http://www.tigr.org/software/pirate/>

PIRATE (Prediction Informatics Resources at TIGR & Elsewhere) is a repository of freely available software tools relevant to microbial genome annotation. It also contains documentation, training data, experimental results and external links.

### GlimmerHMM

<http://www.tigr.org/software/GlimmerHMM/index.shtml>

GlimmerHMM is a gene finding tool based on a Hidden Markov Model (HMM). Gene finding is often one of the first steps in microbial genome annotation and crucial for further annotation of the genes and functions found in the microbe under study.

### Comprehensive Microbial Resource

<http://www.tigr.org/tigr-scripts/CMR2/CMRHomePage.spl>

The Comprehensive Microbial Resource (CMR) is a tool that provides access to many of the bacterial genome sequences completed to date, both at TIGR and elsewhere. For genomes not sequenced at TIGR, additional annotation is generated at TIGR by an automated annotation process and this is available freely to users.

### MUMmer

<http://www.tigr.org/software/mummer/>

MUMmer is a system for aligning whole genome

sequences, able to rapidly align sequences containing millions of nucleotides.

### Unfinished Microbial Genomes

<http://www.tigr.org/tdb/ufmg/>

This webpage contains a list of microbial genomes currently being sequenced at TIGR and elsewhere. It permits the user to run a BLAST search using the deposited, but as yet unfinished, genome sequences.

### Visualization Tools for Bacterial Genome Alignments

<http://globin.cse.psu.edu/enterix/>

This website provides tools for the comparative viewing of a reference genome with sequences from several related bacteria. It is largely focused on the enteric bacteria such as *Escherichia* and *Salmonella*.

### Artemis

<http://www.sanger.ac.uk/Software/Artemis/>

Artemis is a genome viewer and annotation tool for visualization of sequence data and the results of sequence analyses. It is freely available for download from the Sanger Center website.

### TIGR's annotation engine

[http://www.tigr.org/edutrain/training/annotation\\_engine.shtml](http://www.tigr.org/edutrain/training/annotation_engine.shtml)

This site provides service to all prokaryotic sequencing centers, funded by the U.S. Department of Energy (DOE). The service is free automated annotation of any prokaryotic sequence submitted to the annotation engine. The site also offers a free course in 'Prokaryotic Annotation and Analysis'.

### **GMP-Tool-Box**

<http://www.pasteur.fr/applications/dri/English/DI/01-43.html>

This website, housed at the Institut Pasteur, offers a software package developed to aid in the three major steps of a shot-gun genome project: shotgun follow-up, genome closure and gene annotation.

### **Microbial genome checker**

<http://www.genoscope.cns.fr/agc/tools/micheck/Form/form.php>

The MICheck website software provides a tool for rapid verification of sets of annotated genes and frameshifts in completed bacterial genomes that are presently available in public databanks.

### ***In silico* experiments with complete genomes**

<http://www.in-silico.com/>

This website offers tools that can run computational experiments on genomes, predicting results for: PCR amplification, multiplex PCR, restriction digestion, PFGE, PCR-RFLP, and DNA fingerprinting.

### **Reannotation of microbial genomes**

<http://www.biomedcentral.com/1471-2105/3/5>

This webpage describes a software tool that automatically identifies biologically significant gene candidates in a bacterial genome.

### **HAMAP**

[http://us.expasy.org/sprot/hamap/hamap\\_doc.html](http://us.expasy.org/sprot/hamap/hamap_doc.html)

HAMAP (High-quality Automated and Manual Annotation of Microbial Proteomes) is offered by Swiss-Prot and provides automatic annotation of a significant percentage of proteins originating from bacterial and archaeal genome sequencing projects. The method uses a rule-based system and is only applied in cases where the automatic system is able to produce the same quality as manual annotation results.

### **Lawrence P. Wackett**

*McKnight Professor and Head  
Microbial Biochemistry and Biotechnology  
Department of Biochemistry  
Molecular Biology and Biophysics  
University of Minnesota  
St Paul, MN 55108, USA*