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MicrobesOnline: A Community Resource for Data-Integrated Comparative Functional Genomics

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# MicrobesOnline: A Community Resource for Data-Integrated Comparative Functional Genomics (R-009)

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http://vimss.lbl.gov/

### INTRODUCTION

Since 2003, the MicrobesOnline.org web site of the Environmental Stress Pathway Project (ESPP) has provided novel web-based tools for comparative genomics of prokaryotes.

- •To describe the potential functions of genes, MicrobesOnline includes protein family analyses (from InterPro and COG), metabolic maps (from KEGG), and links to characterized genes (from UniProt).
- \*To examine each gene's evolutionary history, MicrobesOnline includes precomputed phylogenetic trees for all the gene families, and displays them with the genes' genomic context, or it compares the gene tree to the species tree.
- Users can also compute their own sequence alignments and phylogenetic trees. \*To examine the potential regulation of genes of interest, MicrobesOnline also includes tools for finding sequence motifs and for finding regulatory sites.
- •MicrobesOnline includes microarray data: it shows up-regulated or downregulated genes or operons, shows changes in expression patterns in a metabolic map, or gives an overview of the expression pattern for specific genes of interest. •Finally, users can use our gene annotation interface to add or revise gene names, descriptions, EC or GO assignments, or comments.

Currently MicrobesOnline hosts over 350 public genomes and 20 private genomes, and ~300 public and private microarrays. Our web site is unique in that, in addition to providing our own automated analyses, it allows users to perform their own analyses of genes of their choice.

All of these tools are freely available at our web site:

### MicrobesOnline



Our examples concern perR and related genes in Desulfovibrio vulgaris Hildenborough. Searching for perR (above) returns search results (below) where there are links to view the various pages relating

Search results for perR in Desulfovibrio vulgaris Hildenborough

	From Synonym: 1 four	d. Add all genes to cart		
	Genes			
1	GODHSTB VMSS208612 P	erR DVU3095.0RF04117 3237384 - 32	27770 (-) Desulfovibrio	vulgaris Hildenborough Ad

COG735. Fe2+/Zn2+ uptake regulation proteins linorganic ion transport and metabolism.

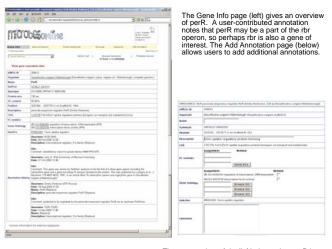
Every gene page has links for viewing basic gene annotatations, operon predictions, domain alignments from InterPro, BLASTp homologs, and the public annotation interface.

# **Future Work**

- More links to external databases/web sites, such as RegTransDB. EcoCyc, IMG, STRING, PhIGs
- •More microarray data, and a new interface including heat maps Protein-protein interaction data
- Metabolomic and proteomic data
- Operon-wise significance analysis of microarray data



## **Gene Information and Annotation Pages**



VMSS Predicted Operon

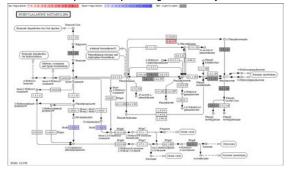
The operon view of rbr (left) shows that perR is not predicted by our methods to be part of the rbr operon. User contributed annotations allow for manually-entered information to supplement

# Microarray Data Display and Analysis

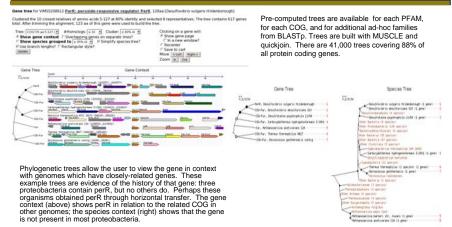


In ESPP experiments, perR was significantly up-regulated, as well as rbr2 and rbr (above). The operon view of this microarray experiment (upper right) shows that rbr was up-regulated, as was

#### Example KEGG map with integrated Microarray data



## **Phylogenetic Tree Browser**



#### **Gene Cart Workbench Tools**

#### **Gene Cart Multiple Sequence Alignments** Cart Summary / Cart: ASM Cart #1 / Generale MSA



#### Phylogenetic Tree Creation



#### Motif Search : MEME / Weeder / AlignAce



#### Genome Browser



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Website:

http://www.microbesonline.org