

## PATRIC OFFERS:

- **Consistent annotation** across all sequenced bacterial species from GenBank and other sources via RAST, the most widely used and highly cited automated microbial annotation system. Annotate your bacterial genome for free in less than 24 hours.
- **A wealth of associated, descriptive genome meta-data** parsed from a variety of sources in over 60 fields such as: isolation source, geographic location, year of isolation, and the host and/or environment from which the sample was collected.
- **Data integration** across sources, data types, molecular entities, and organisms. Data types include genomics, transcriptomics, protein-protein interactions, 3D protein structures, sequence typing data, and metadata, and are summarized and organized at various taxon, genome, and gene levels.
- **Various search tools** help you easily find data and genomes of interest including single specific genomes, whole genome sets within certain taxa, sets of genomes that share common metadata, and even closely related sets of genomes based on phylogeny.
- **Upload your own data** and analyze it privately and securely with PATRIC analysis tools by itself or against public datasets.
- **Freely available** data and analysis results, presented in tabular, graphic, and downloadable formats.



- **A personal workspace** to permanently save groups of genomic data, gene associations, and uploaded private data. Both private and public data can be analyzed together using a suite

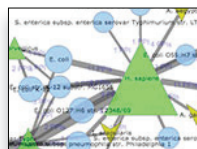
of tools to perform comparative genomic or transcriptomic analysis. Customize PATRIC preferences to streamline searches and data browsing.



Above: Comparing gene neighborhoods across multiple genomes



## OTHER DATA AND FEATURES



- **Pathogen Interactions Gateway** enables a highly interactive and sophisticated exploration of intricate protein-protein interaction networks that may span many different organisms.
- **Disease View** showcases relationships between pathogens, genes, and diseases, while also presenting infectious disease, virulence, and outbreak data.

## KEEP IN TOUCH WITH US



[www.patricbrc.org](http://www.patricbrc.org) (website)



[www.youtube.com/user/patricbrc](http://www.youtube.com/user/patricbrc)



Pathosystems Resource Integration Center



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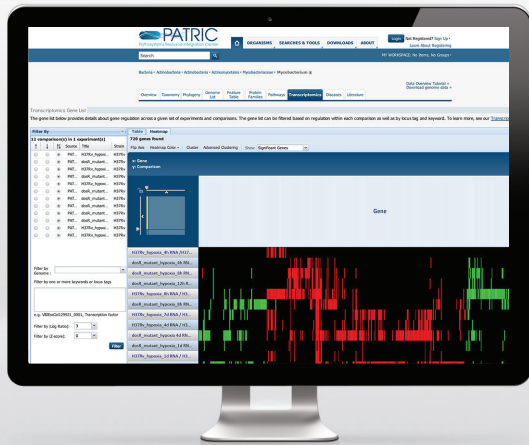


## NOT JUST ANOTHER DATA REPOSITORY

...a data analysis resource providing the power to respond to real-life problems in real-time.

[www.patricbrc.org](http://www.patricbrc.org)

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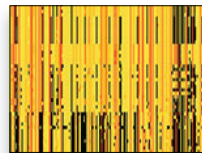
Above: Transcriptomics Heatmap

## WHAT IS PATRIC?

PATRIC is the bacterial **Bioinformatics Resource Center (BRC)**, an information system designed to support the biomedical research community's work on bacterial infectious diseases via integration of vital pathogen information with rich data and analysis tools. PATRIC is one of the most comprehensive data analysis resources available for bacteria, providing thousands of consistently annotated bacterial genomes, related 'omics data and metadata, and a suite of analysis tools. The freely available PATRIC platform provides an interface for biologists to privately upload their own data, search public data, and conduct comprehensive comparative genomics, transcriptomics, and other analyses in a one-stop shop. PATRIC is an NIH-NIAID -funded project.

## COMPARATIVE GENOMIC ANALYSIS

PATRIC's compilation of all public bacterial genomes with consistent RAST annotations provides a powerful platform for comparative genomic analysis.

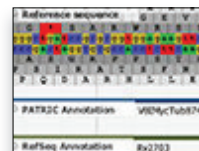
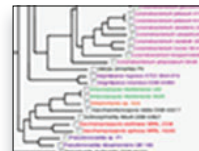


The Protein Family Sorter and Heatmap tools enable selection of a set of genomes of interest and provide a bird's-eye ('pan-genome') view of the distribution of

the protein families across them, with clustering and anchoring functions to show relative conservation of synteny and identify lateral transfers. The Comparative Pathway Tool allows identification of a set of metabolic pathways based on taxonomy, EC number, pathway ID, pathway name, and/or specific annotation type. Use interactive KEGG Maps and Heatmaps to summarize data, including presence/absence of individual EC numbers within the selected genomes.

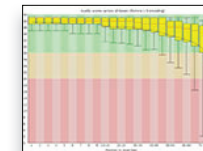
Additional Analyses Include:

- View and select genomes from interactive Phylogenetic Trees.
- Use the Compare Region Viewer to compare gene neighborhoods by viewing flanking regions across related genomes.
- Construct gene trees and/or alignments with the Multiple Sequence Alignment tool.
- Compare RAST, RefSeq, and your own uploaded annotations using the Genome Browser.
- Analyze data via all types of BLAST, including plasmid-specific.



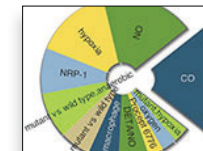
## COMPARATIVE TRANSCRIPTOMIC ANALYSIS

PATRIC integrates transcriptomic and genomic data, allowing researchers to explore gene expression across species, within a specific genome, or for a gene of interest.



Analyze public data, your own private uploaded data, and/or stream data from your RNA-Rocket workspace directly to PATRIC analysis tools. RNA-

Rocket is an RNA-Seq analysis pipeline, where you can upload your data, align it against a BRC provided genome, and generate quantitative transcript profiles using BRC annotations.



Interactive Gene Lists and Heatmaps with clustering tools provide quick access to genes that are differentially expressed or have similar expression patterns across various conditions. These genes can be selected and mapped to metabolic pathways.



At the gene level, a graphical summary of metadata for the comparisons relevant to differential expression of the gene, a summary of genes with correlated expression profiles, and transcriptomics BLAST help assess or hypothesize potential function of a gene, making it a valuable resource for researchers who are interested in studying specific genes or identifying potential function of hypothetical genes.