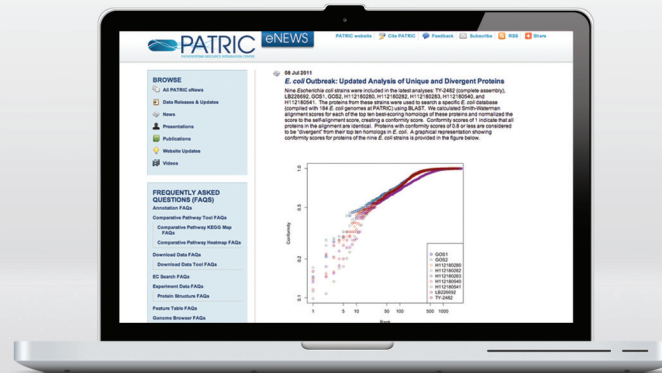


## WHAT PATRIC OFFERS

- Consistent annotations across all sequenced bacterial species from GenBank.
  - » Annotate your bacterial genome for free in less than 24 hours using the same RAST annotation service that is used at PATRIC.
- Data and Information Searches.
  - » Perform a PATRIC global search or conduct advanced searches based on Taxonomy, Gene Name, Locus Tag, Protein Function/Families, Pathways, EC Numbers, GO Terms, Host-Pathogen Interactions, and more.
  - » Perform a BLAST search against plasmid-specific BLAST databases containing genomic sequences or proteins in PATRIC.
  - » PATRIC provides enhanced literature search and text mining techniques to identify genes, proteins, diseases, drugs, organisms, and other entities of interest.
- Personal workspace that allows users to permanently save sequences of interest collected from PATRIC. From here manage and analyze saved data within your customized groups.
- Numerous comparative analysis and interactive visualizations help investigators to discover emergent properties in complex systems. Sequences and other specifics about the data used to create your custom visualizations is easily captured.
- Rich, interactive visualizations that support analyses such as, a bird's-eye view of the conservation (or lack thereof) of particular genes of interest, discerning how many proteins have the same function within a single genome, and identifying proteins with multiple homologs or paralogs across a set of genomes.
- Freely available data and analysis results, presented in tabular, graphic, and downloadable formats.








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-  [www.patricbrc.org](http://www.patricbrc.org) (website)
-  [www.youtube.com/user/patricbrc](http://www.youtube.com/user/patricbrc)
-  Pathosystems Resource Integration Center
-  [www.twitter.com/patricbrc](http://www.twitter.com/patricbrc)
-  [patric@vbi.vt.edu](mailto:patric@vbi.vt.edu)



## 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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VIRGINIA BIOINFORMATICS INSTITUTE  
AT VIRGINIA TECH

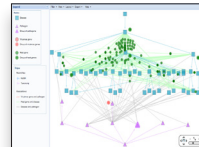


Above: Groups within your personal workspace.

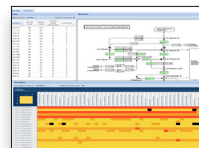
## WHAT IS PATRIC?

PATRIC is the **Bacterial Bioinformatics Resource Center**, 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 sharpens and hones the scope of available bacterial phylogenomic data from numerous sources specifically for the bacterial research community, in order to save biologists time and manpower when conducting comparative analyses. The freely available PATRIC platform provides an interface for biologists to discover data and information and conduct comprehensive comparative genomics and other analyses in a one-stop shop. PATRIC is a NIH-NIAID -funded project of Virginia Tech's Cyberinfrastructure Division.

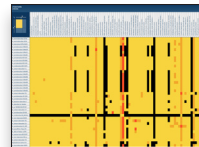
## PATRIC TOOLS & COMPARATIVE ANALYSES



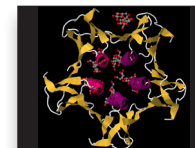
**Disease View:** Presents infectious disease, virulence, and outbreak data associated with various taxon. Includes an interactive graph presenting relationships between pathogens, genes, and diseases and a disease map, which geolocates reports of associated diseases around the globe in real-time.



**Comparative Pathways:** Compares consistently annotated metabolic pathways across closely related or diverse groups of genomes and visualizes them using interactive KEGG maps and heatmaps. The heatmap view is an interactive visualization tool that provides an overview of the distribution of genomes across the set of EC numbers within a selected pathway.

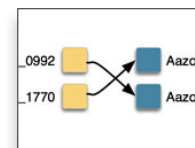


**Protein Family Sorter:** Compares protein families across closely related or diverse groups of genomes, visualizes them using interactive heatmaps, and generates multiple sequence alignments and phylogenetic trees for an individual families. The heatmap view is an interactive visualization tool that provides an overview of the distribution of proteins across a selected set of genomes.

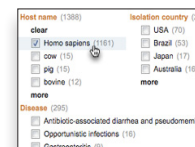


## 3D Structures and Experiment

**Data:** Provides consolidated and uniform data access via summaries of all relevant post-genomic datasets available in various public repositories, such as GEO, ArrayExpress, the (former) Proteomics Resource Centers, PRIDE, NCBI structure, IntAct, and BIND.

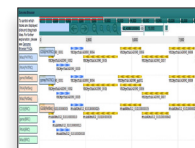


**ID Mapping:** Quickly maps PATRIC identifiers to those from other prominent external databases, such as GenBank, RefSeq, UniProt, etc. Alternatively, researchers can start with a list of external database identifiers and map them to the corresponding PATRIC features.



**Metadata:** Supports searches for and locates genomes of interest based on various combinations of 61 different metadata fields.

For instance, all genomes that have been isolated from humans, genomes related by phylogeny, or genomes related by lifestyle.



**Genome Browser and Compare Region Viewer:** Visualizes and compares genome annotations from multiple sources and allows users to view gene neighborhoods.