PATRIC: THE BACTERIAL BIOINFORMATICS RESOURCE CENTER

PATRIC, the PAThosystems Resource Integration Center, is the NIH/NIAID-funded Bacterial Bioinformatics Resource Center, a webbased resource providing integrated omics data and analysis tools to support biomedical research on bacterial infectious diseases and antimicrobial resistance. At PATRIC, users can upload their private data into a workspace, analyze it using high-throughput services, compare it with other public data using visual analytics tools, and share results with other PATRIC users.

Visit: https://patricbrc.org

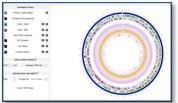


KEY FEATURES

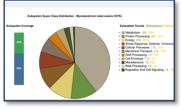
- Comprehensive collection of microbial genomes and related 'omics data
- Uniform microbial genome annotations
- Curated genome metadata and AMR phenotypes
- Easy to use high-throughput computational analysis services
- Integrated analysis and visualization tools
- Private workspace for analysis of user data
- User data sharing and publishing
- Programmatic access via Command-line Interface
- Bulk data upload and download via FTP

VISUAL ANALYTICS

GENOME METADATA



CIRCULAR GENOME VIEWER



SUBSYSTEM OVERVIEW

OUTREACH

- Online tutorials and guides
- > 66 workshops worldwide
- > 2000 workshop participants
- Monthly webinars
- Twitter @PATRICBRC
- > YouTube PATRICBRC
- Facebook facebook.com/patricbrc



- 185,000 public microbial genomes
- 10,000 plasmids, 4,800 bacteriophages, 10 eukaryotic hosts
- Genome annotations: genes, RNAs, repeats, CRISPRs, and protein functions
- Protein families, subsystems, and pathways
- AMR genes, virulence factors, drug targets, essential genes, and transporters
- AMR phenotype data for 25,000 genomes and 130 antibiotics
- > 829 transcriptomic datasets

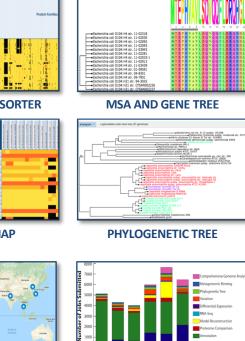
Percent protein sequence identity 100 99.9 99.8 99.5 99 99 89 95 90 80 72 60 50 40 20 20 10 100 99.9 99.8 95 99 96 95 90 80 72 60 50 40 30 20 10

PROTEOME COMPARISON

65M protein-protein interactions

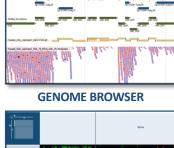
ANALYSIS SERVICES

- Comprehensive Genome Analysis
- Genome Assembly and Annotation
- Similar Genome Finder and BLAST
- Proteome Comparison
- Protein Family Sorter
- Pathway Comparison and Metabolic Model Reconstruction
- Phylogenetic Tree Construction
- Variation/SNP Analysis
- RNA-Seq and Expression Analysis
- Tn-seg Analysis
- Metagenomic Binning
- ID Mapping



COMPARE REGION VIEW







GENE EXPRESSION



PROTEIN INTERACTIONS

PATRIC USAGE

- > 8,100 registered users
- > 6,000 analysis jobs/month
- > 150,000 page views/month
- > 5,000 unique visitors/month
- 7,700 PATRIC/RAST citations

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PROTEIN FAMILY SORTER

PATHWAY MAP



WORKSHOPS