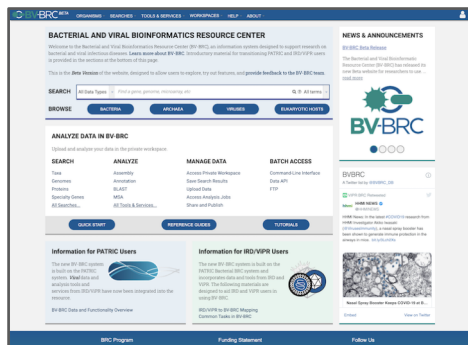


What is the BV-BRC?

The **Bacterial and Viral Bioinformatics Resource Center (BV-BRC)** combines and integrates the data, tools, and technologies from two long-running centers, **PATRIC**, the bacterial BRC, and **IRD / ViPR**, the viral BRCs. It is designed to support bacterial and viral infectious disease research.



bv-brc.org

New Pathogens

In addition to providing a single resource where users can access both bacterial and viral data, we have added **6 new virus families**. These include several priority pathogens and consist of the following families:

- [Adenoviridae](#)
- [Asfarviridae](#)
- [Polyomaviridae](#)
- [Hepadnaviridae](#)
- [Hepeviridae](#)
- [Parvoviridae](#)

Those interested in bacteria-specific viruses will also be able to browse through bacteriophage data.

[All Viruses](#)

[All Bacteria](#)

New Tools

As part of the merger of PATRIC and IRD/ViPR, BV-BRC integrates tools and services from both resources, including extending existing tools to support both bacteria and viruses, where appropriate.

New to IRD/ViPR Users:

In addition to the key viral analysis tools already available in IRD/ViPR, BV-BRC provides the following:

- [SARS-CoV-2 Genome Assembly and Annotation](#)
- [SARS-CoV-2 Variant Tracker](#)
- [Taxonomic Classification](#)
- [Metagenomic Binning](#)
- [RNA-Seq Analysis](#)
- [Expression Import](#)
- [Fastq Utilities](#)
- [3-D Protein Structure Viewer](#) (new)

New to PATRIC Users:

In addition to the bacterial analysis tools already available in PATRIC, BV-BRC provides the following:

- [MetaCATS](#) (Metadata-driven Comparative Analysis Tool)
- [Primer Design](#)
- [MSA and SNP Analysis](#)
- [Gene Tree](#)
- [Taxonomic Classification](#) (with support for viral data)
- [Metagenomic Binning](#) (with support for viral data)
- [3-D Protein Structure Viewer](#) (new)

[All Tools and Services](#)

FAQs

Q: Will I need to create a new account?

A: No. You can use your previous PATRIC/IRD/ViPR login credentials to access the BV-BRC database.

Q: Can I still use the old websites?

A: Yes. The PATRIC, IRD, and ViPR websites will remain active while users migrate to the new site. However, updates and support for these legacy websites will be discontinued sometime after September 2022.

Q: What will happen to my data stored on the old sites?

A: For PATRIC users, your data is available in the BV-BRC workspace. For IRD/ViPR users, your data is still available in those sites. We can help migrate it to BV-BRC, if desired.

Q: I need help using the new site. Where can get help?

A: [Click here](#) to request assistance, report issues, and make suggestions.

Learning Resources

[Quick Start Videos](#)

[Information for PATRIC users](#)

[Information for IRD/ViPR users](#)

[Quick Reference Guides](#)

[Tutorials](#)

[Webinars](#)

Contact Us

Questions? Problem? Suggestions?
[Click Here](#)

See 2nd page (reverse) for additional information



Key Features

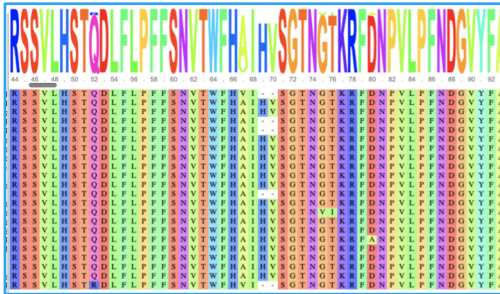
- Extensive collection of bacterial and viral genomic and related data
- Standardized genome annotations to facilitate comparative analysis
- Curated genome metadata, AMR phenotypes, and variants of concern
- Easy-to-use high-throughput computational analysis services
- Integrated, interactive data analysis and visualization tools
- Private user workspace for data analysis, sharing, and publishing
- Programmatic access via CLI, API, FTP
- Extensive help documentation, tutorials, and educational materials

Data Types

- Total 9.1M+ microbial and viral genomes
 - 604K+ public and 768K+ private microbial genomes
 - 8.4M+ public viral genomes, including 6.2M SARS-CoV-2
 - 22K+ bacteriophage genomes
 - 10 eukaryotic host genomes
- Annotations using RAST and VIGOR4
 - 5B+ genes/proteins, 90M+ mat peptides, and other features
- Curated metadata and AMR phenotypes
- 300K+ experimentally verified epitopes
- 77K+ protein structures
- 900+ curated 'omics datasets
- 56M+ microbial and host-pathogen PPIs
- 1.6M surveillance, 47K serology records

Tools and Services

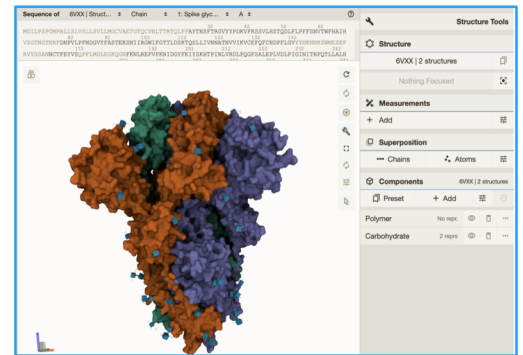
- Genome Assembly and Annotation
- Comprehensive Genome Analysis
- SARS-CoV-2 Assembly & Annotation
- Similar Genome Finder and BLAST
- Meta-CATS
- Phylogenetic Tree Inferencing
- Genome Alignment
- Primer Design
- Variation and MSA/SNP Analysis
- Tn-seq Analysis
- Proteome Comparison
- Metagenomic Read Mapping, Binning, & Taxonomic Classification
- RNA-Seq and Expression Analysis
- Fastq Utilities
- ID Mapping



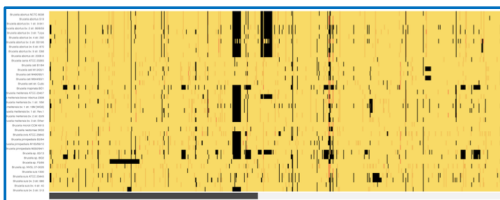
Multiple Sequence Alignment



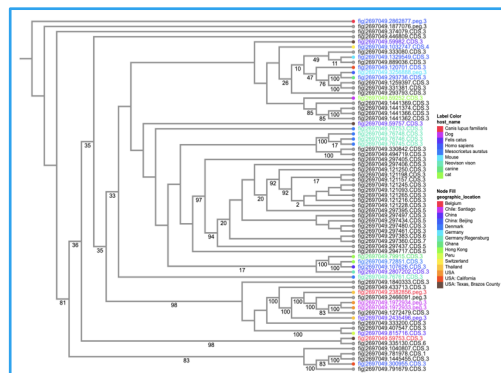
Variation/SNP Viewer



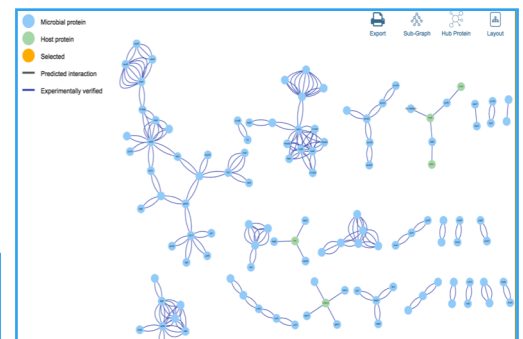
3-D Protein Structure Viewer



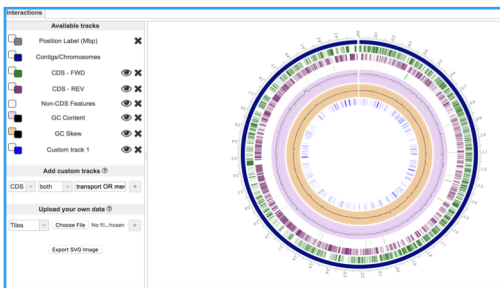
Protein Family Sorter



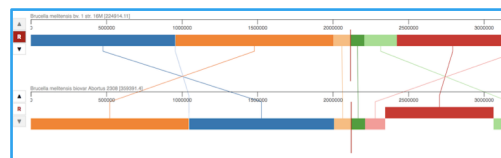
Phylogenetic Tree Viewer



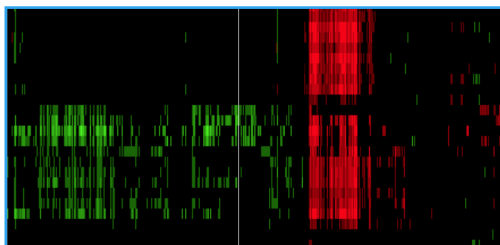
Protein-Protein Interaction Viewer



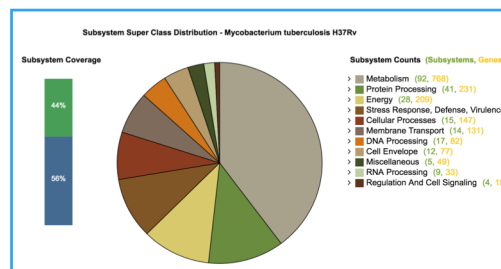
Circular Genome Viewer



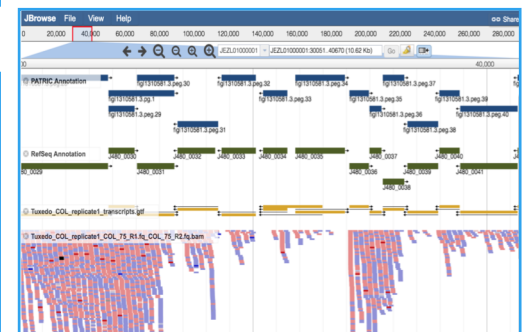
Genome Alignment Viewer



Transcriptomic Heatmap



Subsystem Analysis



Linear Genome Browser