

BV-BRC Renewal

We are pleased to announce that the BV-BRC resource will continue to be supported by NIAID under Award Number U24AI183849 through 2029. See the details [here](#).

BV-BRC will continue to maintain & expand existing data, analysis tools, & public & private workspaces & support batch & programmatic access to data & tools via Data API, Command Line Interface (CLI), & public FTP site.

Over next five years, we will develop innovative tools & technologies to enable in-depth characterization of bacterial & viral pathogens, microbiomes, & host pathogen interactions; enhanced genotype & phenotype predictions; advanced capabilities for functional genomics & drug & vaccine development; & an AI-driven user interface for accessing data & tools to improve usability & user experience.

BV-BRC will also provide cutting edge bioinformatics support & tools to rapidly respond to emerging outbreaks, pandemics, & public health emergencies.

We will continue our outreach & training program, offering several in-person & virtual bioinformatics workshops & webinars each year. We will also provide online & freely accessible tutorials, user guides, & MOOC courses.

The BV-BRC team is excited & looking forward to continue advancing infectious disease research with cutting-edge bioinformatics tools, innovative technologies, & comprehensive data resources that empower global community of researchers to respond effectively to public health challenges.

Outreach

The BV-BRC team conducted several outreach events this summer & it was great connecting & interacting with our users in person.

Dr. Rebecca Wattam gave a two-day workshop on Analyzing Bacteriophages using BV-BRC on June 20-21 at the George Eliava Institute of Bacteriophages, Microbiology & Virology in Tbilisi Georgia. The workshop material and tutorials can be found in the [BV-BRC Workspace for Workshops](#).



The BV-BRC team had a great time at ASV 2024 in Columbus Ohio. It was awesome to get connected with the virology community at our booth & hear from our users in this way. Thanks for stopping by and chatting with the team. We are looking forward to seeing you next year.



Please contact us if you are interested in hosting the BV-BRC team to offer a workshop at your institution. The workshop can be customized & cover broad range of topics, such as Bacterial and/or Viral Bioinformatics, Metagenomics, AMR Analysis, & Bacteriophages. Past workshops can be found in the [BV-BRC Workshop folder](#).

Upcoming Webinars

With our fall outbreak webinar series, we will analyze our H5N1 and MPOX data, outbreak pages, and tools. These meetings will be on Thursdays, October 3rd, 10th, and 17th, at 11:00 a.m. PT.

- [Register now](#) for Data Searching (October 3rd)
- [Register now](#) for Outbreak pages & phylogenetics Searching (October 10th)
- [Register now](#) for BV-BRC Influenza & Monkeypox Virus Tools (October 17th)

Surveillance Data

New surveillance data for influenza has been added- check it out on either our table or map feature now! Surveillance data can be accessed from the [influenza a taxon view](#) or [surveillance advanced search](#). To view the map, from the surveillance tab taxon view- click on any subset of data you are interested in then click "map" on the green bar.



This figure is 2023 surveillance data colored by flyway from our surveillance pages.

BV-BRC User Support

BV-BRC offers an online helpdesk, accessible through the 'Contact Us' option in the 'About' menu on our website. Our dedicated team actively monitors the helpdesk to provide prompt assistance with any questions or requests. We manage these requests using a Jira service desk to track & review recurring questions & suggestions, which in turn help us develop new features & functionality.

Sequence Feature Variant Types

We are pleased to reinstate IRD's Sequence Feature Variant Types (SFVT) on the BV-BRC platform. SFVT offers advanced insights into genotype-phenotype associations by defining distinct sequence features based on nucleotide or amino acid variations. This feature supports detailed analysis of pathogen genomes, aiding in the understanding of how specific genomic changes impact functional characteristics. You can find SFVT across structural, functional, epitopes, & sequence alterations. Initially available for Influenza A data.

We are excited to bring this powerful tool back to support your research efforts. We will be showcasing this data in our upcoming webinar. [Register here](#). Please stay tuned for more updates.

You can find Sequence Feature Data [here](#).



Sequence Feature Variant Type Data

- Sequence Feature Variant Types Table on Influenza A virus Taxonomy Page
- Variant Types table for each sequence feature
- Advanced Search Sequence Feature Variant Type Search from home page
- Quick Reference Guide to explain data

Sequence Feature & Variant type data can also be searched for on the [advanced search pages](#) shown below.

Advanced Search
Sequence Feature Variant Type (SFVT) Search - BETA

Search for Sequence Feature Variant Type data for select viral families using generic keywords, subtype, segment, or sequence feature type. For further explanation, please see the Advanced Search Quick Reference Guide.

Keyword
Search term

Pathogen Group
Influenza A virus

Segment / Protein
1 / PB2
2 / PB1
2 / PB1-F2
3 / PA
4 / HA
5 / NP
6 / NA
7 / M1
7 / M2
8 / NS1
8 / NS2

Sequence Feature Type
Epitope
Functional
Sequence alteration
Structural

Sequence Feature Variant Type Sequence
eg. "RERE"

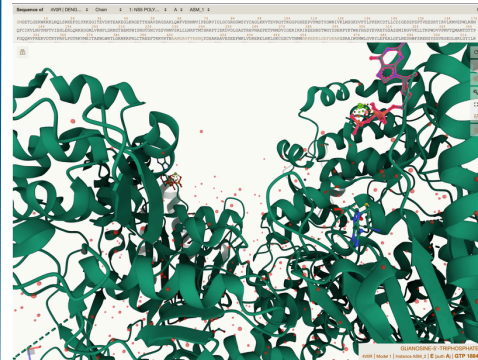
Reset Search

Molecular Docking

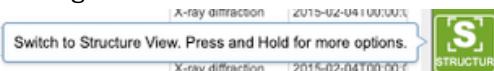
We are excited to release our [protein docking service](#). Explore protein-ligand interactions generated by advanced artificial intelligence (AI) & machine learning (ML). This service utilizes a diffusion model, DiffDock, to compute a set of poses for a target protein structure & small-molecule ligands. Our protein viewer gives a 360-degree, three-dimensional interactive view of the protein & docked ligands. The aim is to simulate & analyze potential binding scenarios "in silico," offering a crucial advantage by predicting the success of protein-ligand combinations ahead of costly & time-consuming in vivo experiments.

Showcase: Protein Viewer

This is one example of the power of the [protein structure](#) viewer data. Check out the awesome resource for structures & all of the functionality encased in that data for both bacteria & viruses.



1. Find bacteria or virus of interest
2. Click on protein structure tab from taxon view
3. Click on "STRUCTUR" icon on green bar



4. View structure in interactive format seen above
5. Click around & explore the possibilities!

Monkeypox Virus Spotlight

Monkeypox virus (MPXV) is a member of the *Orthopoxvirus* genus, which also includes variola virus (the cause of smallpox), vaccinia virus, & cowpox virus. The MPXV genome is a double-stranded DNA molecule, approximately 197 kb in size, encoding over 190 proteins. The virus is divided into two major clades 1 & 2.

Monkeypox Virus Timeline

1958



Mpox detected in a colony of research monkeys, but the original host is unknown.

1970



First human infection detected in the Democratic Republic of the Congo (DRC). This case was in a 9-month-old in Basankusu County. This area had a high concentration of monkeys but no sick monkeys had been detected.

1980



Smallpox, caused by Variola virus was eradicated. Variola virus & MPXV are classified into different species within the *Orthopoxvirus* genus. One major difference between these viruses is host.

2003



First case detected outside of Africa due to introduction from prairie dogs which were infected by imported small mammals from Ghana. Forty seven cases were detected in the United States.

2017



Nigeria had an outbreak of clade 2 virus. Cases surged between children & young adults, with 198 suspected cases. The animal host & nature of spread are not well classified.

2022



Clade 2 infection spread around the globe. Clade 2 is less severe compared to Clade 1. Clade 2 is still circulating globally through today.

2023/4



Clade 1 spread across DRC & neighboring countries. Leading to in 2024, both WHO & Africa CDC reported a Global Emergency over outbreak as cases of Clade 1 continue to rise.

2024



An imported case of Clade 1 was detected in Sweden. This is the first time Clade 1 was seen outside of Africa- & has not spread. It was determined to be Clade 1b. A case in Thailand was also detected.