BRC Analytics

Yes, we automated it on purpose.

brc-analytics.org

Our Mision

Seamless Data Integration

Automatically manage reference genomes and annotations from NCBI and other public data sources.

Community-Driven Knowledge

Establish community standards for analysis and incorporate these into workflows and results reports for consistency and reproducibility.

Accessible Bioinformatics

Leverage Galaxy, TACC and AI to eliminate the need for command-line interfaces and hardware administration.

BRC Analytics, Today

- Intuitive workflow configuration tool to browse and select public resources (including ENA) as inputs
- General purpose and organism-specific Galaxy workflows tailored for pathogen research
- Nearly 2,000 reference assemblies currently available, with projections to exceed 5,000 assemblies in the next release
- Integration with NCBI Datasets and UCSC Genome Browser
- Free access to high-performance computing resources at TACC
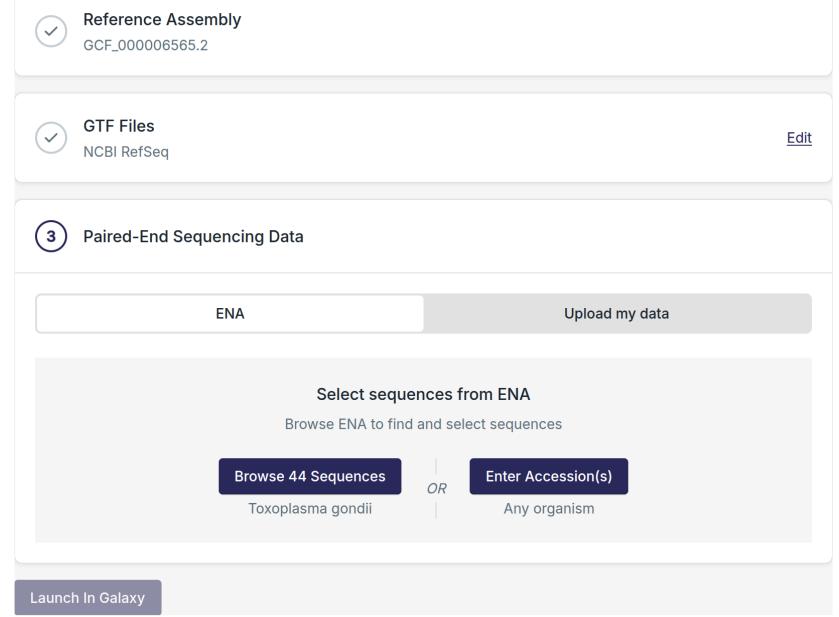
Chat Interface

AI Assistant

Can you tell me about the *Toxoplasma gondii* SAG1 gene? I'm trying to interpret my workflow results.

I queried the NCBI database for information on the *Toxoplasma gondii* SAG1 gene. SAG1 encodes a major surface antigen important for host cell adhesion and invasion. I can also provide links to public resources such as NCBI Gene and VEuPathDB for more details.

Type a message...

Workflow Configuration

Reference Assembly
GCF_000006565.2

GTF Files
NCBI RefSeq   Edit

3 **Paired-End Sequencing Data**

| ENA | Upload my data |

Select sequences from ENA
Browse ENA to find and select sequences

| Browse 44 Sequences | OR | Enter Accession(s) |
| *Toxoplasma gondii* | | Any organism |

Launch In Galaxy

BRC Analytics, Tomorrow

- Advanced AI-powered assistants for querying public resources and providing biological context
- Comprehensive analytical reports with interactive visualization for workflow results, which can optionally be shared
- Sophisticated comparative genomics pipelines for phylogenetic analysis and evolutionary studies
- Format workflow results to be compatible with VEuPathDB user dataset requirements
- Direct integration of VEuPathDB gene models as primary workflow inputs

Building Bridges in Molecular Parasitology

BRC Analytics complements the foundational knowledge provided by VEuPathDB by offering accessible workflow tools that enable researchers to process and analyze their data with ease. We would like to see a collaborative ecosystem where researchers can leverage both platforms' strengths - VEuPathDB's curated knowledge and BRC Analytics' workflow capabilities - to accelerate discovery in molecular parasitology research.