

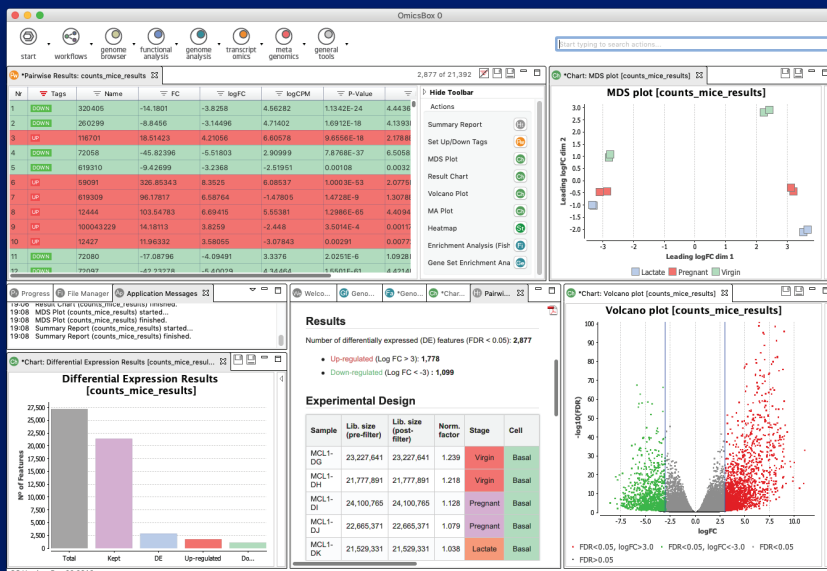


OmicsBox

BIOINFORMATICS  
MADE EASY

# OmicsBox Overview

- Leading bioinformatics platform for the analysis of novel genomes.
- Internationally recognized as a leader in functional genomics, which is demonstrated by over 7000+ scientific research citations.
- User-friendly bioinformatics desktop application for industry, academic and governmental research biologists.
- Allows to gain biological insights fast and easy even for completely novel genomes.



## Developed by BioBam

- OmicsBox is developed and maintained by BioBam Bioinformatics.
- BioBam is a bioinformatics solution provider based in Valencia, Spain.
- BioBam's solutions accelerate research in disciplines such as agricultural genomics, microbiology and environmental NGS studies; amongst others.

# OmicsBox Modules

## Genome Analysis

De-Novo Assembly, Gene Finding, Repeat Masking, Coding Potential, Rfam

## Transcriptomics

FastQC, Assembly, Quantification, Differential Expression (Pairwise, Time Series)

## Functional Analysis

Blast2GO Annotation (GOs, COG, Enzymes, Domains), Enrichment Analysis, Visual Exploration

## Metagenomics

Taxonomic and Functional Classification, MetaAssembly and GenePredictions, Comparative Analysis

## OmicsBox

Workflows, Genome Browser (gff, vcf, fasta and bam), Projects, CloudComputation, Data Manipulation, Filtering, etc.

# Subscription Options

**1 Module**  
**1 Year**  
**1 User**

**Your  
Personal  
Plan**

**Multiple  
Modules, Years  
and Users**

**REQUEST YOUR FREE TRIAL**

# Genome Analysis

## Quality Control

Use FastQC and Trimmomatic to perform the quality control of your sequencing data, to filter reads and to remove low quality bases.

## De-Novo Assembly

The assembly features based on ABySS allows to reconstruct whole genome sequences without a reference and specific hardware requirements.

## Repeat Masking

Mask repeats and low complexity DNA sequences of your eukaryotic genome assemblies to improve the downstream gene predictions.

## Gene Finding

Perform prokaryotic (Glimmer) and eukaryotic (Agustus) gene predictions to generate GFF genome annotations. The eukaryotic gene predictions offers RNA-seq intron hint support.

## Genome Browser

Visualize your annotations in form of tracks to combine the genome sequences (.fasta) with alignments (.bam), the intron-exon structure (.gff) as well as variant data (.vcf).

# Functional Analysis

## High-Throughput Blast and InterProScan

Use CloudBlast and CloudInterPro to perform fast sequence alignments and domain searches against a reference datasets of your choice.

## Gene Ontology Mapping

Link potential homologs and domains with available functional information.

## Blast2GO Annotation

The Blast2GO methodology allows to flexibly assign most reliable functional labels to novel sequence datasets, taking into account source quality and ontology hierarchies.

## Enrichment Analysis

Use different enrichment analysis approaches to identify over and under represented molecular functions.

## Functional Interpretation

Many different visualizations allow to evaluate the annotation process as well as help with the biological interpretation of experimental and functional analysis results.

# Transcriptomics

## De-Novo Assembly

Assemble short reads with Trinity to create a de-novo transcriptome without a reference genome.

## RNA-Seq Alignment

Alignment of RNA-seq data to your reference genome making use of STAR, an ultrafast universal RNA-seq aligner via the OmicsBox Cloud.

## Quantify Expression

Quantify expression at gene or transcript level via HTSeq or RSEM and with or without a reference genome.

## Differential Expression Analysis

Detect differential expressed genes between experimental conditions or over time. All used frameworks, NOISeq, edgeR and maSigPro, are well-known and versatile statistical packages used for these types of analysis. Rich visualizations help to interpret results.

## Enrichment Analysis

By combining differential expression results with functional annotations, enrichment analysis allows to identify over- and under-represented biological functions.

# Metagenomics

## Quality Control

Use FastQC and Trimmomatic to perform the quality control of your samples, to filter reads and to remove low quality bases.

## Taxonomic Classification

Identify present species (Bacteria, Archaea, Virus) with Kraken and visualize results with multilevel pie-charts (Krona) as well as inter-sample comparison bar-charts.

## Metagenomic Assembly

Choose between MetaSPAdes and MEGAHIT to assemble large datasets easy and fast in the cloud.

## Gene Prediction

Use FragGeneScan for plain reads and Prodigal for assembled data to identify and extract possible genes and proteins.

## Functional Interpretation

Use EggNOG-Mapper (orthologous groups) and PfamScan (domains and families) to perform high-throughput functional classifications. Results can be represented and compared visually with GO graphs and charts.

# Examples, Tutorials, Videos

In our blog you can find many video tutorials, example analysis and datasets as well as information about the latest developments.

The BioBam blog is also a great resource to learn about all the different analysis steps and to stay up to date.

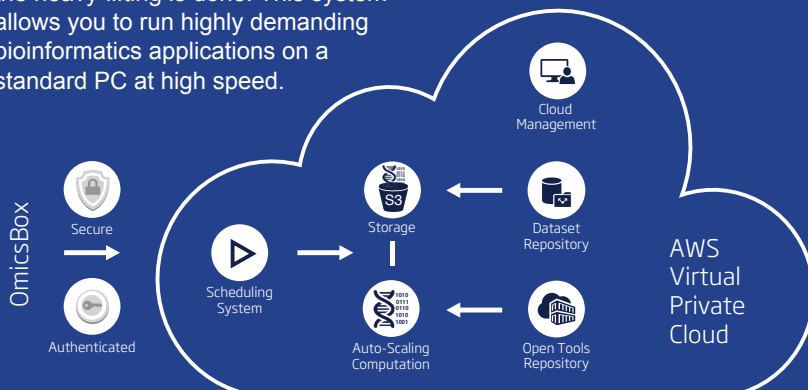


## Omics Cloud Platform

aws partner network

Standard  
Technology  
Partner

Our cloud platform provides a secure, robust and auto-scalable backend to OmicsBox where most of the heavy-lifting is done. This system allows you to run highly demanding bioinformatics applications on a standard PC at high speed.



\* The Cloud Cloud Platform is also available as dedicated solution. Please ask us for details.

powered by **aws**

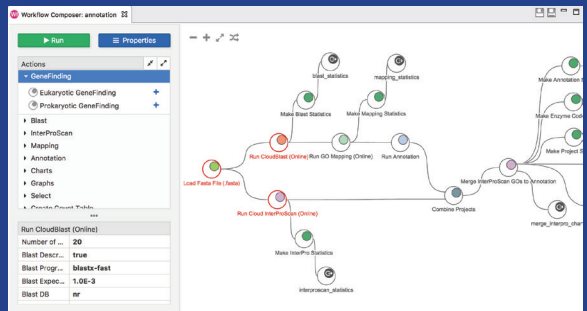
# One Box - One Solution

# Powerful Tables

The rich user interface allows to process large datasets with ease. All tables can be filtered, sorted and, most importantly, combined with other result sets. It is easy to create and extract subsets for subsequent analysis steps.

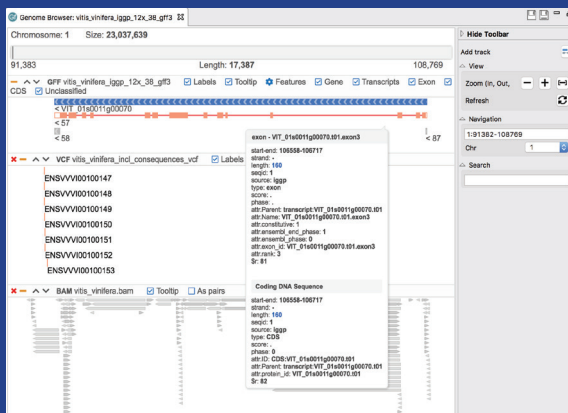
# Workflows

The Workflow Manager allows to create, run and save bioinformatics workflows. Create a workflow by dragging and dropping the analysis steps of your choice and configure and review all parameters in one place.



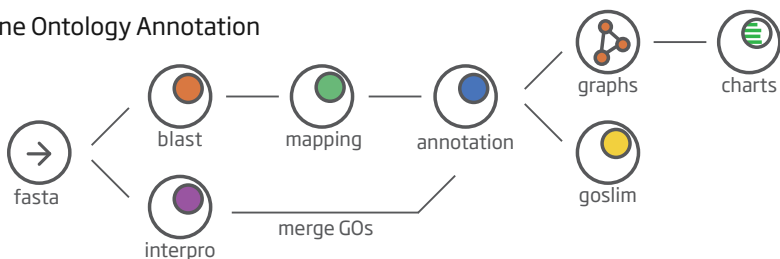
# Genome Browser

The Genome Browser offers the possibility to combine alignments (.bam) with gene annotations (.gff) and variant information (.vcf) via multiple tracks. Navigation, filter and search options allow to review results in an easy and explorative way.

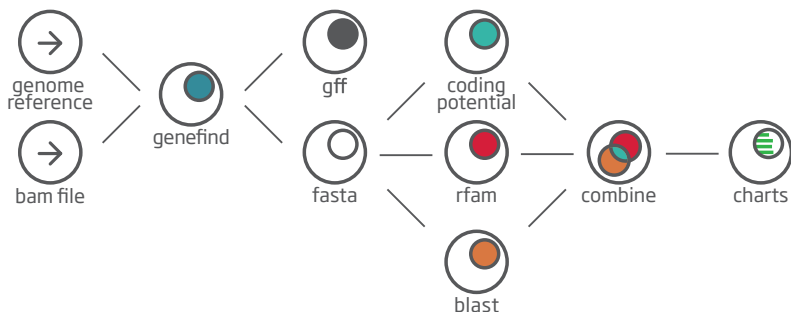


# Example Workflows

## Gene Ontology Annotation



## Genome Characterization



## Differential Expression with Enrichment



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