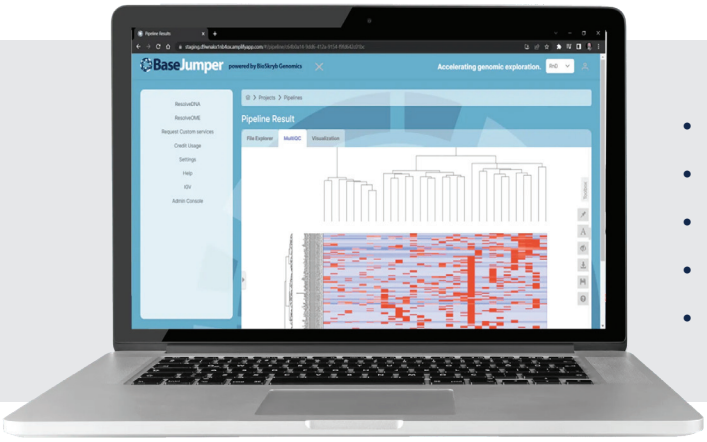
BioSkryb GENOMICS

Cells explored. Answers revealed.

BaseJumper™

Accelerate genomic exploration today with the BaseJumper™ Bioinformatics platform. Discover what you've been missing!



- **Cloud-based platform to accelerate single-cell informatics**
- **Single cell multiomics data analysis for both DNA and RNA**
- **Fast track the interpretation and visualization of large data sets**
- **Ultrafast filtering of millions of biomarkers in a study**
- **Generate publication-quality figures and reports**

THE MISSION

The BaseJumper™ Bioinformatics Platform, powered by BioSkryb Genomics, is designed to provide bioinformatics analysis and interactive visualization at scale. Uncovering biomarkers and mechanisms of disease demands high volumes of complex data and the ability to quickly slice layers of analyses. Since multiomic (DNA, RNA, and Protein) data can be generated across a single cell, organization and mapping of the results are necessary to empower interplay of molecular features. BaseJumper™ brings speed and ease of use directly into the hands of its users, shifting time from computation to interpretation of results.

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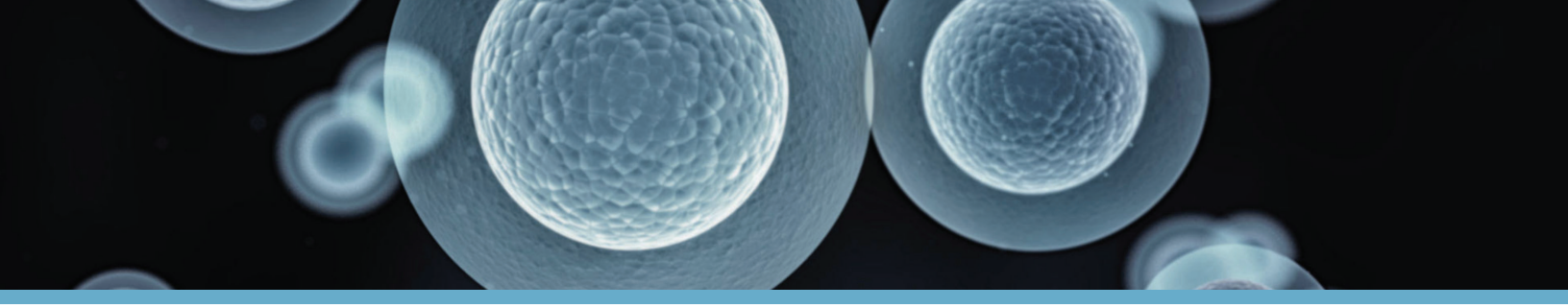

THE ANSWER – BASEJUMPER™

The BaseJumper platform provides a number of rich interactive visualizations, RNA/DNA analysis workflows and QC tools. With dynamic data filtering capabilities, researchers from all disciplines can accelerate the interpretation of results in common formats without deep expertise in computational and visual methods.

A suite of visualization apps is available to users within the analysis project that can cover common areas of analysis such as:

- Genome browsing for allele changes and expression levels
- Cellular phenotype identification to colorize figures and drive significance analyses
- Sample grouping based on similarity of copy number, expression, genotype etc.
- Prevalence of genetic loci within copy aberrations across studies
- Expression-level views like heatmaps, PCAs and differential expression.
- Filtering of variants based on dozens of annotation databases and common genetic and cancer databases

Users create projects and organize data from their repositories of sequencing results and put through several pre-design bioinformatics workflows to derive a variety of biomarkers: variants (SNVs/Indels), repetitive regions, copy number aberrations, structural variants, isoform variation, gene fusions, etc.

Access **Build** **Compute** **Display** **Export**

Unlock the discovery potential from your single cell experiments with BaseJumper™ Bioinformatics

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