# Frequently Asked Questions for BaseJumper

## General

1) **Requesting a BaseJumper account/personal workspace.**
   a. To request a BaseJumper account, contact an administrator at: BaseJumper@bioskryb.com or Request New Account
   b. Once registered, you will be assigned to BioSkryb Demo Organization and BioSkryb Demo Workspace. You will have limited access until an administrator assigns you into a workspace. You can access your organization and workspace by signing in with google.
   c. To request to Add a New Organization or Users to Your Current Organization, use the following link: Request New Account

2) **Accessing my BaseJumper workspace.**
   a. After registering, **Create an Account.**
   b. You will see the current workspace selected in the top right of your screen.



   c. When you open the dropdown menu, you will see all workspaces you currently have access to.
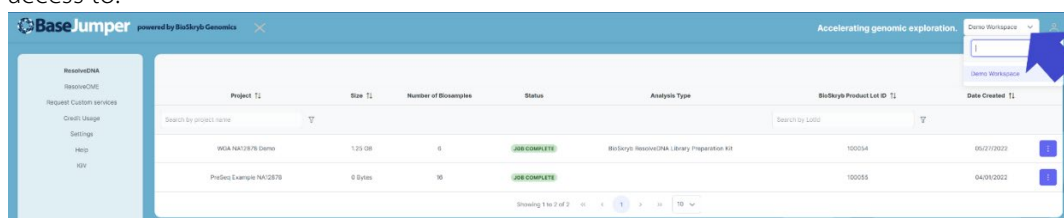


   d. You can find your workspace of interest by scrolling down in the search box. After you select   a workspace, all projects inside that workspace are loaded.

3) **Creating a new project.**
   a. If you've selected a workspace, you should see a table containing all of the projects in that workspace. If you see the notice "*No projects found*" it indicates that the workspace you've chosen is empty.
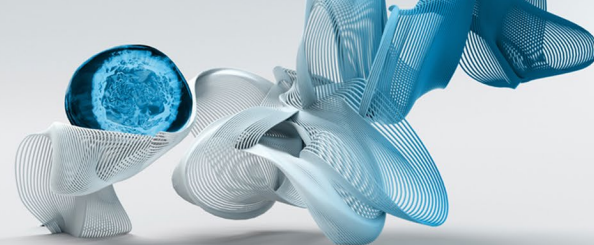
**b.** To create a project, first choose the appropriate Resolve technology for your single cell workflow. If you're unsure, visit the **BaseJumper Glossary** for clarity.
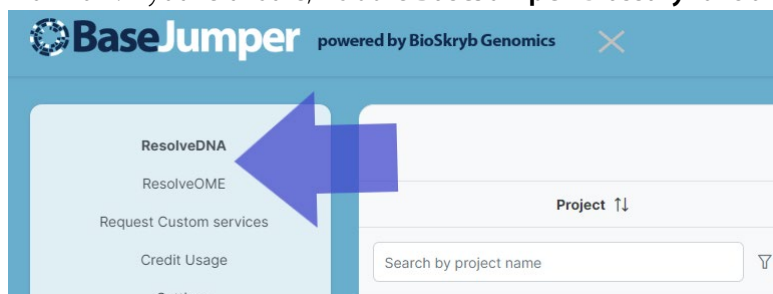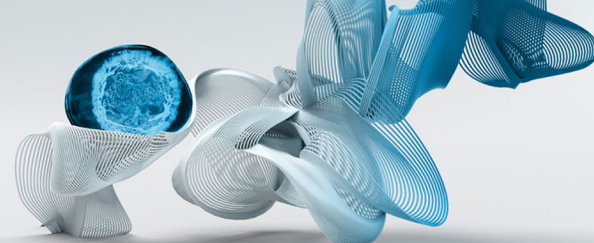


**c.** Next, click the **New Project** button in the upper right of the table.
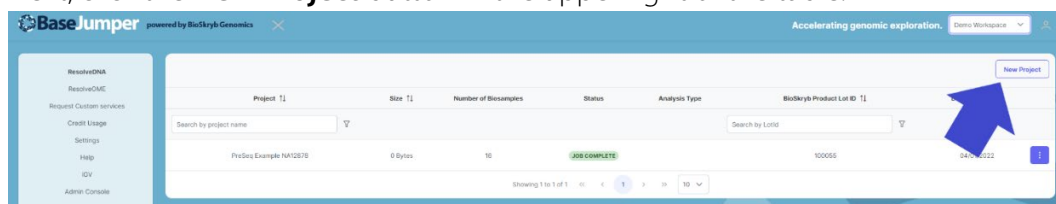


**d.** Once selected, a **Create Project** dialog pops up. If you see a loading spinner wait a few seconds for all of the available biosamples to be loaded from the BaseSpace Sequence Hub.
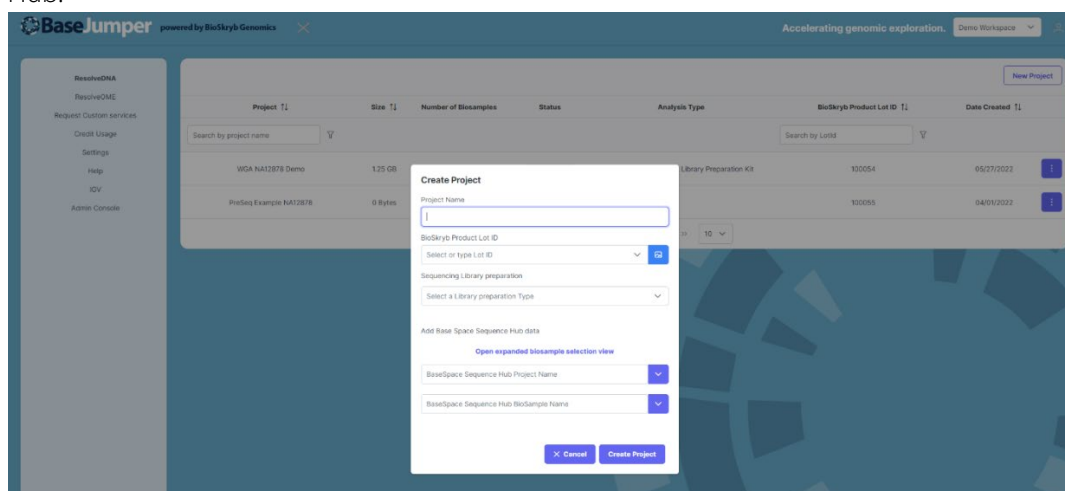


**e.** List of available inputs:
   i. **Project Name** - The name of your project. Cannot contain special characters.
   ii. **BioSkryb Product Lot Id** - The lot number printed on your reagent box. The lot id can be found on the box by clicking the image icon next to the "Lot ID" section.
   iii. **Sequencing Library Preparation** - List of all available sequencing types.
   iv. **BaseSpace Sequence Hub Project Name** - List of all available projects from BaseSpace Sequence Hub. If you select a project (or multiple), only the biosamples belonging to that project will be show in the Biosample Name input field. You have the option to import all the biosamples belonging to that project by clicking the arrow button that will appear on the left of the input field.

      v.    **BaseSpace Hub Biosample Name** - If no projects wore selected, all of the available biosamples will be shown.

Clicking on create project will add the project to the data table. Upon creation, the projects status will be *"No Data"*. The status will change after a few seconds to *"Job Started"*, this indicates that the download process from BaseSpace Sequence Hub to the project specific S3 location has started. Once the download is finished, the status will change to *"Job Complete"*.

4) **Triggering BaseJumper Pipelines.**

Triggering a pipeline in BaseJumper can be accomplished in two ways: in combination with the BaseSpace download prompt and after the download is complete in the home prompt.

    a.  **Approach 1:**

When you create a new project by selecting **Create Project**, a window will appear inquiring if you want to run a pipeline when the BaseSpace download is complete.



Select **Yes** to confirm that you wish to launch a pipeline.

Then, in the following window, choose the pipeline you want to activate.
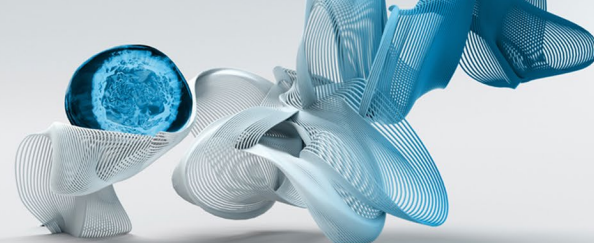


Following that, a window with pipeline-specific settings will emerge.

Select the parameters of interest, then click **Check** at the bottom of the prompt.



This will bring up another screen to "check" the provided specifications before launching the pipeline using the **Launch Pipeline** button.
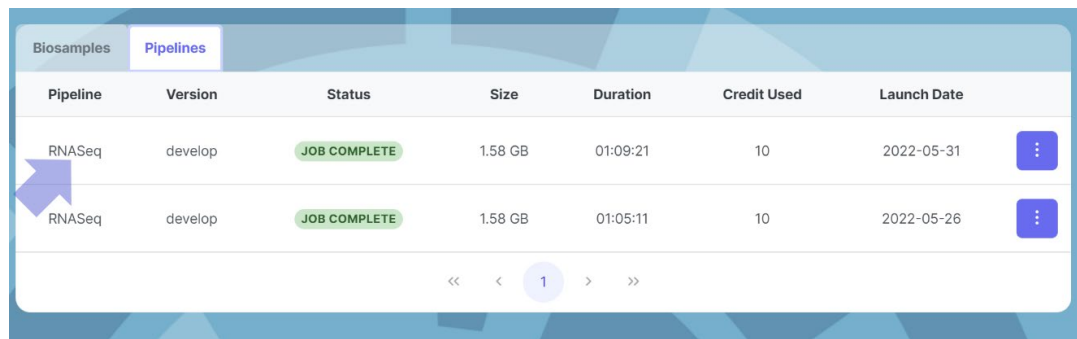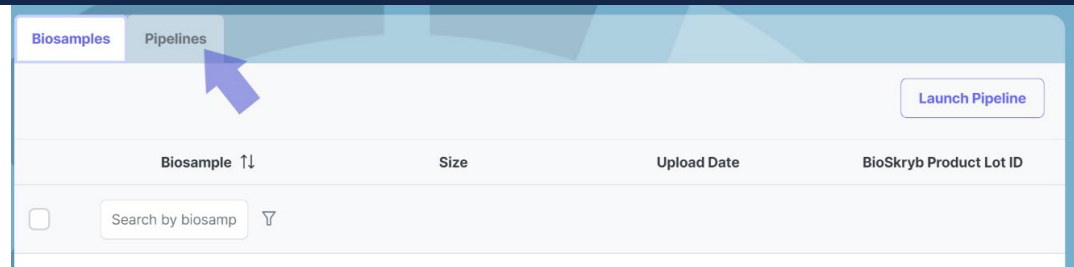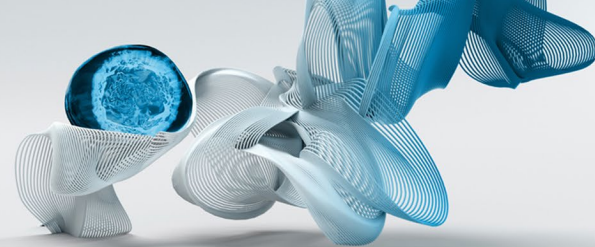


Once the pipeline is complete (you will receive an email marking the pipeline's initiation and completion), select your project, then under the **Pipelines** tab, click the pipeline run to browse results.

**b. Approach 2:**

After the BaseSpace download is complete, just click on the project name to choose the project of interest. You'll be sent to the **Biosamples** page, where you can choose specific biosamples.
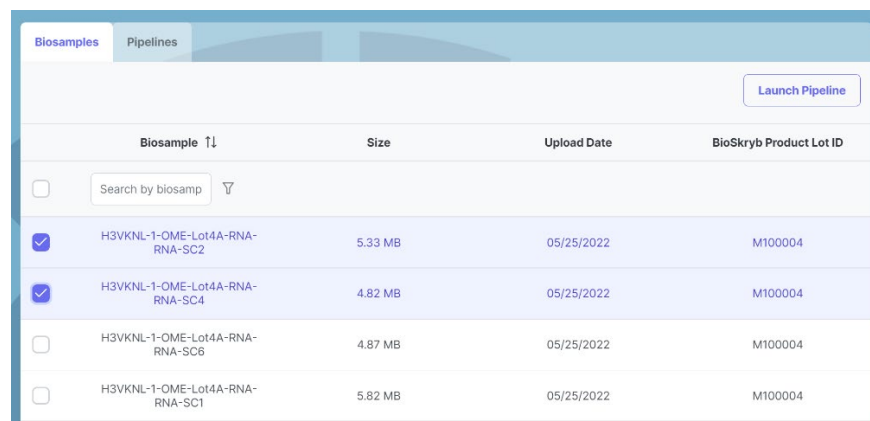


After you've selected your biosamples, click the **Launch Pipeline** button and repeat steps 3 through 7 from Approach 1.

**5) Downloading results/files.**

After triggering the pipeline, you will receive a notification that it has finished. Upon completion, files and figures will be available under the **Pipelines** tab (see **Triggering BaseJumper Pipelines**, step 7).



Downloading can be executed in **File Explorer** by selecting a specific data file(s) of interest and then clicking the **Download** button. Data will export in the specified format.
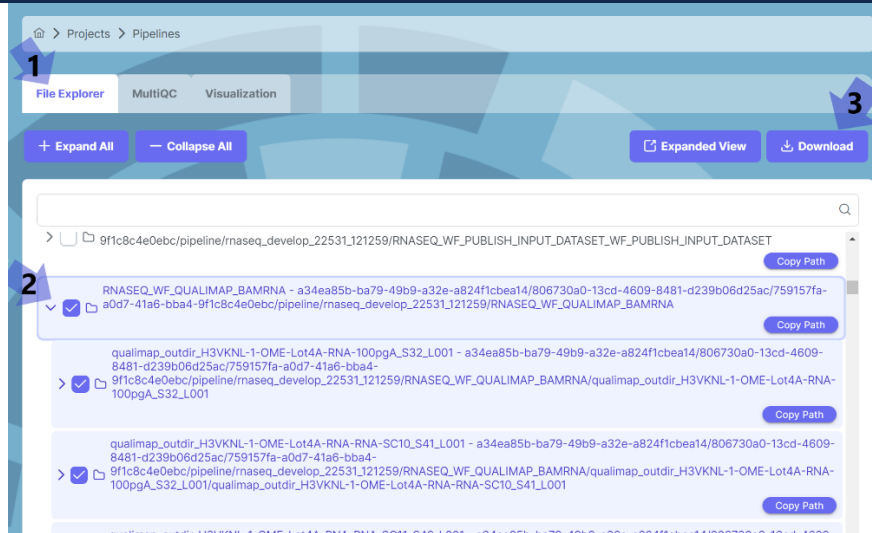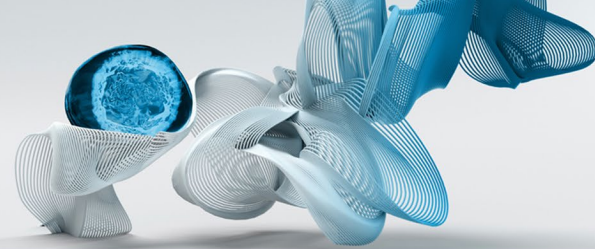
The **MultiQC** tab contains MultiQC Reports and Figures.
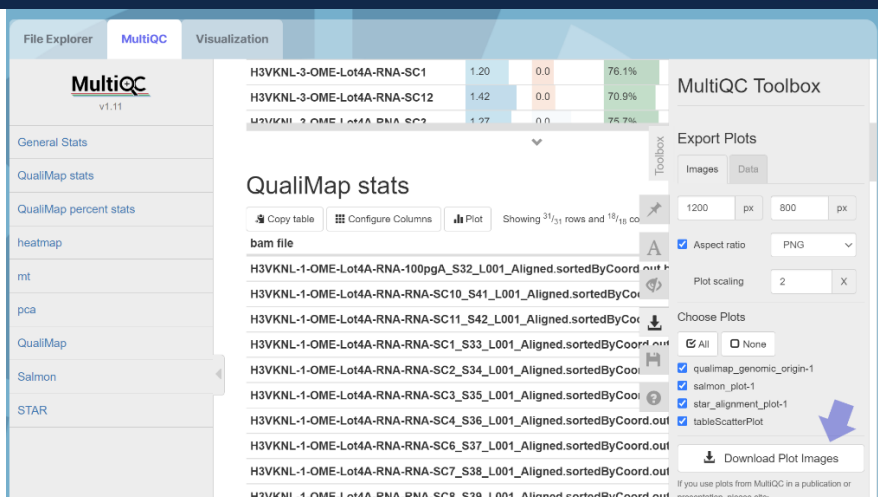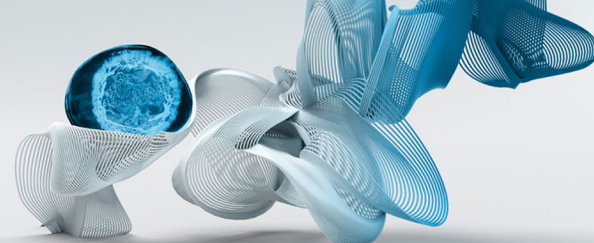
Click the tab, then the **export** button on the right side.
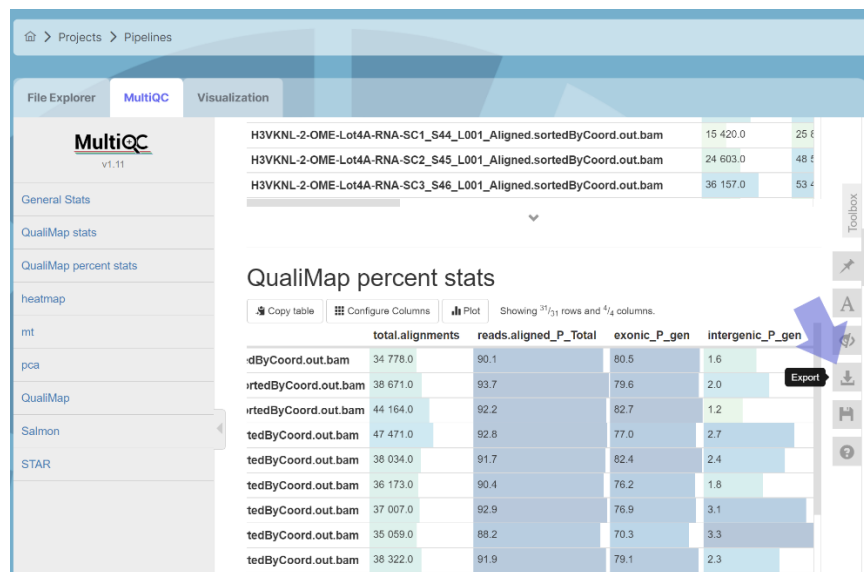


The toolbox will appear, allowing you to alter parameters, select for specific figures, and eventually **Download Plot Images.**

These will download directly to your computer.

Note: that additional data/ tables are saved in multiqc_report_data under the **File Explorer** tab.

6) **Which browser should I use?**

For best performance, we suggest Chrome, but also supports Safari, and Microsoft edge.

7) **Reporting usage issues/bugs/errors/feedback.**

Use the **Request Customer Services** tab in the left panel or BaseJumper Help to report any issues/questions/feedback/requests.
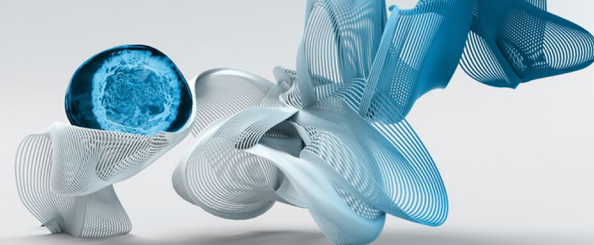


# Datasets

1) **Test Data/Workspaces.**

Data and pipelines for ResolveOME and ResolveDNA preparation kits are available within your Demo Workspace. Here, you can explore general operations and view the output results/figures.

To execute the pipeline on test or external data, use the link below to contact a BaseJumper admin and create a new workspace:
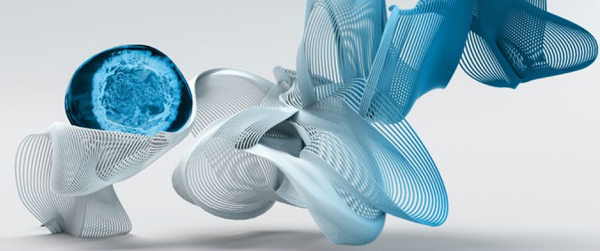
Request New Account

**2) How do I find/sort for my files/data?**

Within each project, you can search for biospecimens at the header row. There is a drop down menu to change the number of biosamples shown in the project view at the bottom of the panel



When in a pipeline view, you can select the tab for file explorer. You can search for biosample, ID or file extension to bring one or more files visible in the file explorer

**3) Is my data secure?**

Yes! Your data is only available to specified users within your organization. It will be secure stored in a personal S3 space, specific to your organization and specified users within your organization.

**4) How long do you store my data/results?**

When launched, BaseJumper will keep data for a project alive for 3 months from project creation. After that point, data will be removed for that project (including pipelines). You will receive an email within 2 weeks of that data requesting additional time and pricing options.

## Pipeline Parameters/Data Analysis

**1) Can I import a specific genome annotation file?**

At present, no; however, if you have a specific genome that you would want to integrated into your workspace, please contact our team at BaseJumper Help.

**2) Can I do exome analysis?**

Yes, the WGS pipeline allows you to switch between wgs and exome mode.

To enable this, go to the WGS pipeline and, when configuring parameters, select **exome** under **Mode** (**wgs** is default).
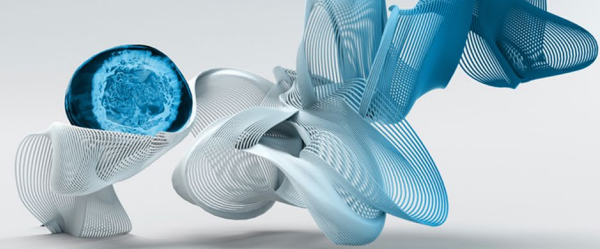
3) **What software do you use in your pipeline?**

Each pipeline has a manual in the BaseJumper landing page that describes the methods used in each pipeline, with citations to tools.  In addition, an explanation of file deliverables and content can be found within.

4) **Can I upload and compare more than one project?**

You can open more than one window or tab of BaseJumper but within a single session, only one project can be viewed at one time.

**For more information about BaseJumper, see our user manuals, materials, and tutorial videos available at https://www.bioskryb.com/BaseJumper/.**

# BaseJumper Glossary

**ResolveOME** : The ResolveOME technology enables for the simultaneous probing of both RNA and DNA from the same individual cell, and it does so in a holistic, comprehensive manner, providing full genomic DNA variant information as well as full mRNA transcript profiling.

**ResolveDNA**: ResolveDNA amplification, driven by primary template-directed amplification, provides nearly complete amplification coverage of the genome, with robust representation of
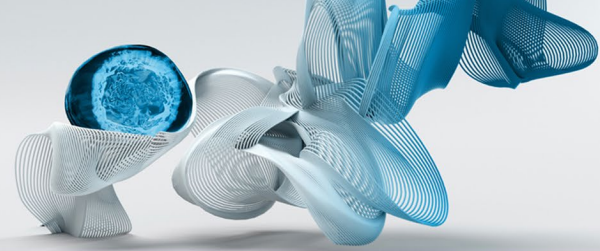
both alleles and overall uniformity. ResolveDNA thereby eliminates the peaks and valleys of coverage and inadequate coverage associated with previous techniques, boosting the capacity to gain single cell genomic insights critical for understanding both disease and normal biology.

**IGV**: The Integrative Genomics Viewer (IGV), which is completely integrated into BaseJumper, is a high-performance visualization tool for interactive study of massive, integrated genomic datasets.

**Ginkgo**: Ginkgo, a copy number call tool, takes a deduplicated (or deduplicated and compressed).bam file, transforms it to a.bed file, and generates plots and a.tsv table containing copy number information.

**DNAscope**: The Sentieon DNAScope tool is used for germline calling, which takes a deduplicated (or deduplicated and compressed) .bam file and a machine learning model and produces variants in a .vcf file.

**SEQTK**: The seqtk tool performs read subsampling on data provided in .fastq files, resulting in an output of subsampled .fastq files.

**STAR**: STAR is an aligner that uses a spliced alignment technique to overcome several of the issues of RNA-seq data mapping.