

Release Notes for SeqSense Cloud Application

Version 2.2

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Introduction

SeqSense Cloud is a cloud-based application for analyzing and visualizing the next-generation sequencing (NGS) data. Using SeqSense Cloud, you can analyze and visualize NGS data from your FASTQ sample files. You can run the SeqSense Cloud analysis pipelines using data generated from the SEQuoia Complete Stranded RNA Library Prep Kit, the SEQuoia Express Stranded RNA Library Kit, and the Omnitron ddSEQ 3' scRNA-seq Kit.

General Information and Resources

Supported Browsers

SeqSense Cloud is supported on the latest versions of Google Chrome and Apple Safari.

Documentation

The following documents are accessible from SeqSense Analysis Solution, Version 2.2:

- SeqSense Cloud Solution User Guide, Version 2.2
- SeqSense Cloud Solution Frequently Asked Questions, Version 2.2

Sample Reports

To access Omnitron Cloud sample reports, see the Analysis section of the Omnitron user guide.

New Features and Improvements

SeqSense Cloud Now Supports Analysis of Data Generated Using ddSEQ Single-Cell 3' RNA-Seq Kits

You can now use the Omnitron pipeline in SeqSense Cloud with ddSEQ Single-Cell 3' RNA-Seq Kits to perform whole transcriptome analysis (WTA) at the single-cell level, capturing hundreds to thousands of cells with high sensitivity and recovery.

Required Prep Kits

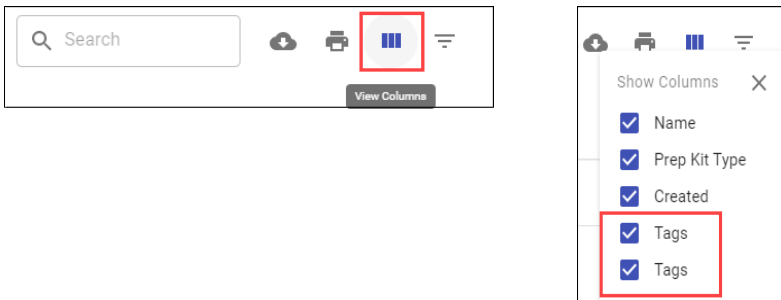
To use the SeqSense Cloud, you must purchase one of the following kits from Bio-Rad (<https://www.bio-rad.com>)

- SEQuoia Express Stranded RNA Library Prep Kit (Catalog No. 12017265)
- SEQuoia Complete Stranded RNA Library Prep Kit (Catalog No. 17005710)
- ddSEQ Single-Cell 3' RNA-Seq Library Prep Kit (Catalog No. 17009671)

To purchase the kits, you must create a Bio-Rad website user account. From the landing page, click Log In/Register and follow the prompts. To use SeqSense Cloud to analyze your data, you must create a SeqSense Cloud user account. From the application landing page, click New User Form and follow the prompts. For more information, see the SeqSense Cloud User Guide. (SCP-1318)

Known Issues

- SeqSense Cloud has a four-hour timeout. You must upload all experiment files within this timeframe to avoid interruptions.
- When you click the View Columns icon on the Samples and Experiments pages, the Tags checkbox is displayed twice in the pop-up and the Tags column can appear twice in the pages. You must clear the second checkbox to display only one Tags column in the Samples page.



- When you click in the Experiment Title field as you create a new experiment, the dropdown list of existing experiment names appears; however, if you select a name from the dropdown list, you receive an error message. You must modify the experiment name before you can continue.
- If you click the browser Back button, you might be returned to the Home page instead of the previous page.
- If you add more than 20 tags to an experiment, an error message appears. You must delete a tag before you can continue.
- When uploading multiple large files, the application might time out. Save your progress frequently to prevent data loss.

Contacting Technical Support

The Bio-Rad Technical Support department in the U.S. is open Monday through Friday, 5:00 AM to 5:00 PM, Pacific Time.

Phone: 1-800-424-6723, option 2

Email: Support@bio-rad.com (U.S./Canada Only)

For technical assistance outside the U.S. and Canada, contact your local technical support office or click the Contact Us link at www.bio-rad.com.

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