SeqSense Analysis Solution

User Guide

Version 1.0
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Chapter 1 Logging into SeqSense

To log into the SeqSense Analysis Solution

2. Click the URL to open the Login page.
3. Read the Terms and Conditions on the right.
4. Enter the user name provided by Bio-Rad.
5. Enter the associated password.
6. Click Login.
   **Important:** When you click Login, you accept the Terms and Conditions.
7. Continue to the Introduction on page 3.
Chapter 1 Logging into SeqSense
Chapter 2 Introduction

The SeqSense Analysis Solution allows you to view and manage your FASTQ sample files and related analysis.

After your login credentials are validated, the Home page appears.

The tabs described in Table 1 are available in the left panel.

Table 1. Functional tabs

<table>
<thead>
<tr>
<th>Tab name</th>
<th>Tab function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Samples</td>
<td>Create and manage your sample file records.</td>
</tr>
<tr>
<td>Tags</td>
<td>Create and manage tags to associate with sample file records.</td>
</tr>
<tr>
<td>Profile</td>
<td>View your profile information.</td>
</tr>
<tr>
<td>Help</td>
<td>Access online help information.</td>
</tr>
<tr>
<td>Feedback</td>
<td>Use the Feedback modal to ask a question, request a feature, or report a bug.</td>
</tr>
<tr>
<td>Logout</td>
<td>Log out of the application.</td>
</tr>
</tbody>
</table>
Chapter 2 Introduction
Chapter 3 Samples Page and Toolbar

Use the options on the Samples page to view and manage files relating to your SeqSense samples.

From the Samples tab, you can access the top toolbar icons described in Table 2.

Table 2. Samples tab icons

<table>
<thead>
<tr>
<th>Icon</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>+</td>
<td><strong>Create New Sample</strong> — allows you to upload samples files and create a matching record that appears in the grid</td>
</tr>
<tr>
<td><img src="icon" alt="search" /></td>
<td><strong>Search</strong> — allows you to search through file names and metadata to display a corresponding list of sample files</td>
</tr>
<tr>
<td><img src="icon" alt="download" /></td>
<td><strong>Download CSV</strong> — creates a list of all active sample files with metadata in a CSV file</td>
</tr>
<tr>
<td><img src="icon" alt="print" /></td>
<td><strong>Print</strong> — allows you to print the current view of your active samples</td>
</tr>
<tr>
<td><img src="icon" alt="viewcolumns" /></td>
<td><strong>View Columns</strong> — allows you to show or hide various available columns</td>
</tr>
<tr>
<td><img src="icon" alt="filter" /></td>
<td><strong>Filter Table</strong> — allows you to filter samples based on a single or multiple parameters</td>
</tr>
<tr>
<td><img src="icon" alt="edit" /></td>
<td><strong>Edit</strong> — allows you to view the status of the pipeline</td>
</tr>
</tbody>
</table>
Table 2. Samples tab icons, continued

<table>
<thead>
<tr>
<th>Icon</th>
<th>Description</th>
</tr>
</thead>
</table>
| Remove — allows you to remove a sample record from the grid  
Note: Removed samples are archived rather than deleted. |
| Restore — allows you to restore an archived sample record to the active samples list  
For information on archiving and restoring files, see Archiving and Restoring Sample Records on page 16. |

From the bottom toolbar you can
- Specify the number of rows per page (10, 15, or 100)
- Use the < and > arrows to navigate to subsequent or previous pages

Creating a Sample Record

Use the Samples tab to upload files and create sample records.

To create a sample record

1. In the left panel, click Samples.
2. Click the Create New Sample (.addButton) button in the upper right corner.

The Sample Add page appears.
Creating a Sample Record

3. To upload one or more FASTQ files, do one of the following:
   - Drag and drop one or more files to the boxed area under Sample Add.
   - Click in the boxed area and select the files from the dialog box, and then click Open to upload the files.

   **Important:** You can upload FASTQ files in the .gz (GZIP) format only. If your internet connection is interrupted during the upload, refresh the browser. You may need to upload your files again.

   When the files are uploaded, they appear below the upload area with a success message.

   ![Sample Add]

<table>
<thead>
<tr>
<th>File Name</th>
<th>Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lib32_Sub_R1_001.fastq.gz</td>
<td>4.01 MB</td>
</tr>
<tr>
<td>Lib32_Sub_R2_001.fastq.gz</td>
<td>1.24 MB</td>
</tr>
</tbody>
</table>

   **Files uploaded successfully!**

   In the remaining steps, enter or select the applicable information in the Bioinformatics Pipeline section.

4. In the Sample Name field, enter the sample name.

5. **(Optional)** For Skip UMI processing, select Yes or No.

   **Important:** UMIs are strings of random nucleotides attached to the start of reads. Each R1 read has a corresponding R2 read that contains the UMI. Prior to mapping, each UMI is attached to its corresponding R1 read and used to identify PCR duplicates following mapping. After the deduplication step, each UMI is detached from the R1 reads, leaving the original R1 read intact.

   **Note:** This process is applicable only if both R1 and R2 are present.

6. **(Optional)** For Species, select from the dropdown list.

   You can select the reference genome used to map the reads in order to create a BAM file from the results.
Currently, three reference genomes are provided:

- Homo sapiens (human) genome assembly GRCh38 (hg38)
- Mus musculus (house mouse) genome assembly GRCm38 (mm10)
- Rat (Rattus norvegicus) genome assembly (rnor6)

7. (Optional) For Spike in type, select from the dropdown list.

   Currently, Bio-Rad supports ERCC RNA Spike-In Control Mixed (ercc) only. The mixes provide a set of external RNA controls, which enable performance assessment used for gene expression experiments. Use the data from the spike-ins for normalization.

8. (Optional) Minimum MapQ score to count — move the indicator to the correct value. The selected value appears on the right.

   MapQ quantifies the probability that a read is misplaced. It equals $-10 \log_{10} \Pr \{\text{mapping position is wrong}\}$, rounded to the nearest integer. Using this option, you can potentially filter out the poorly aligned reads. Reads below this specified score are not used in the mapping.

9. (Optional) Min base pairs per read — move the indicator to the correct value. The selected value appears on the right.

   This removes reads that are shorter than a specific number of base pairs, after trimming of adapters and bad regions.

10. (Optional) Skip read trimming — select Yes or No.

   Skips removing low-quality bases at the 3’-end of a read, reads containing too many N-bases along their length, and more.

11. (Optional) 5’ read quality cutoff — move the indicator to the correct value.

   Removes 5’ end with low-quality, based on a quality cutoff, after adapter removal (if any)

12. (Optional) 3’ read quality cutoff — move the indicator to the correct value.

   Removes 3’ end with low-quality, based on a quality cutoff, after adapter removal (if any)

13. Click Start Pipeline in the bottom right corner to initiate the pipeline.
Creating a Sample Record

You can view the pipeline completion status in the Sample Add page and in the Sample Detail page. Typical statuses are:

- initializing
- running
- succeeded
- failed

**Note:** If you close the Sample Add page while the process is running, you cannot reopen it to display the pipeline processing. However, you can see the statuses as they change on the Sample Detail page (Sample Status).

When the pipeline is completed, the sample appears in the list.

<table>
<thead>
<tr>
<th>Samples</th>
</tr>
</thead>
<tbody>
<tr>
<td>Name</td>
</tr>
</tbody>
</table>

View headline samples
Searching for Files

To use the search feature

1. In the left panel, click Samples.
2. Click the Search icon in the toolbar.

The Search field appears in the top left corner.

3. Enter any combination of text and numbers as your search criteria.

The search activates, and the list narrows as you continue entering text or numbers.

When you finish your entry, associated files appear in the grid below.
Download a List of Sample Files

To download a list of active sample files to a .csv file

1. In the left panel, click Samples.
2. Click the Download icon in the toolbar.
   The file automatically appears in your Downloads folder.
3. Double-click the file to open it and view the results.
   The file contains information under the following headings:
   - Name
   - Owner
   - Created (date the sample file was created)
   - Pipeline (pipeline details)
   - Tags (tags associated with the sample file)
   - SampleID
   - Actions
   - DateasString (download date)
Printing a List of Displayed Files

To print a list of the files displayed on the Samples tab

1. In the left panel, click Samples.
2. Click the Print icon in the toolbar.

The Print modal opens.

![Print modal](image)

The file list that will be printed appears on the left.

3. Click Print.
Showing or Hiding Columns

To show or hide columns in the Samples grid

1. In the left panel, click Samples.
2. Click the View Columns icon in the toolbar.
   A pop-up opens, displaying the current list of columns.

   ![Show Columns]
   - Name
   - Owner
   - Created
   - Pipeline
   - Tags

3. Select or clear checkboxes:
   - When you clear a checkbox, the column is immediately removed from the display.
   - When you select and checkbox, the column is immediately added to the display.
Chapter 3 Samples Page and Toolbar

Filtering the Sample Files

To filter the list of sample files

1. In the left panel, click Samples.
2. Click the Filter icon in the toolbar.

The Filter modal opens.

3. Enter your filter criteria.

The list filters as you enter information in the fields, and each filter criteria appears in the top-left corner of the Samples grid.

4. To remove a filter criteria, click the X on the right.
Editing a Sample File Record

You can edit the name of a sample file record, and you can add or delete tags. To add or delete tags, see Creating and Deleting Tags on page 19.

To edit the record

1. In the left panel, click Samples.

   The Samples page appears.

   ![Samples Page]

   1. In the applicable sample record row, click the Edit icon on the right.

   The Sample Detail page appears.

   ![Sample Detail Page]

2. Click the sample name to open the modal.

   ![Sample Detail Modal]

3. Click the sample name to open the modal.
4. Enter a new sample name in the field.
5. Click Save.

The modal closes and a success message appears.

**Tip:** You can also click Close to close the window without making changes.

## Archiving and Restoring Sample Records

**To archive an active sample record**

1. In the left panel, click Samples.

The Samples page appears.

<table>
<thead>
<tr>
<th>Samples</th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Name</td>
<td>Owner</td>
<td>Created</td>
<td>Pipeline</td>
<td>Tags</td>
<td>Actions</td>
</tr>
<tr>
<td>Sample</td>
<td>Test</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

2. For the applicable record, click the Remove icon on the right.

   The record is immediately moved to the inactive samples list.

**To restore an inactive sample record**

3. In the left panel, click Samples.

   The Samples page appears.

   Click the View Inactive Samples link on the left.
Archiving and Restoring Sample Records

The list of inactive sample records appears on the Samples page.

4. For the applicable record, click the Restore icon on the right.
   The record is immediately moved to the active sample records list.

5. Click View Active Samples to display the list of active sample records.
Chapter 3 Samples Page and Toolbar
Chapter 4 Tags

Tags are simple pieces of descriptive data applied to your sequencing sample files, which provide details about an item and facilitate locating related items with the same tag.

Tags are used to capture various pieces of metadata, such as project name, experiment name, variables, methods, and so forth. You can also group and sort your sample file records based on these tags in lieu of folders.

From the Tags tab, you can view your existing tags, and associate tags with your sample file records.

Creating and Deleting Tags

To create a new tag

1. In the left panel, click Tags.

   The Tag Management page appears.

   ![Tag Management](image)

2. In the Tag Name field, enter a new tag name.

3. Click Save.

   The new tag appears on the right.

To delete a tag

- Click the X in the applicable tag to delete it.
Viewing and Associating Tags

To view tags

1. In the left panel, click Tags.

   The Tag Management page appears.

   Tags you have created are visible on the right.

To associate a tag with your sample record

1. In the left panel, click Samples.

   The Samples page appears.

   2. In the applicable sample record row, click the Edit icon.

      The Sample Details page appears.
3. For Available tags, click the tag to associate.

The tag moves to Associated Tags, and a success message appears below.
Chapter 5 Generating Reports

You can generate a report from a selected file.

1. In the left panel, click Samples.
2. Under Name, for the applicable sample record click the link.
   The Sample Detail page appears.
   
   ![Sample Detail]

3. Click Download Reports to open the Downloadable Reports modal.
4. Click the cloud icon on the right for each report to be downloaded.
5. To close the modal, click Close.

You can download the following reports:

- gene_counts_rpktpm.txt
- trimlog.log
- trimmed_R1.fastq.gz
- _debarcoded_R1.fastq.gz
- debarcode_stats.txt
- Aligned.sortedByCoord.deduplicated.out.bam
Chapter 5 Generating Reports

- Aligned.sortedByCoord.deduplicated.out.bam.bai
- dedup.log
  - _fastqc.html
  - _fastqc.html
  - _fastqc.zip
  - _fastqc.zip
- gene_counts_longRNA
- gene_counts_longRNA.summary
- gene_counts_miRNA
- gene_counts_miRNA.summary
- rna_metrics.txt
- execution_report.html
- execution_timeline.html
- execution_trace.txt
- pipeline_dag.dot
- htmlReport.html
- pdfReport.pdf
- out.longRNAs.bam
- out.miRNAs.bam
- Aligned.sortedByCoord.out.bam
- Aligned.sortedByCoord.out.bam.bai
- Log.final.out
- Aligned.sortedByCoord.tagged.bam
- Aligned.sortedByCoord.tagged.bam.bai

Note: Several of the reports (including _fastqc.html, _fastqc.html, _fastqc.zip, _fastqc.zip) contain the original name of your FASTQ.
Chapter 6 Viewing your User Profile Information

The Profile tab displays your user name and name.

To view this information

► In the left panel, click Profile.

The user profile information appears on the page.

To edit this information

1. Enter the following URL in your browser URL field:
   

   The Bio-Rad website Profile page opens.

2. Click Login/Register.

3. Login with your user name (not the full email address) and password.

4. Follow the prompts to change applicable user information.
Chapter 6 Viewing your User Profile Information
Chapter 7 Accessing the Help System

The Help tab provides online links to a variety of help topics describing the SeqSense Web Application functionality.

To open the online help system

1. In the left panel, click Help.
   A list of help topics appears.
2. Click links to locate applicable topics.
Chapter 8 Feedback Tab

The Feedback tab allows you to send an email to Bio-Rad asking a question, requesting a feature, or reporting an application defect.

To send feedback to Bio-Rad

1. In the left panel, click Feedback.
   
   The Feedback modal opens.

2. In the field provided under message, type your question, feature request, or defect report.

3. To send the message to Bio-Rad, click Send.
Chapter 8 Feedback Tab
Chapter 9 Logging Out of SeqSense

To log out of SeqSense

- In the left panel, click Logout.

  You are immediately logged out of SeqSense. You can close the application or another user can log in.