



# Sequence Data

**Sequence Data** stores the sequencing data files uploaded by the users and displays them in reverse chronological order. Click the  icon in the Utilities menu to access the **Sequence Data** window (Fig. 1). The paginated window displays 10 samples, by default, per page and can be increased to show 20, 40, 60, 80, 100 samples. The search box (Fig. 1) on the top right corner allows users to filter samples with tags, organism names, or pairing information. Validation failed samples are greyed out and displayed with a “Validation Failed” message. The failed samples are not available for selection and should be deleted from the platform by the user. Validation passed samples are shown with a green check . The quality (fastqc) report is available for the validated samples (Fig. 1).

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Show 10 Stanome Search (Case Sensitive)

SEQUENCE DATA

REFERENCES

ANNOTATIONS

METADATA

<input type="checkbox"/>	Name	Organism	Tag	Fastqc Report	File(s)	Paired	Owner	Date
<input type="checkbox"/>	SRR3288171 	Yeast	100SEsample	<a href="#">SRR3288171_fastqc.html</a>	SRR3288171.fastq	No	Stanome	14/Jun/21 7:28 PM
<input type="checkbox"/>	SRR3288172 	Yeast	100SEsample	<a href="#">SRR3288172_fastqc.html</a>	SRR3288172.fastq	No	Stanome	14/Jun/21 7:28 PM
<input type="checkbox"/>	SRR3288164 	Yeast	100SEsample	<a href="#">SRR3288164_fastqc.html</a>	SRR3288164.fastq	No	Stanome	14/Jun/21 7:28 PM
<input type="checkbox"/>	SRR3288165 	Yeast	100SEsample	<a href="#">SRR3288165_fastqc.html</a>	SRR3288165.fastq	No	Stanome	14/Jun/21 7:28 PM
<input type="checkbox"/>	SRR3288170 	Yeast	100SEsample	<a href="#">SRR3288170_fastqc.html</a>	SRR3288170.fastq	No	Stanome	14/Jun/21 7:28 PM
<input type="checkbox"/>	SRR3288163 	Yeast	100SEsample	<a href="#">SRR3288163_fastqc.html</a>	SRR3288163.fastq	No	Stanome	14/Jun/21 7:28 PM

Showing 1 to 6 of 6 entries

First 1 Last

The list view shows eight fields :



- **Name:** Derived sample name from the file name by the platform

Example:

Sequencing Type	File Name	Sample Name
Single End	seq_file.fastq	seq_file
Paired End	seq_file_1.fastq seq_file_2.fastq	seq_file

- **Organism:** Organism name, provided by the user during upload

- **Tag:** Tag name, provided by the user during upload
- **Fastqc Reports:** The FastQC quality report of each sample
- **File(s):** The actual file name(s) associated with the sample name
- **Paired:** Sample pairing information, provided by the user during upload
- **Owner:** Name of the user, who uploaded the samples
- **Date:** Date of upload

Additional sample details can be accessed by clicking on the sample name. Click the  icon on the top right corner of the sample window (Fig. 2) to delete the selected sample. Click the  icon to go back to the **Sequence Data** window.

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Sequence Data : 9987309518 , AN868\_3

Name	Organism	Tag	Fastqc Report
AN868_3	Tomato	AN868samples	AN868_3_FASTQC.HTML

Paired	FileType	File(s)	Date
No	.fastq	AN868_3.fastq	20/Dec/21 8:54 AM

Revision #6

Created 24 January 2022 13:35:56 by Kshama

Updated 3 March 2022 03:35:52 by Stanome