

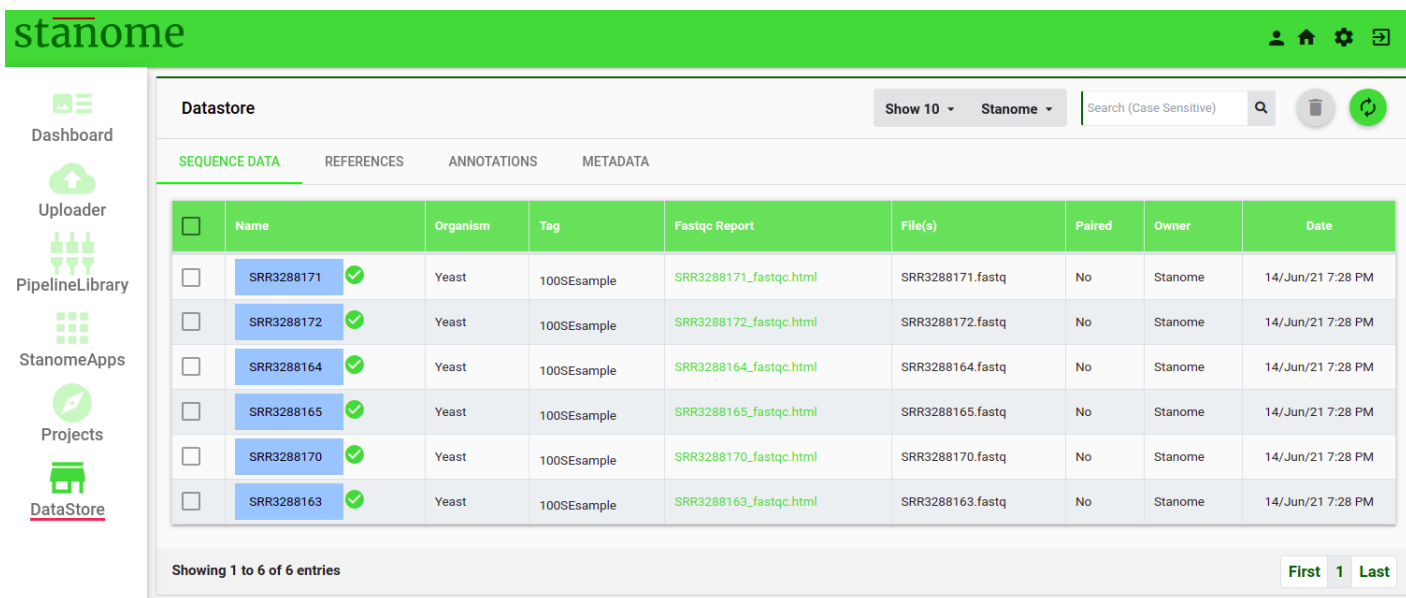


# Sequence Data

**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).



The screenshot shows the Stanome Datastore interface. The top navigation bar is green with the Stanome logo and user icons. The left sidebar contains navigation options: Dashboard, Uploader, PipelineLibrary, StanomeApps, Projects, and DataStore. The main content area is titled 'Datastore' and has a search bar and a 'Show 10' dropdown. Below the search bar are tabs for 'SEQUENCE DATA', 'REFERENCES', 'ANNOTATIONS', and 'METADATA'. The 'SEQUENCE DATA' tab is active, displaying a table with the following columns: Name, Organism, Tag, Fastqc Report, File(s), Paired, Owner, and Date. The table contains six rows of data, all with green checkmarks in the 'Name' column. The bottom of the table shows 'Showing 1 to 6 of 6 entries' and navigation buttons for 'First', '1', and 'Last'.

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

The list view shows eight fields :



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

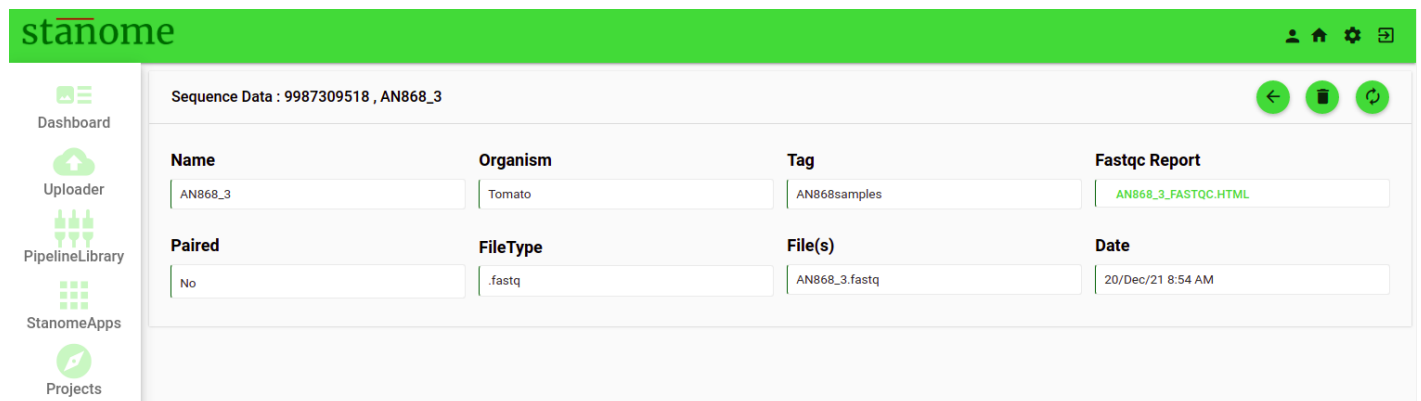
*Example:*

Sequencing Type	File Name	Sample Name
Single End	<i>seq_file.fastq</i>	<i>seq_file</i>
Paired End	<i>seq_file_1.fastq</i> <i>seq_file_2.fastq</i>	<i>seq_file</i>

- **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.



The screenshot shows the Stanome web interface. The top navigation bar is green with the 'stanome' logo on the left and user, home, settings, and help icons on the right. A sidebar on the left contains icons for Dashboard, Uploader, PipelineLibrary, StanomeApps, and Projects. The main content area displays 'Sequence Data : 9987309518 , AN868\_3' with navigation icons (back, delete, refresh) on the right. Below this is a table with the following data:

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