

# Metadata

Click the **Metadata** tab after clicking the  icon to access the **Metadata** window (Fig.). The **Metadata** window shows the list view of Gene lists, Hotspots and Amplicon ranges uploaded by stanome or the user. These files are used as metadata during analysis. The window is restricted to display 10 (or more) Metadata files per page. The search box (Fig.) on the top right corner of the page allows users to filter files with name(s), type (i.e. gene list or hotspots), platform, or organism name. Metadata files are also checked for format and file integrity and their correspondence to a reference genome version. Only the validated files are available for consumption on the platform, and the remaining will be greyed out with the “Validation Failed” message.



The screenshot shows the Stanome web interface. The top navigation bar is green with the 'stanome' logo and user icons. A left sidebar contains navigation options: Dashboard, Uploader, Pipeline Library, Stanome Apps, and Projects. The main content area is titled 'Datstore' and has tabs for 'SEQUENCE DATA', 'REFERENCES', 'ANNOTATIONS', and 'METADATA'. The 'METADATA' tab is active. Below the tabs is a table with the following columns: Name, Organism, Reference Version, File Type, Owner, and Date. Two entries are visible, both with green checkmarks indicating validation success.

<input type="checkbox"/>	Name	Organism	Reference Version	File Type	Owner	Date
<input type="checkbox"/>	tomatoAmplicon.bed	Tomato	SL3.0	AmpliconRange	Stanome	9/Aug/21 12:52 PM
<input type="checkbox"/>	tomatoBedfileSL3.0.bed	Tomato	SL3.0	HotSpots	Stanome	9/Aug/21 11:50 AM

Showing 1 to 2 of 2 entries

First 1 Last

The list view shows following six fields :

- **Name:** Filename
- **Organism:** Name of the organism to which metadata belongs to
- **Reference Version:** Reference version to which metadata file correspond to
- **FileType:** Type of the file e.g. Gene list, Hotspots, or Amplicon range
- **Owner:** Owner of the metadata file
- **Date:** Date of upload

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