
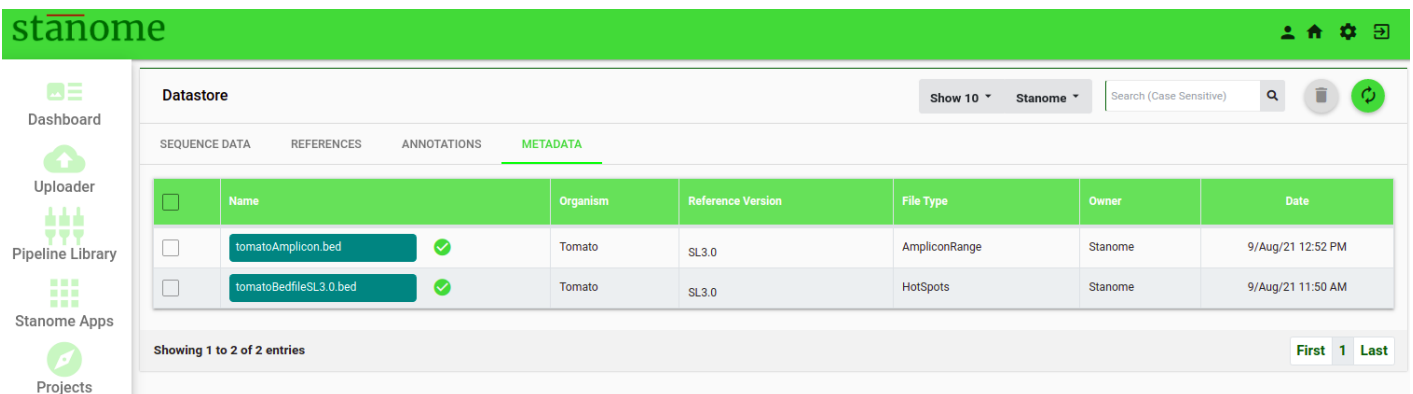


# Metadata

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. The left sidebar contains icons for Dashboard, Uploader, Pipeline Library, Stanome Apps, and Projects. The main content area is titled 'Datastore' and has tabs for SEQUENCE DATA, REFERENCES, ANNOTATIONS, and METADATA (which is selected). The METADATA tab displays a table with the following columns: Name, Organism, Reference Version, File Type, Owner, and Date. Two files are listed: 'tomatoAmplicon.bed' and 'tomatoBedfileSL3.0.bed', both for the organism 'Tomato' and reference version 'SL3.0'. The first file is of type 'AmpliconRange' and the second is 'HotSpots'. Both files are owned by 'Stanome' and were uploaded on '9/Aug/21'. The table also shows a 'Showing 1 to 2 of 2 entries' message and pagination controls for 'First', '1', and 'Last'.

	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

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

Revision #4

Created 24 January 2022 14:48:09 by Kshama

Updated 15 February 2022 08:13:29 by Kshama