

Frequently Asked Questions

Who can use the Stanome platform?

Anyone who has NGS data to be analyzed can take advantage of the platform. The user does not need hardware resources or computational knowledge of NGS tools to use the Stanome platform.

Which browsers and operating systems do I need to use to access the Stanome platform?

The platform is tested and validated on the latest versions of the Chrome browser and works best on any operating system that supports the Chrome browsers.

How can I contact Stanome's technical support team?

Mail your detailed query to support@stanome.com.

How can I use my own custom reference genome?

Upload custom reference genomes through the **Reference/Annotation files** tab on the **Upload** window. Refer to section 4.2 (Upload Reference and annotation files) for detailed instructions on how to upload custom reference and annotation files.

How can I share my data with only my team members?

The multi-tenancy feature allows data sharing and analysis between group members of a shared account. Group members can request other members to join the group.

Can I download analysis files and how?

Yes, analysis files can be downloaded through the Report section. Refer to section 7.5 (Reports) to learn more about accessing all the intermediate output/analysis files.

Can I get a customized report?

Yes, a customized report with custom plots and tables can be obtained upon request. Contact Stanome technical support team (support@stanome.com) with details of the requirement.

How do I troubleshoot my failed pipeline?

Check your mail with the job status update. Issues related to the input data are described in the mail. Contact Stanome technical support team along with the job ID, if you are still not able to troubleshoot the issue.

Can I build a command that only generates standard output?

Yes, a command could be built using the **Command builder** dialog box within a pipeline. However, its output could be found in the output.log on the “sample deep dive” page described in section 7.4. In order to redirect the output to the next step in the pipeline contact the Stanome technical support team with details of the requirement.

How can I delete the data completely from the platform?

Raw sequence data can be deleted from the **Sequence Data** window (Utilities Menu). Analysis data can be deleted from the **Projects** window.

How long is the data retained?

Unless requested, all the data is purged after 30 days.

Why do I see duplicated pipelines?

Duplicate object names are not allowed on the platform. However, in a multi-tenancy setup, it's allowed to create pipelines with the same names between shared users. Please use the owner tag to filter user-specific pipelines.

Are Stanome configured pipelines allowed to add to the favorites?

Stanome configured pipelines are accessible for all the users on the platform. These pipelines can't be added to the favorites but can be copied into your projects.

Why the header line required in the BED files?

The BED file format is adapted from the UCSC <https://genome.ucsc.edu/FAQ/FAQformat.html>. We certify and validate the BED files against the reference genomes. Though header is not generally required, Stanome uses the header (*track name#*) content for the Genome Browser visualization in Stanome Report.