
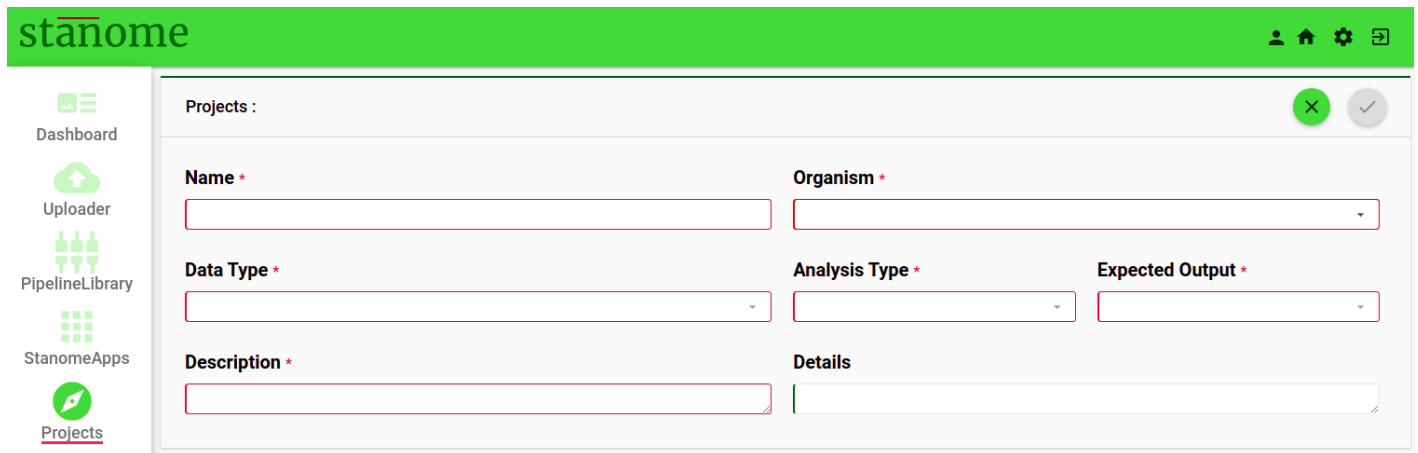


# Project Setup

A new project can be created in two ways.

1. From the **Dashboard** window - click the  icon
2. From the **Projects** window - click  on the upper right corner



The screenshot shows the Stanome web interface. On the left is a sidebar with icons for Dashboard, Uploader, PipelineLibrary, StanomeApps, and Projects (which is highlighted). The main area is titled 'Projects :'. It contains several form fields: 'Name \*' (text input), 'Organism \*' (dropdown menu), 'Data Type \*' (dropdown menu), 'Analysis Type \*' (dropdown menu), 'Expected Output \*' (dropdown menu), 'Description \*' (text input), and 'Details' (text input). There are also close (X) and save (checkmark) buttons in the top right corner of the form.

A new project can be created from the **Project** setup window (Fig. 1). Fill in the seven mandatory fields with details and appropriate descriptions. The data in this form is used for automatic reference file(s) selection and will be exported to the final report.

**CAUTION - Organism enables appropriate reference file(s) selection.**

- o **Name\*** - Provide a unique name for the project.



**HINT** - Project name cannot be longer than 30 characters and alphanumeric characters and spaces are only allowed.

**CAUTION - Project name should be unique.**

- o **Organism\*** - Select the organism from the drop-down menu. We currently support eight main model organisms and some custom species.



**HINT** - Select **Other** if the organism is not listed and contact Stanome technical support team to add a new organism to the list.

- o **Description\*** - Provide a brief description of the project (Example: The gist of the experimental design and the aim of the study).
- o **Data Type\*** - Select sample type from the drop-down list [*Microbiome*, *Targeted Genome*, *Transcriptome*, and *Whole Genome*]. The **Data type** field is tightly connected with the **Hub** field in the pipelines.



**HINT** - Carefully choose the **Data type** to get the relevant pipeline suggestions.


- **Analysis Type\*** - Select the experiment type from the drop-down list [*ABR Screening, Alignment, Annotations, Data Cleaning, Data QC, Differential Expression, Genome assembly, Genotyping, Proband, Serotyping, Species Classification, and Variant analysis*].
- **Expected output\*** - Select expected output(s) from the drop-down list [*BAM, Coverage Metrics, DE Genes (Differentially Expressed Gene list), FASTA, Genotypes, Ontology, Pathways, and VCF (Variant Calling Format)*].



Multiple options can be selected.

- **Details\*** - Provide detailed information about the project. (Example: Aim of the experiment, conditions studied, experimental design, and any other pertinent details).



Click  to save the project. The new project is saved and displays the **Project Main** window (Fig. 2), where the project-specific menu is available on the left menu. The project can be navigated with **Sample Set**, **My Pipelines**, **Jobs**, and **Reports**, and details of these four features are described in the following sections.

**stanome**

Project : 6663595245, DemoProject Variant

**Name \***  
DemoProject Variant

**Organism \***  
Tomato

**Data Type \***  
Targeted Genome

**Analysis Type \***  
Variant Analysis

**Expected Output \***  
Genotypes

**Description \***  
This project demonstrates the complete process of running a pipeline on the platform including sample set selection. It also gives access to Report and its features generated for a small sample set.

**Details \***  
The "Variant Suite 1412" pipeline provided in this project carries out alignment of reads to reference genome. A list of the variants is obtained based on target bed file. The final report provides FastQC statistics, mapping summary and variant summary along with quick visualization. The report also provides IGV interface for the variants.



Projects can be deleted using the  icon from the **Projects** window. All the components within a project (sample sets, pipelines, jobs, and reports) are deleted permanently.

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