

# UPLOAD ANNOTATIONS

Pathways, gene ontology (GO) terms, ABR genes, and VEP (Variant Effect Predictor) files are classified as annotations and can be uploaded through the **ANNOTATIONS** (Fig.) tab.

ABR and GO\_OBO upload has two fields:

1. **Organism:** Name of the organism
2. **Tag:** The version number of the annotation file

Gene Model, VEP, and Variations upload have three fields:

1. **Organism:** Name of the organism
2. **Reference version:** Version of the reference file
3. **Tag:** Version of the annotation file

GO and Pathway upload has four fields:

1. **Organism:** Name of the organism
2. **Reference version:** Version of the reference file
3. **GTF version:** Version of the gene model file
4. **Tag:** Version

Different types of annotations and their allowed formats are explained in Table below.

Tag	Data Type	Format	Details
Gene models	Gene annotations	Gtf, Gff3	Source: Ensembl. Should correspond to the Ensembl genome versions
Pathway	Pathways	Tab, Gmt	Source: Wiki pathways
Gene Ontology	Gene Ontology associations	Obo, Tab, Txt	GO terms

VEP	Variant annotations	Custom	Source: Ensembl. Should correspond to the Ensembl genome versions
Variations	GATK variants	VCF	Source: Ensembl

Table. Annotation file formats. Compressed files are allowed as long as each file is compressed separately.

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 (highlighted with a red underline), PipelineLibrary, StanomeApps, and Projects. The main content area is titled 'Uploader' and has four tabs: SEQUENCE DATA, REFERENCES, **ANNOTATIONS** (active), and METADATA. Under the 'ANNOTATIONS' tab, there is a 'Type \*' dropdown menu and a 'Select File' button with a folder icon. A 'SELECT FILE(S)' button is also visible on the right side of the file selection area.

Similar to Sequence and reference file uploads, the following actions are performed on the uploaded annotation files:

- Uncompression of the files
- Validation of the format and integrity of the file and its compatibility to genome/gene annotation file.
- Registration into the **ANNOTATIONS**
- Status notification through email

Successfully uploaded files are stored in **ANNOTATIONS** and can be accessed while executing the pipelines.

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