

Pathway database setup for an organism

- Go to the [STRING website](#) and select the Download category in the upper right corner
- Next to the Update button, type the organism of interest (e.g. Mus Musculus) to specify which annotated pathways you are interested in
- Download the STRING-file
`{number_organism}.proteins.enrichment.terms.{version}.txt.gz`
- Run pathwayDataFormatting.py with the extracted STRING file and the organisms name. The command may look like this:
`python3 pathwayDataFormatting.py
9606.protein.enrichment.terms.v11.5.txt --o HomoSapiens`
- The program will format the STRING file to the desired pathway format and save it as
`{organism}TermsWithProteins.txt`. Grab a coffee, this may take some minutes.
- Add the pathway file to the neo4j database