Tools

- **Data manipulation**
  ‣ ID Converter
  ‣ Filter lines by keywords or numerical value

- **Retrieve annotation**
  ‣ Get annotation from RNAseq/Ab-based experiments (Human species)
  ‣ Protein features (neXtProt)
  ‣ Expression level by tissue (from HPA)

- **Bioinformatic analysis tools**
  ‣ Venn diagram
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- **Other tools**

Filter lines by keywords or numerical value

Filter lines by keywords or numerical value Filter a file by keywords or numerical values (Galaxy Version 0.1.0)   ▼ Options

Input file

1: Lacombe_et_al_2017_OK.txt   ▼

Input file is a tab–delimited file containing proteomics identification and/or quantitative results

Does your input file contain header?

Yes   No

Filter by keywords

+ Insert Filter by keywords

Filter by value

+ Insert Filter by value

✔ Execute

This tool allows to remove unneeded data (e.g. contaminants, non–significant values) from a proteomics results file (e.g. MaxQuant or Proline output).

For each row, if there are more than one protein IDs/protein names/gene names, only the first one will be considered in the output

Filter the file by keywords

Several options can be used. For each option, you can fill in the field or upload a file which contains the keywords.

- If you choose to fill in the field, the keywords should be separated by ":", for example: A8K2U0:Q5TA79:O43175
- If you choose to upload a file in a text format in which each line is a keyword, for example:

REV

TRYP_PIG

ALDOA_RABBIT

History   ⟳ ⚙ ▯

Rechercher des données   ⊗

23/01/18
1 shown

5.38 KB   ☑ 🏷 💬

1: Lacombe et al 2017 OK.txt   👁 ✏ ✖