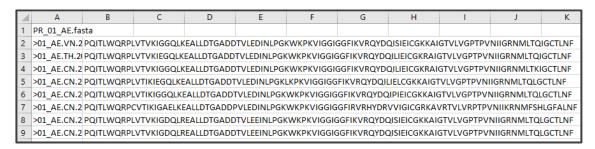
Tools Sequence Search

It allows filtering sequences from .fasta files that contain one or multiple mutations chosen by the user.



- 1 Select the input folder. It should only contain the .fasta files you want to filter.
- (2) Choose the output format between a .csv table or .fasta files.
- 3 Enter one or multiple mutations for filtering, separated by "," without spaces.
- 4 Select the output folder without entering the file name for .fasta format, or enter the name followed by .csv for the .csv format.
- (5) Click Calculate.



The .csv format generates a table with each analyzed file followed by the filtered sequences. If empty rows appear, these would correspond to sequences in the input file where the selected mutations have not been found.

The .fasta format generates a .fasta file for each input file, containing the sequences that include the chosen mutations.

More information about this function can be found in the User Manual, section:

VI. TOOLS VI.1 FILE EDITING VI.1.C) SEQUENCE SEARCH

- page 162 -