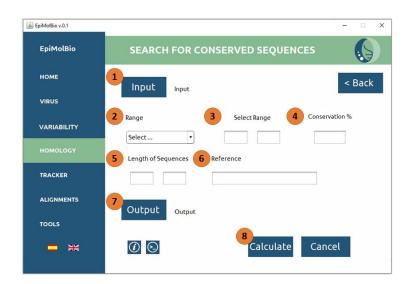# Homology Search for Conserved Sequences

It allows extracting conserved sequence fragments from a set of input sequences. You can search within a specific region, choose the fragment length, and set the conservation percentage.

① Select the input folder. It should only contain .fasta files of sequences to be analyzed in either NT or AA format.

② Choose "Full Range" when you want to search throughout the length of the input sequences or "Select Range" when you want to search within a specific region.

③ If you chose "Select Range," enter the NT or AA positions that encompass the region where you want to search for the conserved fragment.

④ Define the minimum conservation percentage for the fragments to appear in the results.

⑤ Define the desired length for the resulting fragments.

⑥ Enter the reference sequence without line breaks.

⑦ Select the output folder and enter the file name in the following format: /NAME.html.

⑧ Click Calculate.

Homology Search for Conserved Sequences Length 10 - 10 99.0%

File	Length	Region	Fragment	Frequency
PR_71_BF1.fasta	10	Region: 22 - 31	ALLDTGADDT	100.000%
PR_71_BF1.fasta	10	Region: 23 - 32	LLDTGADDTV	100.000%
PR_71_BF1.fasta	10	Region: 24 - 33	LDTGADDTVL	100.000%
PR_71_BF1.fasta	10	Region: 25 - 34	DTGADDTVLE	100.000%
PR_130_A1B.fasta	10	Region: 4 - 13	TLWQRPLVTI	100.000%
PR_130_A1B.fasta	10	Region: 5 - 14	LWQRPLVTIK	100.000%
PR_130_A1B.fasta	10	Region: 19 - 28	LKEALLDTGA	100.000%

The .html file is a table containing the following information: input file name, fragment length, the region where the fragment was found, and the resulting sequence with the conservation percentage colored according to the color code.

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

III. HOMOLOGY III.3 SEARCH FOR CONSERVED SEQUENCES