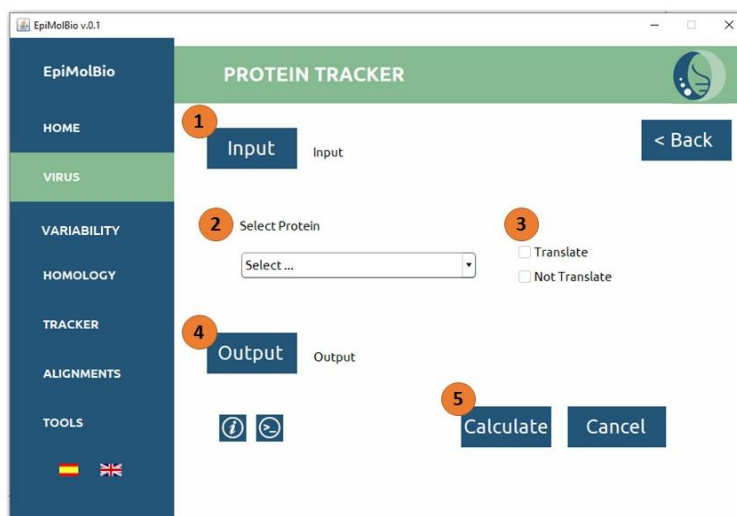


SARS-Cov-2 Protein Tracker

Generates sequences in .fasta format of the chosen proteins from SARS-CoV-2, based on complete genomes, in nucleotides or amino acids.



- ① Select the input folder. It should only contain the .fasta files of the complete SARS-CoV-2 genomes to be tracked, in nucleotide format (1 file or multiple files).
- ② Choose the protein you want to track.
- ③ Select whether you want the output file to be translated to AA or not.
- ④ Choose the output folder. The file will be automatically named as follows: Selected Protein_Traced_InputFileName.fasta.
- ⑤ Click Calculate.

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

I. VIRUS I.2 SARS-CoV-2 protein tracker