Tracker Flanking

It allows searching for proteins within a set of complete genomic sequences using the flanking sequences of the target protein.

① Select the input folder. It should only contain .fasta files of NT sequences where you want to search.

② Select amino acids or nucleotides depending on whether you want the output file to be translated or not.

③ Enter the genomic sequence range where you want to search for the target protein in NT.

④ Enter the length of the protein you are searching for in AA.

⑤ Enter the 15 AA preceding and following the target protein you are searching for.

⑥ Select the output folder without naming the file. It will be automatically named as Tracked_Flanking_InputFileName.fasta.

⑦ Click Calculate.

The output is a .fasta file with the found sequences.

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

IV. TRACKER IV.2 FLANKING