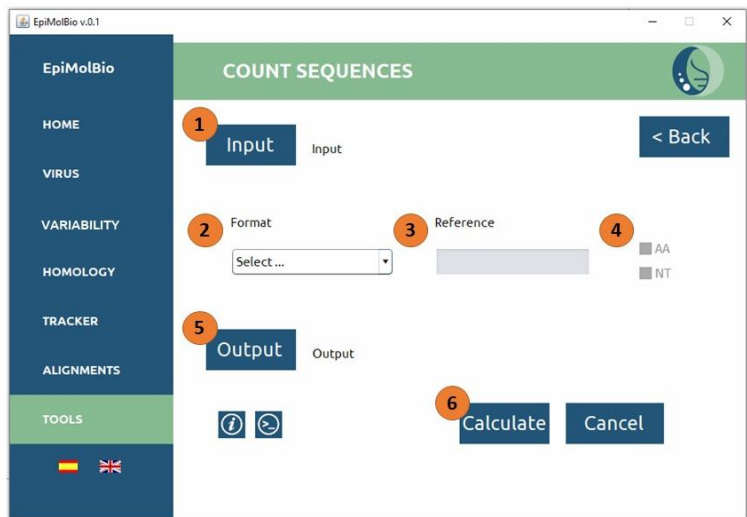


## Tools Count Sequences

It allows counting the total number of sequences in one or multiple .fasta files, or how many of those sequences contain mutations compared to a reference sequence.



- ① Select the input folder. It should only contain the .fasta files you want to count.
- ② Choose the output format: **Table** to count all sequences or **Mutated Sequences** to count only those mutated with respect to the reference.
- ③ If **Mutated Sequences** was chosen, enter the reference sequence without line breaks or spaces, in AA or NT according to the input files.
- ④ If **Mutated Sequences** was chosen, select whether the input files are in AA or NT format.
- ⑤ Select the output folder and name the file by typing .csv at the end.
- ⑥ Click Calculate.

	A	B
1	File	Number of Sequences
2	PR_01_AE.fasta	26849
3	PR_02_AG.fasta	9577
4	PR_03_A6B.fasta	310
5	PR_04_cpx.fasta	15

With the **Table** output, you will obtain a .csv table that displays the names of the input files and the total number of sequences per file. At the end of the table, the total number of sequences across all files will be indicated.

	A	B	C	D
1	File	Mutated	Number of Sequences	Percentage
2	PR_01_AE.fasta	26849	26849	100.00%
3	PR_02_AG.fasta	9577	9577	100.00%
4	PR_03_A6B.fasta	310	310	100.00%
5	PR_04_cpx.fasta	15	15	100.00%
6	PR_05_DF.fasta	24	24	100.00%
7	PR_06_cpx.fasta	746	746	100.00%
8	PR_07_BC.fasta	10916	10916	100.00%
9	PR_08_BC.fasta	2348	2348	100.00%
10	PR_09_cpx.fasta	94	94	100.00%
11	PR_100_01C.fasta	5	5	100.00%
12	PR_101_01B.fasta	4	4	100.00%

With the **Mutated Sequences** output, you will obtain a .csv table that displays the names of the input files, the total number of mutated sequences, the total number of sequences per input file, and the frequency of mutated sequences.

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

### VI. TOOLS VI.4 COUNT SEQUENCES