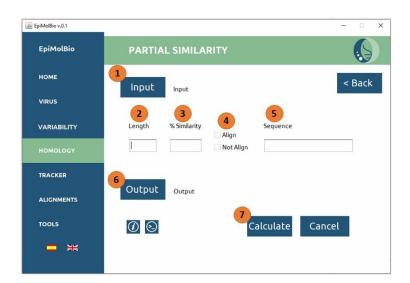
Homology Partial Similarity

It allows comparing a user-introduced sequence with the input sequences to search for similar regions between them, defining the percentage of similarity between the sequences.



- 1 Select the input folder. It should only contain .fasta files of sequences to be analyzed in either nucleotide (NT) or amino acid (AA) format.
- 2 Enter the length of fragments into which the sequences will be divided for comparison.
- 3 Enter the minimum percentage of similarity.
- 4 Select 'Align' for a comprehensive analysis or 'No Align' for a quicker one.
- 5 Enter the sequence for comparison with the input file without line breaks or spaces.
- 6 Select the output folder and enter the file name in the following format: /NAME.html.
- 7 Click Calculate.

Homology Partial Similarity 50.0%				
File	Sequence	Input Sequence	Found Sequence	Similarity
PR_D.fasta	>D.ET.2003.ETH_G_230.AB285830	GHRATGTVLV	GTDTTITVNV	50.000%
PR_D.fasta	>D.ET.2003.ETH_G_230.AB285830	IGRNLLTQLG	NGMNGRTILG	50.000%
PR_D.fasta	>D.ET.2003.ETH_G_230.AB285830	GRNLLTQLGC	GMNGRTILGS	50.000%
PR_D.fasta	>D.ET.2003.ETH_G_230.AB285830	NLLTQLGCTL	NGRTILGSAL	50.000%
PR_D.fasta	>D.JPpatient_88.AB356098	YDQIHVEICG	LTQDHVDILG	50.000%
PR_D.fasta	>D.JPpatient_88.AB356098	DQIHVEICGH	TQDHVDILGP	50.000%

The .html file is a table containing the following information: input file name, sequence headers, a fragment of the introduced sequence, the corresponding found fragment, and the similarity percentage colored according to the color code.

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

III. HOMOLOGY III.2 PARTIAL SIMILARITY

- page 115 -