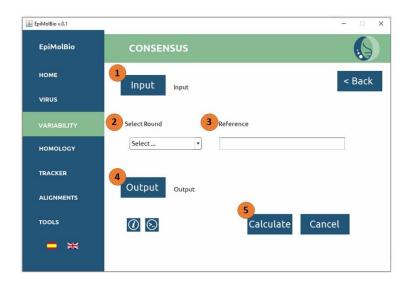# Variability Consensus

It allows obtaining consensus sequences and consensus of consensuses by performing multiple rounds of analysis.
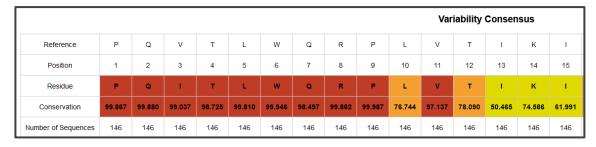

Round 1:

① Select the input folder. It should only contain .fasta files of aligned NT or AA sequences to be analyzed (one or multiple files).

② Choose 'Round 1'.

③ Enter the reference sequence in letters without line breaks.

④ Select the output folder. A .txt file named 'Consensus' will be generated.

⑤ Click Calculate.

Successive Rounds:

① Select the input folder. It should only contain the .txt file generated in the round 1.

② Choose 'Successive Rounds'.

③ Enter the reference sequence in letters without line breaks.

④ Select the output folder. A .txt file and an .html file will be generated.

⑤ Click Calculate.

							Variability Consensus								
Reference	P	Q	V	T	L	W	Q	R	P	L	V	T	I	K	I
Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Residue	P	Q	I	T	L	W	Q	R	P	L	V	T	I	K	I
Conservation	99.867	99.880	99.037	98.725	99.810	99.946	98.497	99.882	99.987	76.744	97.137	78.090	50.465	74.586	61.991
Number of Sequences	146	146	146	146	146	146	146	146	146	146	146	146	146	146	146

The .html file is a table displaying the consensus obtained after analysis. It shows the reference sequence, positions of each residue, the consensus residue, its conservation percentage with cells colored according to the color code, and the number of valid sequences for each position.

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

II. VARIABILITY II.3 CONSENSUS

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