Variability Codon Conservation

It allows obtaining the most conserved codon from an analyzed nucleotide sequence.

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

② Choose the screening percentage between 100% or >75%.

③ Enter the reference sequence in letters without line breaks.

④ Select the output folder and enter the file name in the following format: /NAME.html.

⑤ Click Calculate.

The output file displays the position of the amino acid encoded by each analyzed codon. If the chosen screening is 100%, it shows the residues found [codon and its percentage colored according to the color code] and the number of valid sequences for each position. If the screening chosen is >75%, only the most conserved codon with a frequency greater than 75% will be displayed under "Residues."

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

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