

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.

Variability Conservation Codons 100%		
PR_01_AE.fasta		
Position	Residues	Total Positions
1 P(CCT)	P[CCT(99.810%)] S[TCC(0.011%)] P[CCA(0.011%)] ?[CCY(0.022%)] P[CCC(0.026%)] S[TCT(0.067%)] A[GCT(0.004%)] L[CTT(0.004%)] ?[SCT(0.007%)] ?[CCW(0.004%)] P[CCG(0.007%)] T[ACT(0.007%)] H[CAT(0.004%)] ?[YCT(0.004%)] ?[CMT(0.004%)] V[GTC(0.004%)] L[CTC(0.004%)]	26849
2 Q(CAG)	Q[CAA(96.554%)] Q[CAG(2.503%)] E[GAA(0.071%)] ?[CAR(0.596%)] S[TCA(0.019%)] H[CAT(0.034%)] D[GAC(0.004%)] K[AAA(0.022%)] L[CTG(0.004%)] H[CAC(0.022%)] ?[CAM(0.034%)] ?[CWW(0.004%)] ?[YAA(0.004%)] ?[CAW(0.026%)] ?[CMM(0.015%)] ?[SAA(0.007%)] P[CCT(0.004%)] P[CCC(0.004%)] L[CTC(0.011%)] ?[CWM(0.004%)] R[CGA(0.004%)] R[CGC(0.004%)] T[ACA(0.004%)] ?[CRA(0.019%)] ?[CMA(0.004%)] T[AG(0.007%)] ?[CAV(0.004%)] ?[MAR(0.004%)] ?[CWA(0.007%)] R[AGA(0.004%)]	26844

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:

II. VARIABILITY II.2 CONSERVATION II.2.B) CODONS