

Variability Codons Polymorphisms

Detects the codons that are different from those in the reference sequence and their frequency of occurrence.



- 1 Select the input folder. It should only contain the .fasta files of the sequences to be analyzed in NT format (1 file or multiple files).
- 2 Choose the minimum occurrence frequency for codon detection, selecting between 100% or 75%.
- 3 Enter the reference sequence in letters without line breaks (in NT).
- 4 Select the output folder and enter the filename in the following format: /NAME.html.
- 5 Click Calculate.

Variability Polymorphisms Codons > 75%		
PR_01_AE.fasta		
Position	Residues	Total Positions
2 Q(CAG)	Q[CAA(96.554%)]	26844
3 V(GTC)	I[ATC(99.765%)]	26847
10 L(CTC)	L[CCTT(78.234%)]	26840
14 K(AAG)	K[AAA(91.358%)]	26845
17 G(GGG)	G[GGA(92.468%)]	26845
18 Q(CAA)	Q[CAG(89.655%)]	26845
35 E(GAA)	D[GAT(80.933%)]	26847
36 M(ATG)	I[ATA(98.678%)]	26846
37 S(AGT)	N[AAT(90.951%)]	26844

The .html output file is a table that displays each position with the codon corresponding to the reference sequence and the AA it encodes. It also shows the different codons detected by the analysis along with the AA they encode, their frequency of occurrence, and the total number of valid sequences for that codon.

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

II. VARIABILITY II.1 POLYMORPHISMS II.1.B) CODONS