

HIV Pol Conservation

Generates a table with the most prevalent amino acid and its percentage at each position in the sequence of the selected Pol protein. This allows to identify the most conserved residue of the protein for each position.



- ① Select the input folder. It should only contain the .fasta files of the Pol protein to be analyzed, translated into amino acids and aligned (1 file or multiple files).
- ② Choose the type of protein you want to analyze, selecting from PR (protease), RT (reverse transcriptase), and IN (integrase).
- ③ Choose the type of HIV you wish to analyze, selecting between HIV-1 and HIV-2.
- ④ Select the output folder and enter the filename in the following format: /NAME.html.
- ⑤ Click Calculate.

Pol Conservation Protease HIV-1 > 75%		
PR_procesado_traducido_01_AE.fasta		
CONSENSUS	PQITLWQRPLVTVKIGGQLKEALLDTGADDTVLEDINLPGKWKPKMIGGIGGFIKVRQYDQLIEICGKKAIGTVLVGPTPVNIIGRNMLTIQGCTLNF	
Position	Residues	Total Positions
P1	P(99.896%)	26838
Q2	Q(99.782%)	26649
V3	I(99.858%)	26831
T4	T(99.858%)	26816

The output displays the name of the input file, the consensus sequence for each file with residues colored according to their percentage following the color code, and the table with all positions of the analyzed protein. It includes the most conserved amino acid for each position (provided its frequency of occurrence is > 75%), its percentage colored using the color code, and the total number of valid sequences for that position.

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

I. VIRUS I.1 HIV I.1.C) POL CONSERVATION