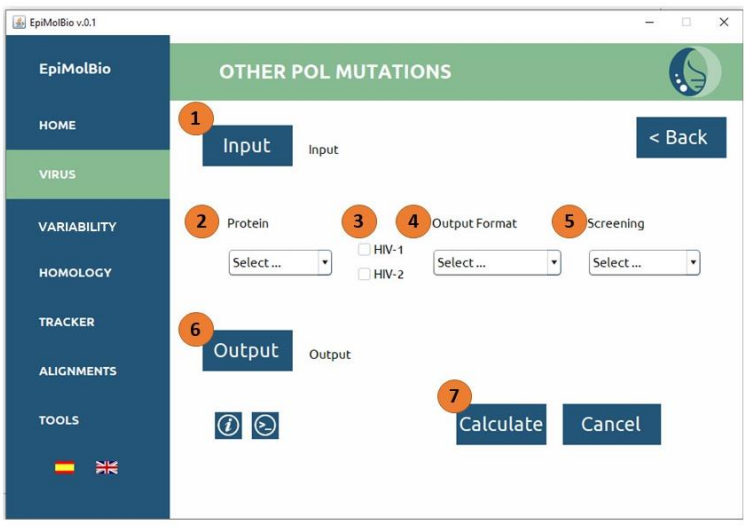
HIV Other Pol Mutations

Allows the detection of any mutation (not only DRM) in HIV-1 or HIV-2 from sequences of Pol proteins, providing their percentage relative to the reference sequence.



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. The program automatically establishes the reference sequence: HXB2 (NCBI K03455.1) for HIV-1 and ALI (NCBI AF082339) for HIV-2.

④ Choose the desired output format by selecting from:

List (100% y >75% screening)

List Other Pol Mutations Protease HIV-1 100%

PR_procesado_traducido_01_AE.fasta

Position	Residues	Total Positions
P1	P(99.896%) S(0.078%) A(0.004%) L(0.007%) T(0.007%) H(0.004%) V(0.004%)	26838
Q2	Q(99.782%) E(0.071%) S(0.019%) H(0.056%) D(0.004%) K(0.023%) L(0.015%) P(0.008%) R(0.011%) T(0.004%) *(0.008%)	26649
V3	I(99.858%) V(0.078%) N(0.015%) L(0.041%) T(0.007%)	26831
T4	T(99.858%) M(0.004%) I(0.048%) N(0.019%) P(0.022%) S(0.034%) F(0.004%) A(0.007%) H(0.004%)	26816
L5	L(99.888%) F(0.075%) V(0.015%) S(0.004%) R(0.007%) I(0.007%) T(0.004%)	26780
W6	W(99.929%) G(0.030%) R(0.022%) *(0.007%) C(0.011%)	26836

Displays the positions with their reference amino acid, followed by the found residues for that position based on the applied screening, and their percentage of occurrence colored according to the color code. At the end of each line, the total number of valid sequences for that position is shown.

Table (>75% default screening)

File	P1	Q2	V3	T4	L5	W6	Q7	R8	P9	L10	V11	T12	I13	K14	I15	G16	G17	Q18	L19	K20	E21
PR_procesado_traducido_01_AE.fasta			I																		
PR_procesado_traducido_02_AG.fasta			I										V							I	
PR_procesado_traducido_03_A6B.fasta			I																		
PR_procesado_traducido_04_cpx.fasta			I																		
PR_procesado_traducido_05_DF.fasta			I																		
PR_procesado_traducido_06_cpx.fasta			I										V							I	
PR_procesado_traducido_07_BC.fasta			I																		
PR_procesado_traducido_08_BC.fasta			I									S			V				I		
PR_procesado_traducido_09_cpx.fasta			I										V								

Shows in the first column: the names of the input files used to generate the table. In the first row, the table displays the name of the analyzed protein, and below it, each position with its reference amino acid and the mutated residue, with the cell colored according to the color code, indicating the percentage of occurrence for that position based on the default screening >75%.

Summary Table (>75% default screening)

Summary Table Other Pol Mutations Protease HIV-1 > 75%

File	Residues	Total Sequences
PR_procesado_traducido_01_AE.fasta	V3I, E35D, M36I, S37N, R41K, H69K, L89M	26849
PR_procesado_traducido_02_AG.fasta	V3I, I13V, K20I, M36I, R41K, H69K, L89M	9577
PR_procesado_traducido_03_A6B.fasta	V3I, E35D, M36I, S37N, R41K, H69K, L89M	310

Shows in the first column: the names of the input files. In the next column, displays each position with its reference amino acid and the mutated residue, colored based on the percentage of occurrence for that position with a screening >75%. The third column shows the total number of sequences for each input file.

⑤ If "List" is chosen, select the desired screening: >75% or 100%.

⑥ Select the output folder and enter the filename in the following format: /NAME.html.

⑦ Click Calculate.

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

I. VIRUS I.1 HIV I.1.B) OTHER POL MUTATIONS