

HIV Transmitted Drug Resistance Mutations

It allows obtaining the percentage of transmitted resistance mutations, relative to a reference sequence, from amino acid sequences of the Pol proteins of HIV-1.



- 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 SDRM analysis you want to perform, selecting from mutations against PIs (Protease Inhibitors), NRTIs (Nucleoside Reverse Transcriptase Inhibitors), NNRTIs (Non-Nucleoside Reverse Transcriptase Inhibitors), and INSTIs (Integrase Strand Transfer Inhibitors).
- 3 Choose the desired output format by selecting from:

List

List Transmitted Resistance Mutations SDRM-PI OMS		
PR_procesado_traducido_01_AE.fasta		
Position	Residues	Total Positions
L23	L(99.935%) I(0.019%*) F(0.015%) V(0.019%) Q(0.004%) P(0.004%) S(0.004%)	26251
L24	L(99.940%) I(0.015%*) V(0.019%) S(0.019%) F(0.007%)	26714
D30	D(99.985%) K(0.004%) H(0.004%*) G(0.007%)	26741
V32	V(99.928%) A(0.015%) I(0.028%*) L(0.023%) E(0.008%)	26584
M46	M(98.733%) I(0.661%*) L(0.531%*) V(0.064%) R(0.011%)	26764

It displays the positions with mutations along with the corresponding residues and their percentage, indicating SDRMs with an asterisk (*). The total number of valid sequences for each position appears at the end of each line.

Table

	Table Transmitted Resistance Mutations SDRM-PI WHO																			
	L23I	L24I	D30N	V32I	M46I	M46L	I47V	I47A	G48V	G48M	I50V	I50L	F53L	F53Y	I54V	I54L	I54M	I54A	I54T	I54S
PR_procesado_traducido_01_AE.fasta	0.019%	0.018%	0.004%	0.026%	0.681%	0.821%	0.048%	0.019%	0.010%	0.018%	0.026%		0.119%	0.022%	0.222%	0.022%	0.011%	0.011%		0.019%
PR_procesado_traducido_02_AG.fasta	0.021%	0.021%	0.002%	0.021%	0.699%	0.179%	0.084%		0.011%	0.042%			0.010%	0.118%	0.118%	0.489%	0.002%	0.021%		0.189%
PR_procesado_traducido_03_A6B.fasta				0.990%	1.302%	0.651%		0.649%				0.647%	0.324%	0.329%		0.329%				0.324%
PR_procesado_traducido_04_cpi.fasta		0.667%	0.667%			13.332%			0.667%				13.332%		28.871%					7.143%
PR_procesado_traducido_05_DF.fasta																				
PR_procesado_traducido_06_cpi.fasta	0.137%				1.784%	0.270%	0.368%						0.138%	0.269%	0.369%	1.387%				
PR_procesado_traducido_07_BC.fasta			0.018%		0.086%	0.027%					0.003%									0.042%
PR_procesado_traducido_08_BC.fasta		0.042%	0.042%		0.128%		0.042%				0.128%					0.042%				
PR_procesado_traducido_09_cpi.fasta													1.064%		2.181%					

Displays in the first row: the type of SDRM. In the first column: the names of the input files. In the rest of the columns, it shows the detected SDRMs with cells colored according to the percentage of occurrence in each input file.

Summary Table

Summary Table Transmitted Resistance Mutations SDRM-PI WHO	
File	SDRM PI WHO
PR_procesado_traducido_01_AE.fasta	L23I, L24I, D30N, V32I, M46IL, I47V, G48VM, I50V, F53LY, I54VLMAS, G73ST, L76V, V82ATFSML, N83D, I84V, I85V, N88DS, L90M
PR_procesado_traducido_02_AG.fasta	L23I, L24I, D30N, V32I, M46IL, I47V, G48VM, I50L, F53LY, I54VLM, G73SA, L76V, V82ATFSCL, N83D, I84VAC, I85V, N88DS, L90M
PR_procesado_traducido_03_A6B.fasta	V32I, M46IL, I47A, I50VL, F53L, I54V, G73S, L76V, V82AT, I84V, L90M

Displays in the first column the names of the input files, in the next column, the type of SDRM, and below this, the corresponding found residues for the SDRMs, colored based on their percentage according to the color-code.

The color code used for the percentages can be found in the output file.

- 4 Select the output folder and enter the filename in the following format: /NAME.html.
- 5 Click Calculate.

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

I. VIRUS I.1 HIV I.1.A) RESISTANCE MUTATIONS (Individual Transmitted Mutations)