

Section II.5: Mutation Frequency (p105 - p109)

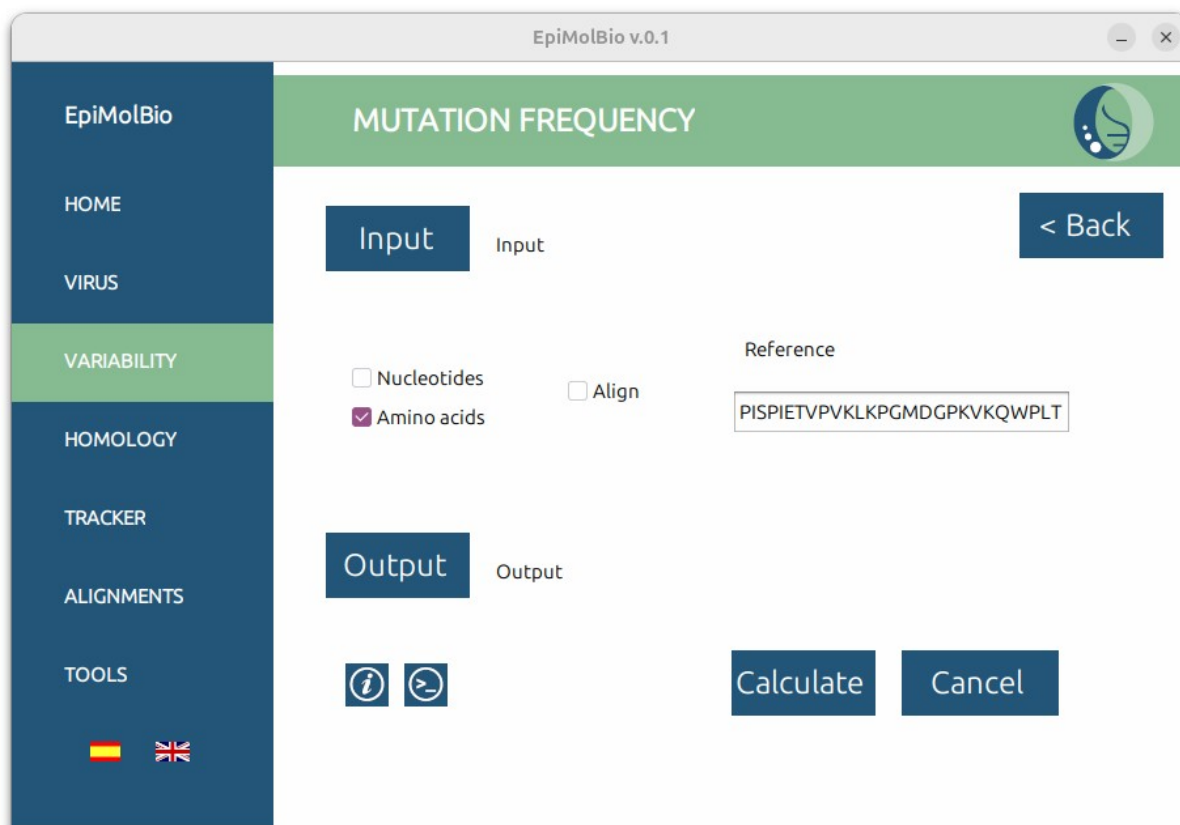
See the full manual [here](#).

Example File

File Name: MUTATION FRECUENCY RT HIV-1.csv

Parameter Selection

- **Nucleotides/Amino acids:**
 - *Amino acids*
- **Align:**
 - *Do not mark*
- **Reference:**
 - *PISPIETVPVKLPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKKD
STKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTI
PSINNETPGIRYQYNVLPQGWWKGSPAIFQSSMTKILEPFRKQNPDIVIYQYMDDLTVGSDLEIGQ
HRTKIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWTVQPIVLPEKDSWTVNDIQKL
VGKLNWASQIYPGIKVRQLCKLLRGTKALTEVIPLTEEALELAENREILKEPVHGVYYDPSKDLIA
EIQKQGQGQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFKL
PIQKETWETWWTEYWQATWIPEWEFVNTPLVLKLYQLEKEPIVGAETF*



The screenshot shows the EpiMolBio v.0.1 web application interface. The left sidebar contains navigation links: HOME, VIRUS, VARIABILITY (highlighted), HOMOLOGY, TRACKER, ALIGNMENTS, and TOOLS. At the bottom of the sidebar are flags for Spanish and English. The main content area is titled 'MUTATION FREQUENCY' and features a green header bar with a DNA helix icon. Below the header, there are input and output fields. The 'Input' field is empty, and the 'Output' field is empty. The 'Reference' field contains the sequence: PISPIETVPVKLPGMDGPKVKQWPLT. There are checkboxes for 'Nucleotides' (unchecked) and 'Amino acids' (checked). There is also an 'Align' checkbox (unchecked). At the bottom right, there are 'Calculate' and 'Cancel' buttons. A '< Back' button is located in the top right corner of the main content area.