

Prediction of minor variants and drug resistance

Alt-text Figure 34 - Selection of reference genome

Screenshot of IGV tool showing the dropdown menu with a list of reference sequences.

Alt-text Figure 35 - SARS-CoV-2 reference genome

Screenshot of IGV tool showing the annotation of the SARS-CoV-2 genome. It shows the genome represented by blue horizontal bars, indicating the nucleotide positions of each virus gene. Details in the main text.

Alt-text Figure 36 - Mapping to reference

Screenshot of the IGV tool showing the genome mapped to the reference. The reference genome is represented by blue horizontal bars. Below there are grey horizontal bars representing the query sequence aligned to the reference genome. There are thin vertical lines within the grey bars, these represent the differences between the query and the reference sequences.

Alt-text Figure 37 - Zooming in a mutation

Screenshot of the IGV tool showing the nucleotide count in a zoomed position of the mapped genome. Total count: 104, A=0, C=0, G=1, T=103, N=0, del=0, ins =0. It means that in this position the reference has guanine (G), while the query has a change to thymine (T).

Alt-text Figure 38 - Translating the amino acid codons

!Screenshot of the IGV tool showing the settings menu. On the right-hand side of the reference genome there is a cog icon showing two options: reverse and three-frame translate.

Alt-text Figure 39 - Sotrovimab epitope mutations

!Schematic illustration showing the SARS-CoV-2 Spike protein sequence and the mutations that impact in Sotrovimab activity: GAT E>D ↓10-fold, GTA E>V ↓200-fold, GCA E>A ↓100-fold, AAA E>K ↓297-fold.