

Viral Instant Mutation Viewer (VIMVer): a tool to speed up the identification and analysis of new SARS-CoV2 emerging variant

Two years after its outbreak, COVID-19 still represents a major public health problem as it keeps spreading at an alarming rate through the rise of many pathogenic variants (1). The severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), responsible for the COVID-19 pandemic, has become one of the most studied viruses since its emergence. The divergence of these variants from the original strain has a real impact on the efficiency of the vaccination. In this context, our main goal is to understand the differences behind the mutations observed simultaneously in the proteome and the genome. To act accordingly, we developed an user-friendly web-service software (Viral Instant Mutation Viewer or VIMVer) which allows a fast identification of new mutations and displayed them in both the nucleotide and protein sequences in comparison to a reference sequence (wuhan-1). Given a SARS-CoV-2 nucleotide sequence (as a newly sequenced genome), our software will instantly extract, analyze and visualize mutations on the genome and the proteome with the proper numbering and positioning. Furthermore, the lineage or the relative position to known lineage of the variant of interest is available on the link to Phylogenetic Assignment of Named Global Outbreak LINEages (Pangolin COVID-19) (2). We believe this tool will help many in their daily process to analyze their data. The source code is released under public license and can be adapted for further development.

(1).Rochman, Nash D., et al. "Ongoing global and regional adaptive evolution of SARS-CoV-2." *Proc. Natl. Acad. Sci. U.S.A.*, vol. 118, no. 29, 20 July 2021, doi:10.1073/pnas.2104241118.

(2).Rambaut, A., Holmes, E.C., O'Toole, Á. et al. A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. *Nat Microbiol* 5, 1403–1407 (2020). <https://doi.org/10.1038/s41564-020-0770-5>