

## Materials and Methods

The amino acid sequences of the 10 coronavirus proteins of the SARS-CoV-2 reference strain were obtained from NCBI's Protein database (<https://www.ncbi.nlm.nih.gov/protein>). Subsequently, they were aligned to each of the 17 coronaviral isolate genomes by TBLASTN (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>), without filtering low-complexity regions, thereby excluding the 5' ends of the genes. The regions in the respective genomes aligning to the peptide sequences were downloaded in FASTA format. The corresponding nucleotide sequences were translated into amino acid sequences using the EMBOSS Transeq online translation tool ([https://www.ebi.ac.uk/Tools/st/emboss\\_transeq/](https://www.ebi.ac.uk/Tools/st/emboss_transeq/)). For each protein, the translated amino acid sequences, along with the 10 reference protein sequences, were collected into a single file, and were provided as input to the online multiple sequence alignment (MSA) tool MUSCLE (<https://www.ebi.ac.uk/Tools/msa/muscle/>). The generated (or computed) MSAs were downloaded as a FASTA file, and visualized with the Jalview MSA analysis software.