



Figure S1: Model of 3D Structure of N (A) S1 (B) and RBD (C) proteins was predicted using Alphafold server. Signal peptide is colored in yellow, and His tag is colored in red. (E-F) Glycosylation sites were predicted in NetNGlyc 1.0 server. Mayor values of 0.5 was considered as positive. Then we analyze by using the server UCLA-DOE LAB), we found the next Overall Quality Factors, S1=77.21,N=80.83 and RBD= 72.77