Supplementary Figure

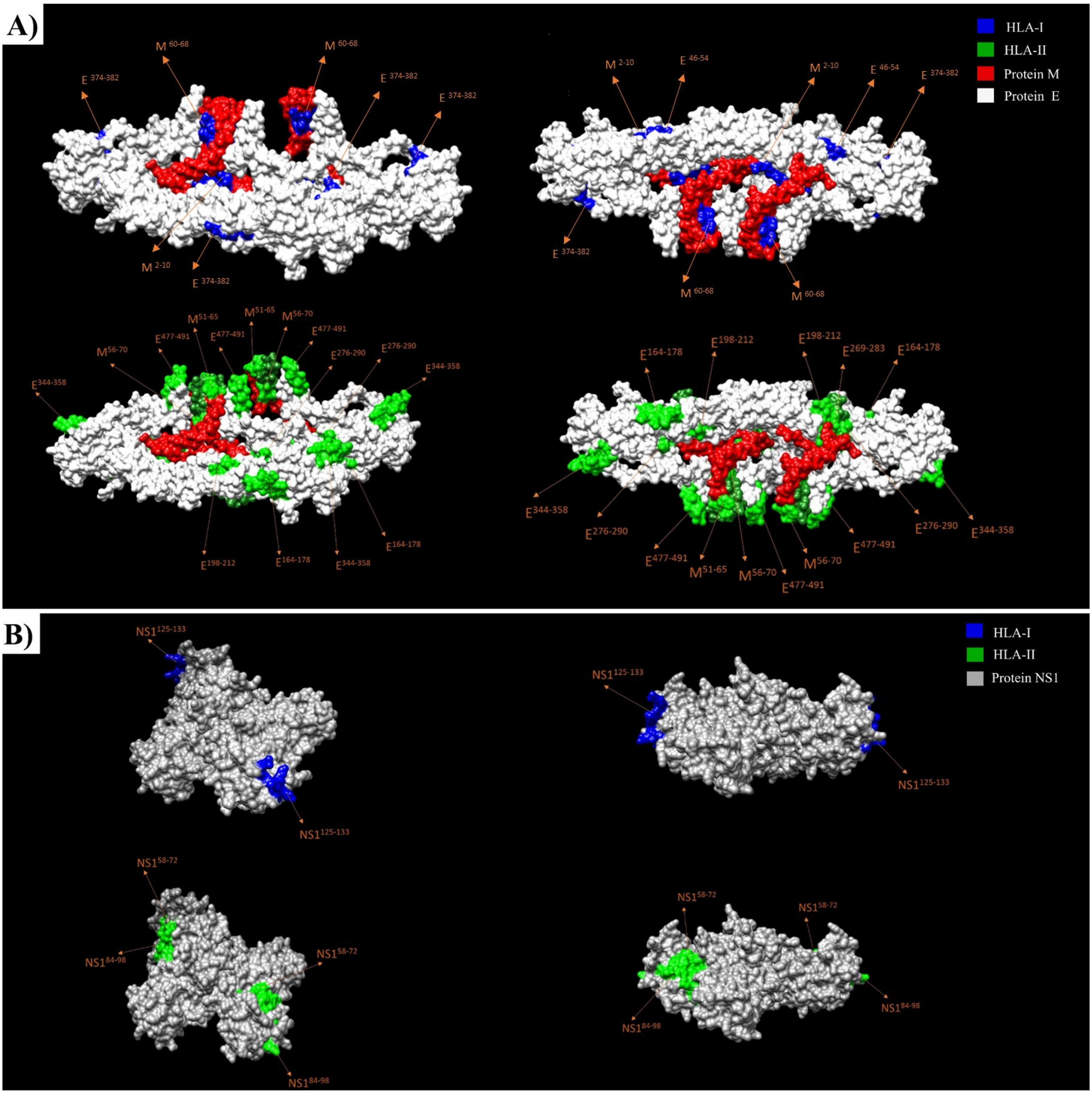

Figure 1: Localization of predicted epitopes on E, M and NS1 proteins. The predicted epitopes on M, E and NS1 proteins were evaluated for the solvent accessible surface (SAS) in the corresponding protein using the UCFS Chimera software version 1.12 and the 3D cryo-structure of E and M protein trimer (5IRE) and NS1 dimer protein (5GS6) deposited on the Protein Data Bank server (PDB). The HLA-I binding epitopes were highlight in blue and the HLA-II bindng epitopes in green. Envelope protein was highlight in white, membrane protein in red and NS1 protein in grey.