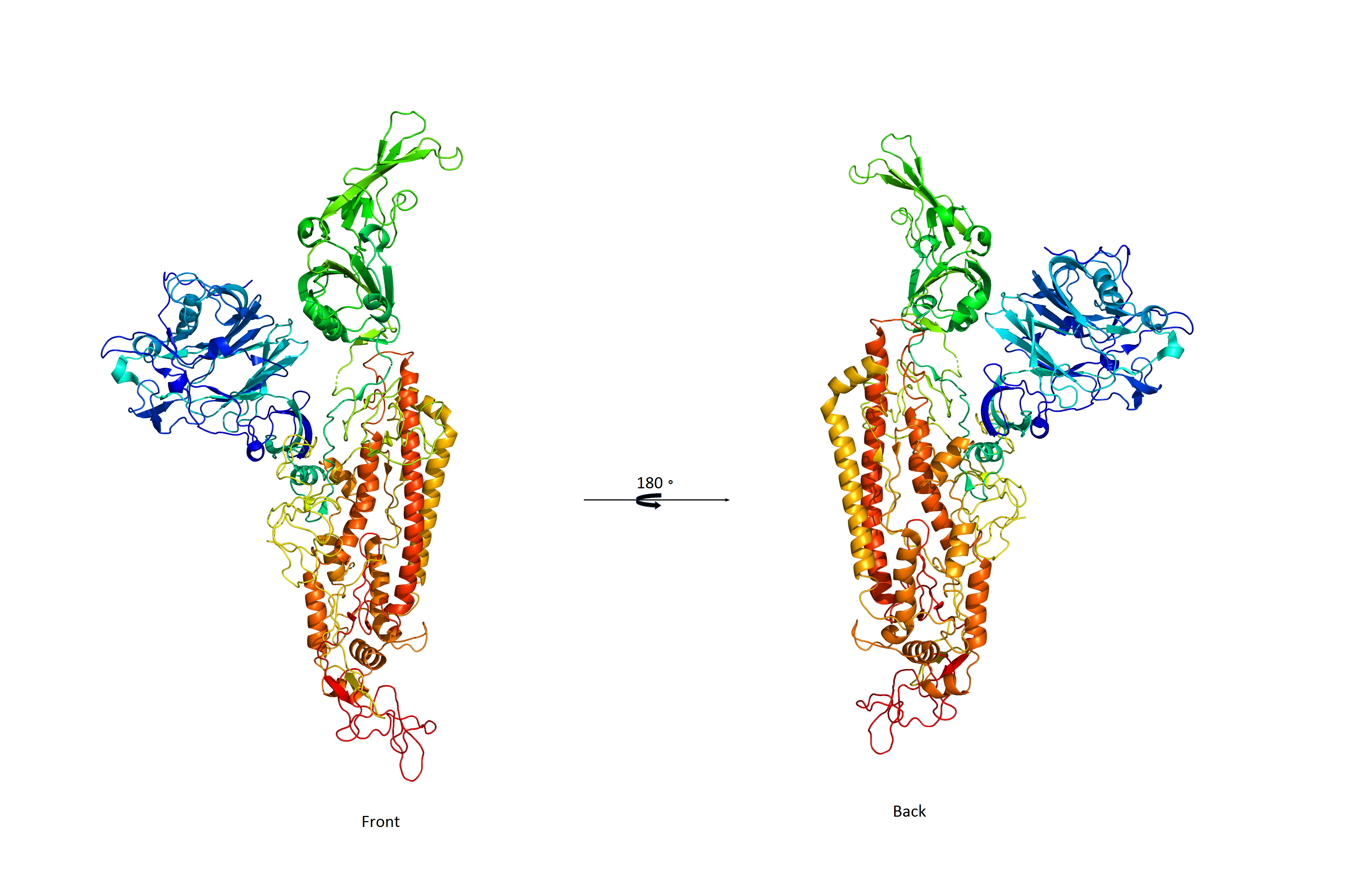
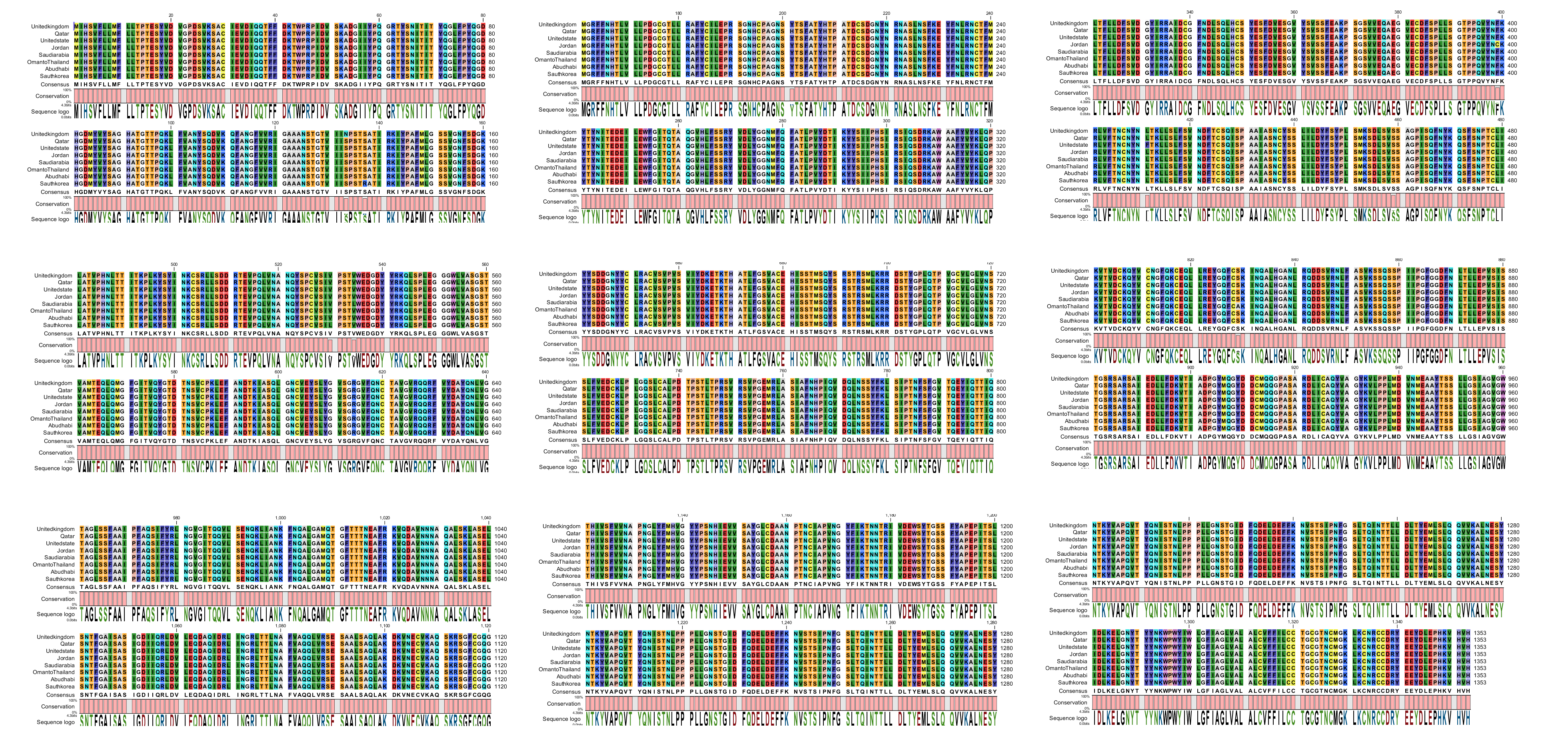


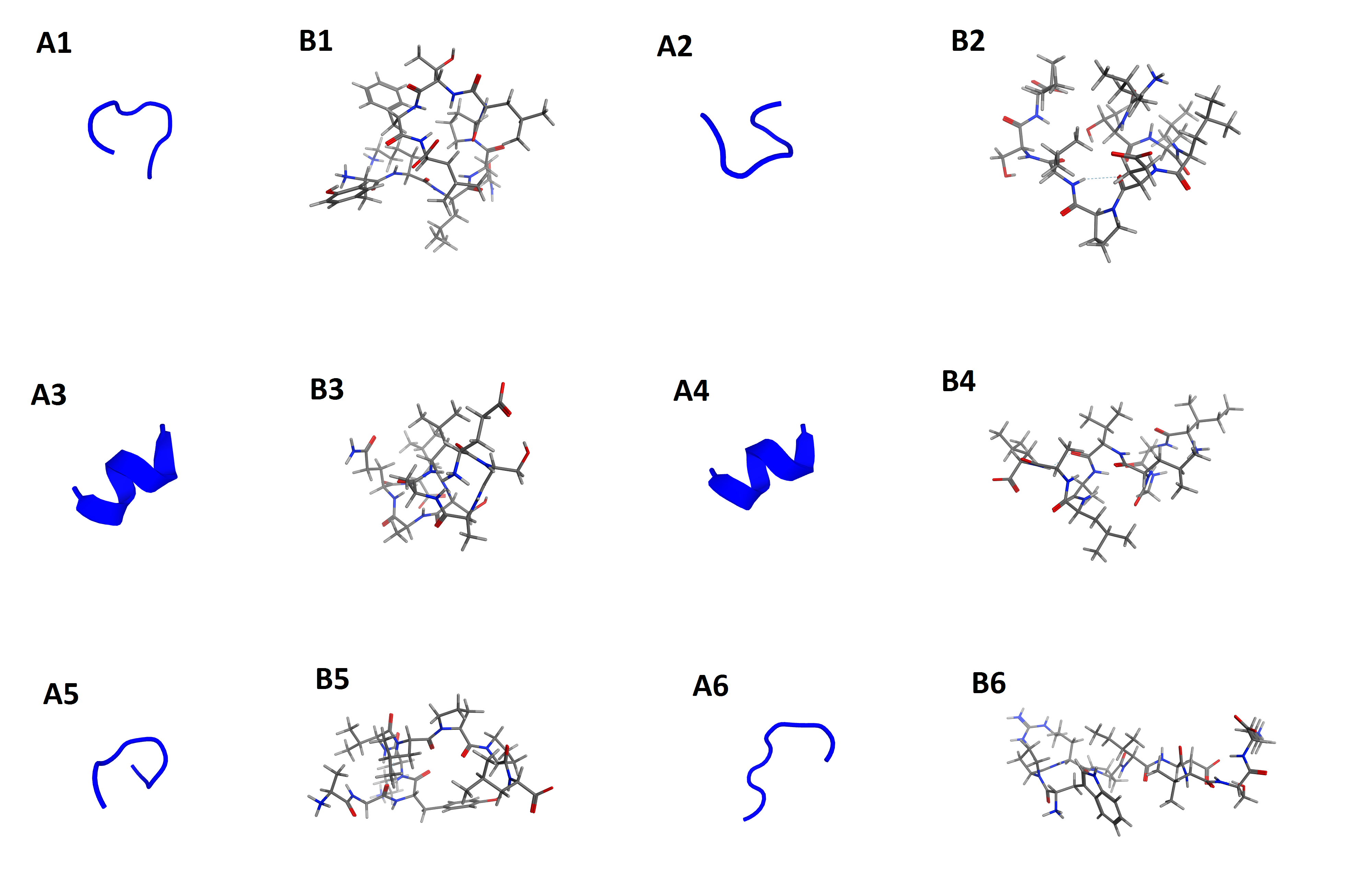
**Figure S1**. PSIPRED analysis of the MERS-COV S protein. Helixes are cylindrical and coloured pink, beta-strands are shown as arrows and coloured yellow, and random coil regions are black.



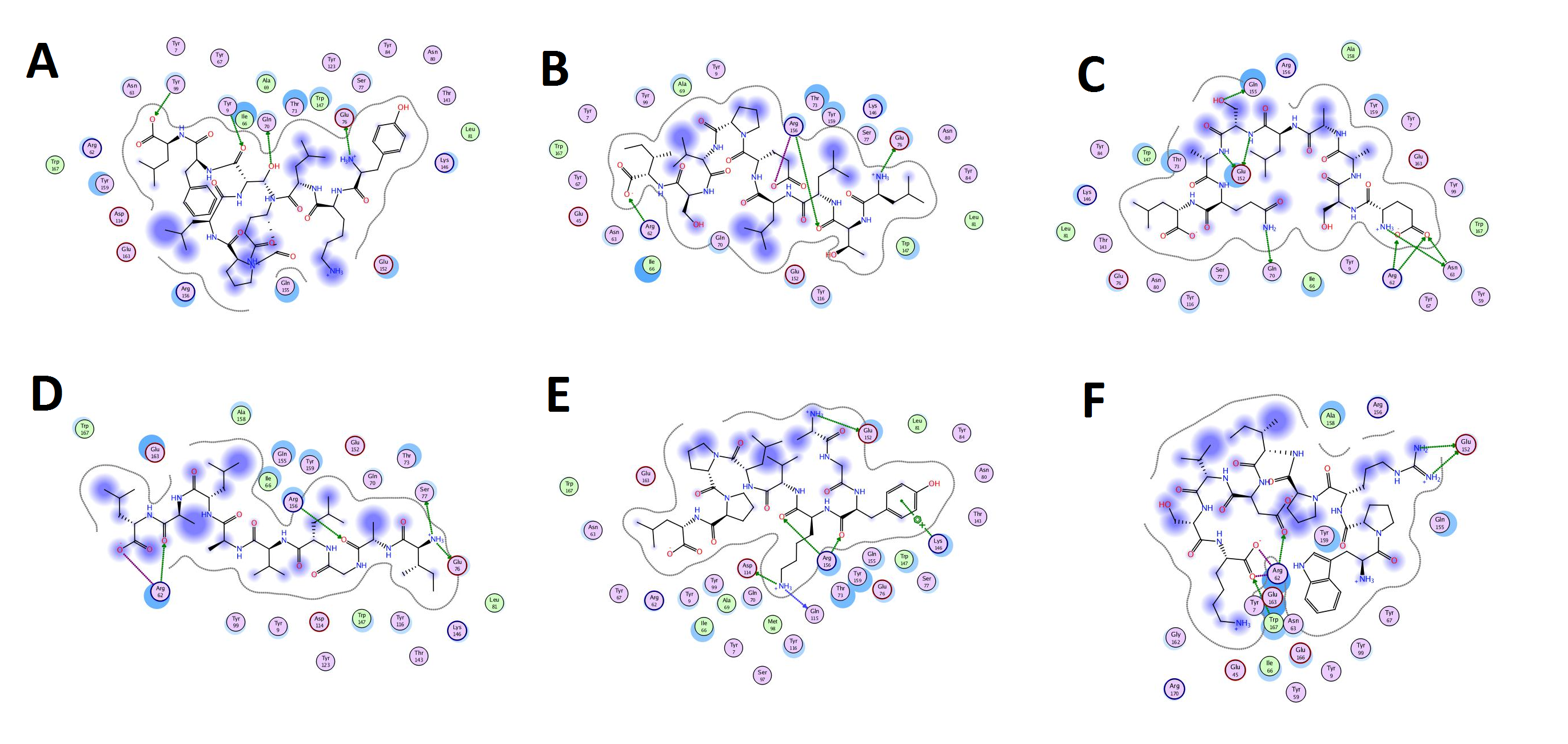
**Figure S2**. The 3D structure of the MERS-COV S protein (front and back conformations).



**Figure S3**. Multiple sequence alignment showing conservation of the S protein of MERS-COV isolated from eight different countries.



**Figure S4**. 3D (A1-6) and stick structures (B1-6) representation of selected MHC class-I alleles binding peptides. The figure is in symmetry with the information provided in Table 3.



**Figure S5**. 2D graphical representation of interaction analyses between human HLA-B7 protein and MHC class-I alleles binding peptides. The figure is in symmetry with the information provided in Table 6 and Figure 6 and showing the residues interacting with strong hydrogen bonding.