Supplementary materials



**Figure S1. Pairwise sequence alignments between the virulent SARS-CoV-1, -2 and MERS-CoV, and nonvirulent HCoV-229E and HCoV-NL63 human (h) coronavirus (CoV) envelope (E) proteins and the respective template used to generate each three-dimensional (3D) model.** Sequence alignments were generated using Jalview (v2.11.1.3) and coloured by sequence identity (blue). **A.** Pairwise sequence alignment between the SARS-CoV E protein (Accession number: P59637) and template 5x29. Sequences shared 91% identity with all residues conserved in the PDZ-binding motif (DLLV). **B.** Pairwise sequence alignment between the SARS-CoV-2 E protein (Accession number: P0DTC4) and template 5x29. Sequences shared 91% identity with all residues conserved in the PDZ-binding motif (DLLV). **C.** Pairwise sequence alignment between the MERS-CoV E protein (Accession number: K9N5R3) and template 2mm4. Sequences shared 35% identity with no conserved residues in the PDZ-binding motif (DEWV). **D.** Pairwise sequence alignment between the hCoV-229E E protein (Accession number: P19741) and template 5x29. Sequences shared 29% and PDZ-binding motif residues **V**IDF were conserved. **E.** Pairwise sequence alignment between the hCoV-NL63 E protein (Accession number: Q6Q1S0) and the hCoV-229E E protein homologous structure. Sequences shared 47% identity and PDZ-binding motif residues **V**LNV were conserved.



**Figure S2.** **Principal component analysis (PCA) indicating the covariance matrix value of the human (h) coronavirus (CoV) envelope (E) proteins for SARS-CoV-1, -2, MERS-CoV, HCoV-229E, and HCoV-NL63 based on the projection of two eigenvectors.** Red: SARS-CoV-2 E protein, Green: SARS-CoV-1 E protein, Blue: HCoV-229E E protein, Pink: HCoV-NL63 E protein, Cyan: MERS-CoV E protein.