Figure S1 Schematic representation of hACE2. PD domain is shown in green, transmembrane region in purple and the cytoplasmic domain in blue. The S protein binding sites, ADAM17 and TMPRSS2 cleavage sites have been mapped on the model. Multiple sequences alignment was performed using Clustal Omega for hACE2, cavACE2, dogACE2, catACE2, ratACE2, rabACE2, ferACE2, musACE2.

Figure S2 Sequences identity matrixes resulting from the ACE2 and TMPRSS2 multiple sequences alignments. Sequence alignment was performed using Clustal Omega using the HHalign algorithm and Gonnett as transition matrix.

Figure S3 Cartoon representation of the hACE2-RBD complex. RBD F486 side chain (teal sticks) is inserted in a relatively hydrophobic patch formed by the hACE2 residues F28, L79, M82 and Y83, shown as hot pink sticks.

Figure S4 Schematic representation of hTMPRSS2. The cytoplasmic domain is shown in blue, the transmembrane helix is purple, the LDL domain in red, the SRCR domain in orange and the Peptidase S1 in green. The catalytic triad residues H296, D345 and S441 have been mapped on the model. Normalised β-factor and estimated accuracy plots of the I-TASSER hTMPRSS2 model. The estimated local accuracy shows that the LDL (1-150) has relatively higher modelling error while most of other regions are accurate with estimated distance to native smaller than 4 Å.