

Supplementary Figures

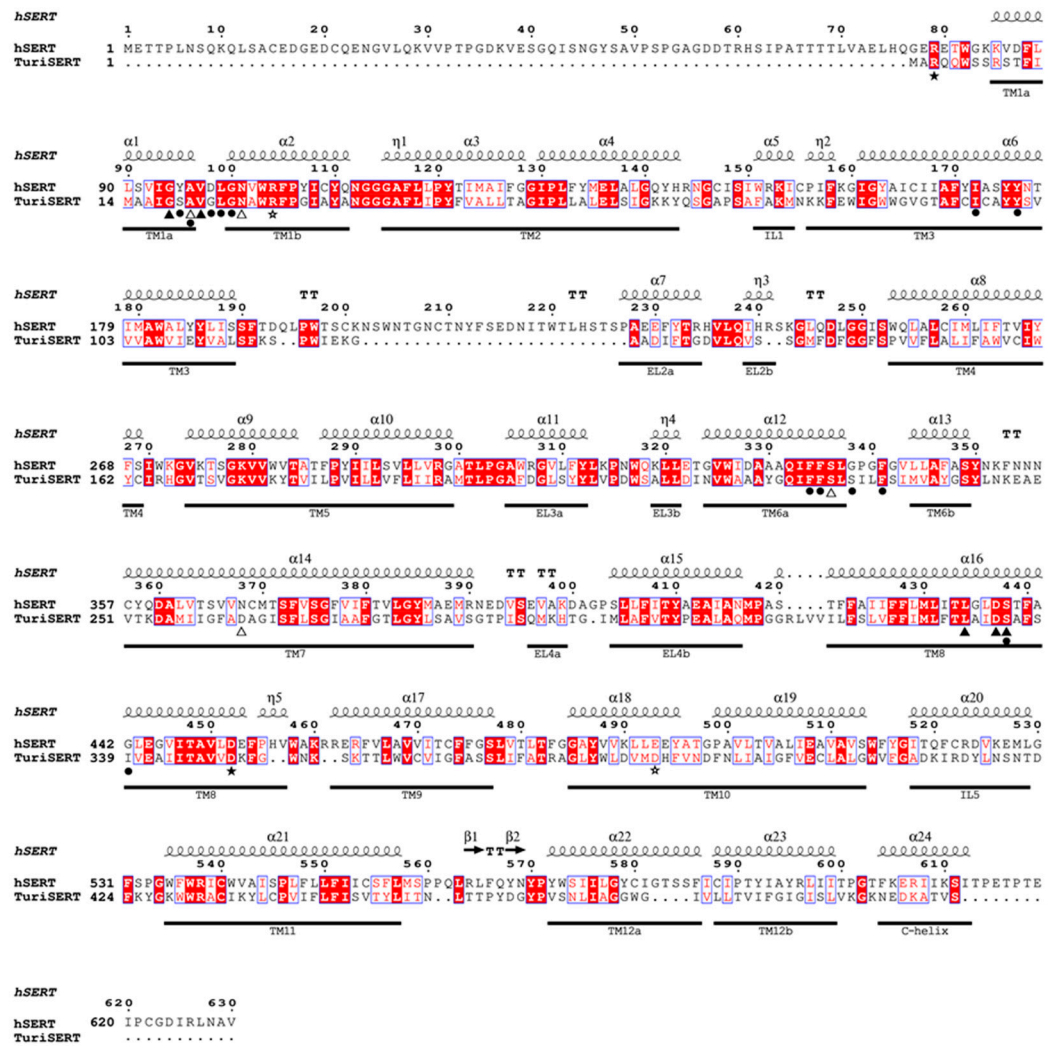


Figure S1. Amino acid sequence alignment of hSERT with TuriSERT. The sequence alignment was obtained with ClustalX2. Identical residues are highlighted in white letters with a red background and similar residues are shown in red letters. α -Helices and β -strands in hSERT are depicted as coils and arrows respectively. The open and filled triangles show residues coordinating sodium ions Na1 and Na2, respectively. The filled black circles indicate the residues involved in 5-HT binding in hSERT. The open and filled stars indicate the ion pairs at the extracellular and cytoplasmic entrances, respectively.

Homology model
AlphaFold

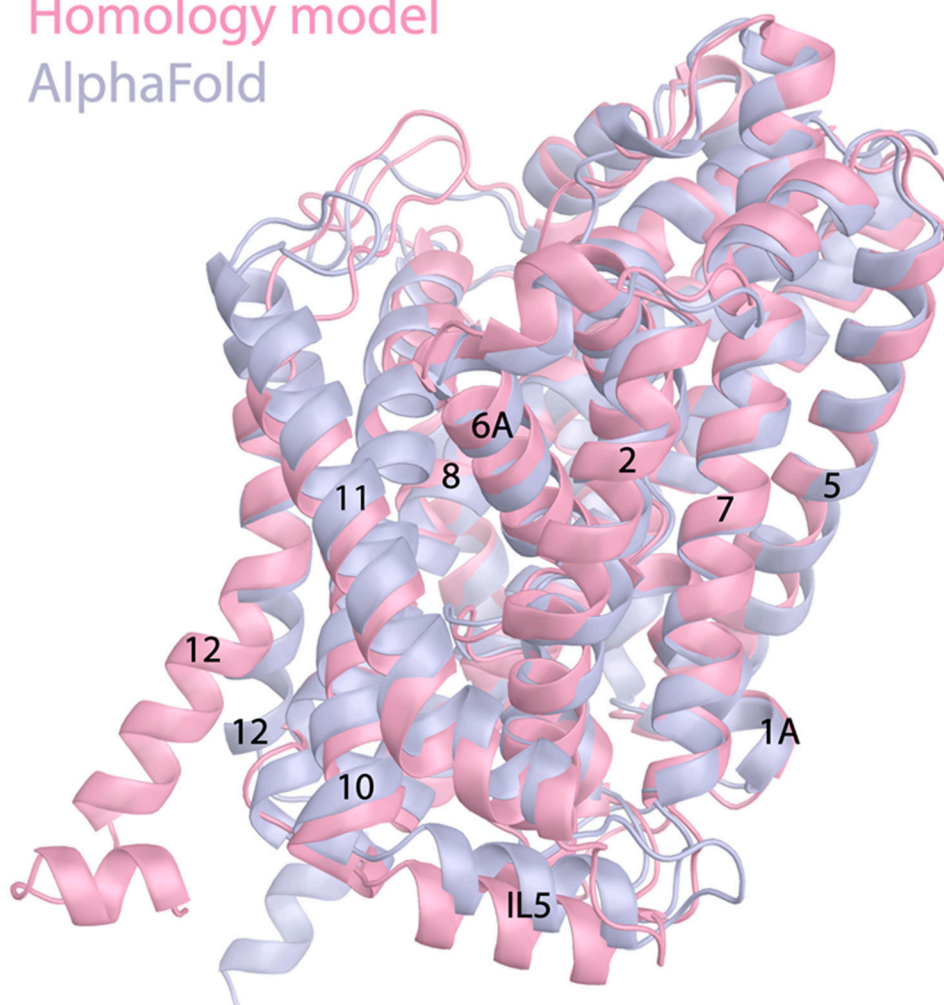


Figure S2. Superimposition of TuriSERT models generated by homology modeling (light pink) and AlphaFold2 (blue white). Numbers represent # of transmembrane α -helices in transporters.