Allosteric Modulation of Human Dopamine Transporter Activity under Conditions Promoting its Dimerization

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Running title: *Human dopamine transporter dimerization*

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Supplementary Figures

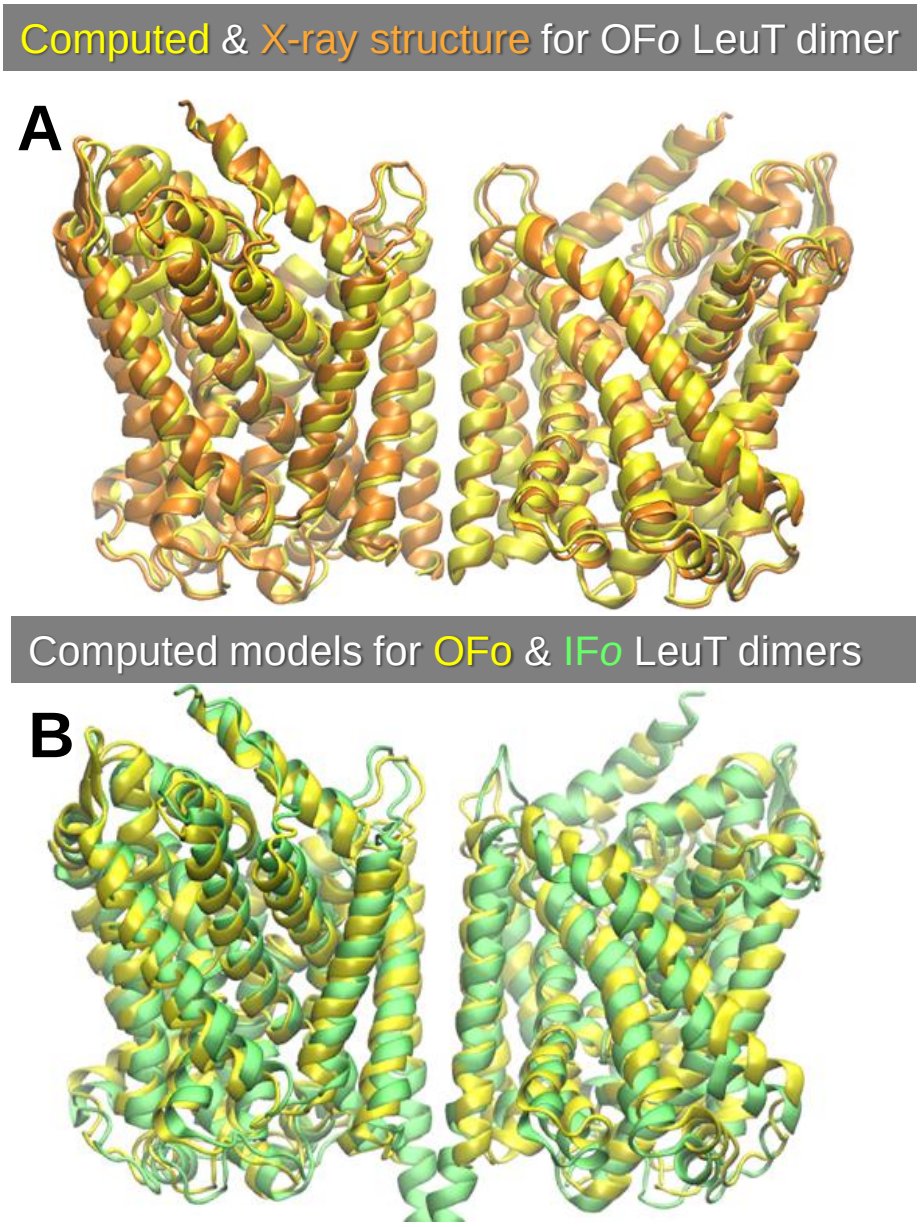

Figure S1: **The computed LeuT dimer in different conformation states**. (**A**) Comparison of the computed OF*o* LeuT dimer structure (*yellow*) with that structurally resolved (*orange*) (PDB: 3TT1). (**B**) Alignment of the computed OF*o* LeuT dimer (*yellow*) with the computed IF*o* LeuT dimer (*green*).

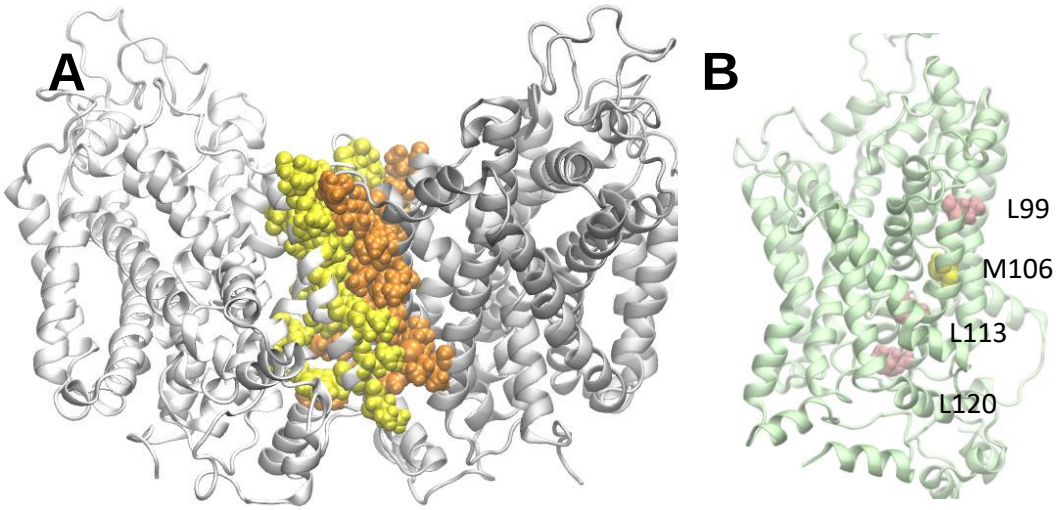

Figure S2: **Large hydrophobic patch at the interface of the two subunits in the hDAT dimer**. (**A**) Hydrophobic interfacial contact colored differently (*yellow* and *orange* represent hydrophobic residues from different subunits); (**B**) The predicted Leucine zipper (L99, M106, L113 and L120) (1) is not in direct contact. Instead one residue shift: V100, V107 and P112 contribute to direct interfacial interactions.