

Supporting material

Diffusion Mechanism Modeling of metformin in Human Organic Cationic Amino Acid Transporter one and Functional Impact of S189L, R206C, and G401S Mutation.

Leydy Cano¹, Alejandro Soto-Ospina^{1,2}, Pedronel Araque^{2,5}, Maria Antonieta Caro-Gomez¹, Maria Victoria Parra-Marin³, Gabriel Bedoya¹ and Constanza Duque^{4*}

1. Universidad de Antioquia, Medellín, Colombia.
2. Universidad EIA, Envigado, Colombia.
3. Tecnológico de Antioquia, Medellín, Colombia.
4. Universidad Cooperativa de Colombia, Medellín Colombia.
5. Cecoltec, Medellín, Colombia

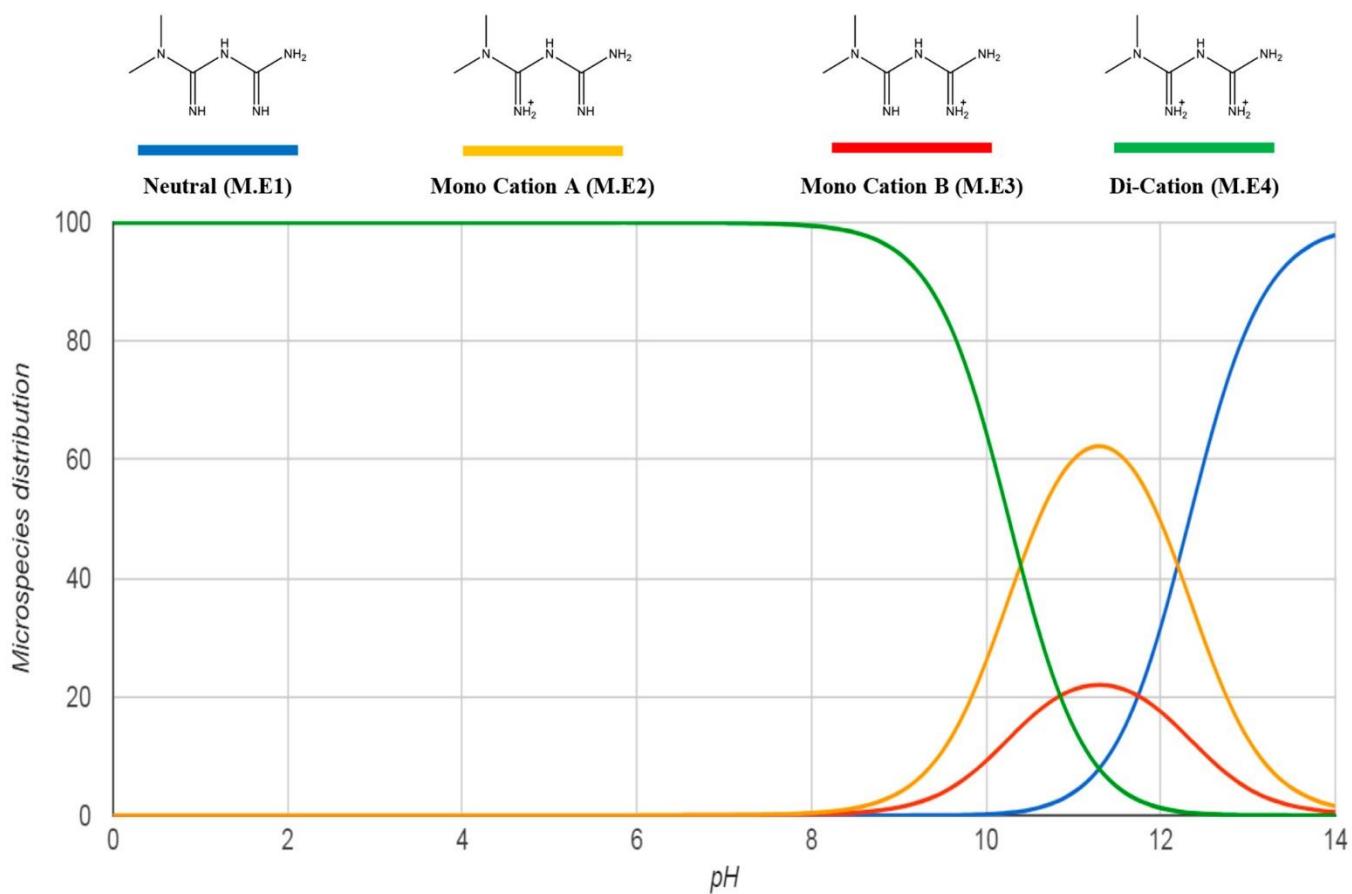


Fig. S1 Metformin characterization for calculation of the α (alpha) fractions

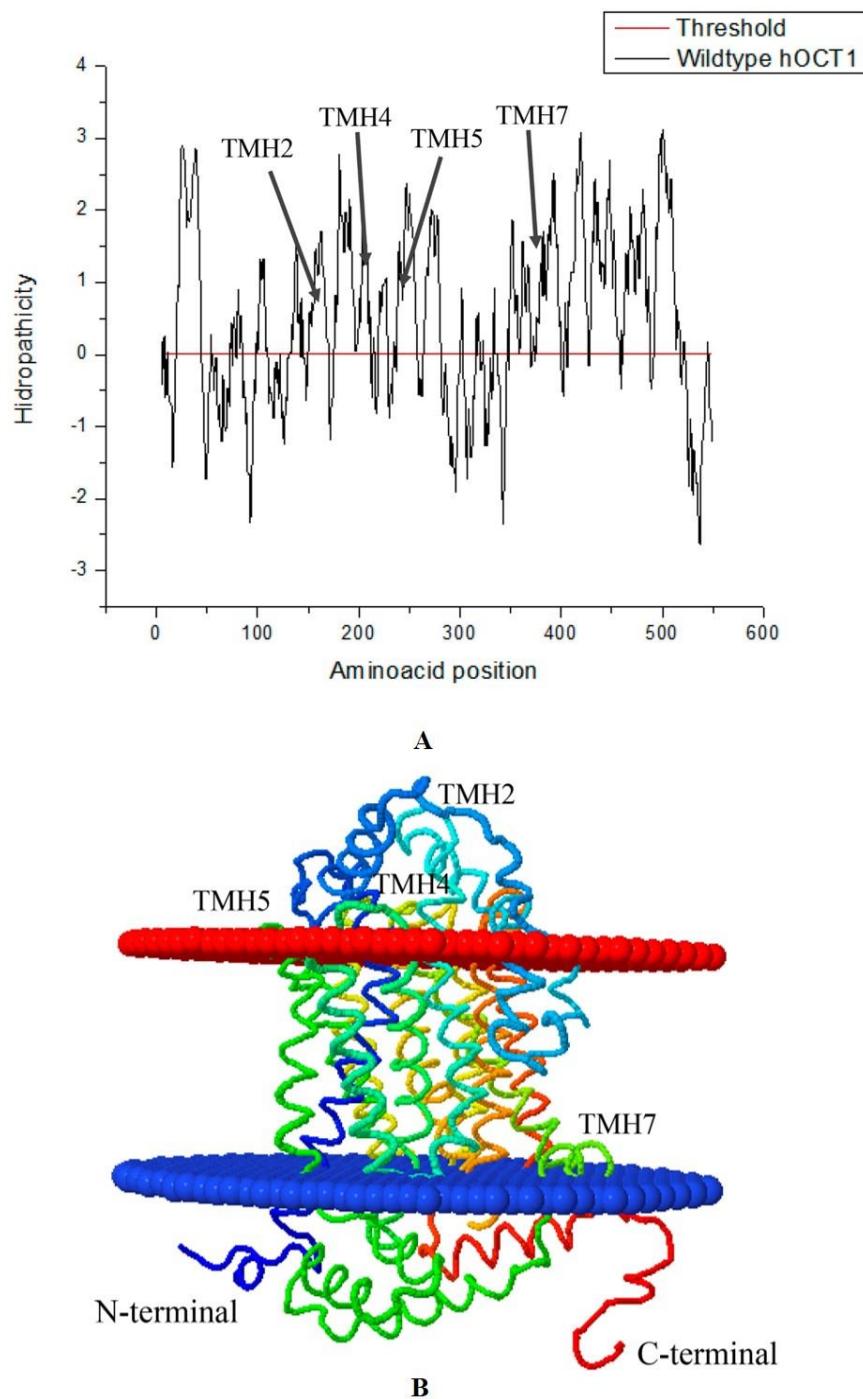


Fig. S2 Characterization of Human Organic Cation Transporter hOCT1: A) Hydropathy index plot for hOCT1; B) Structure of transmembrane α -helices involved in the passive diffusion of the metformin cation

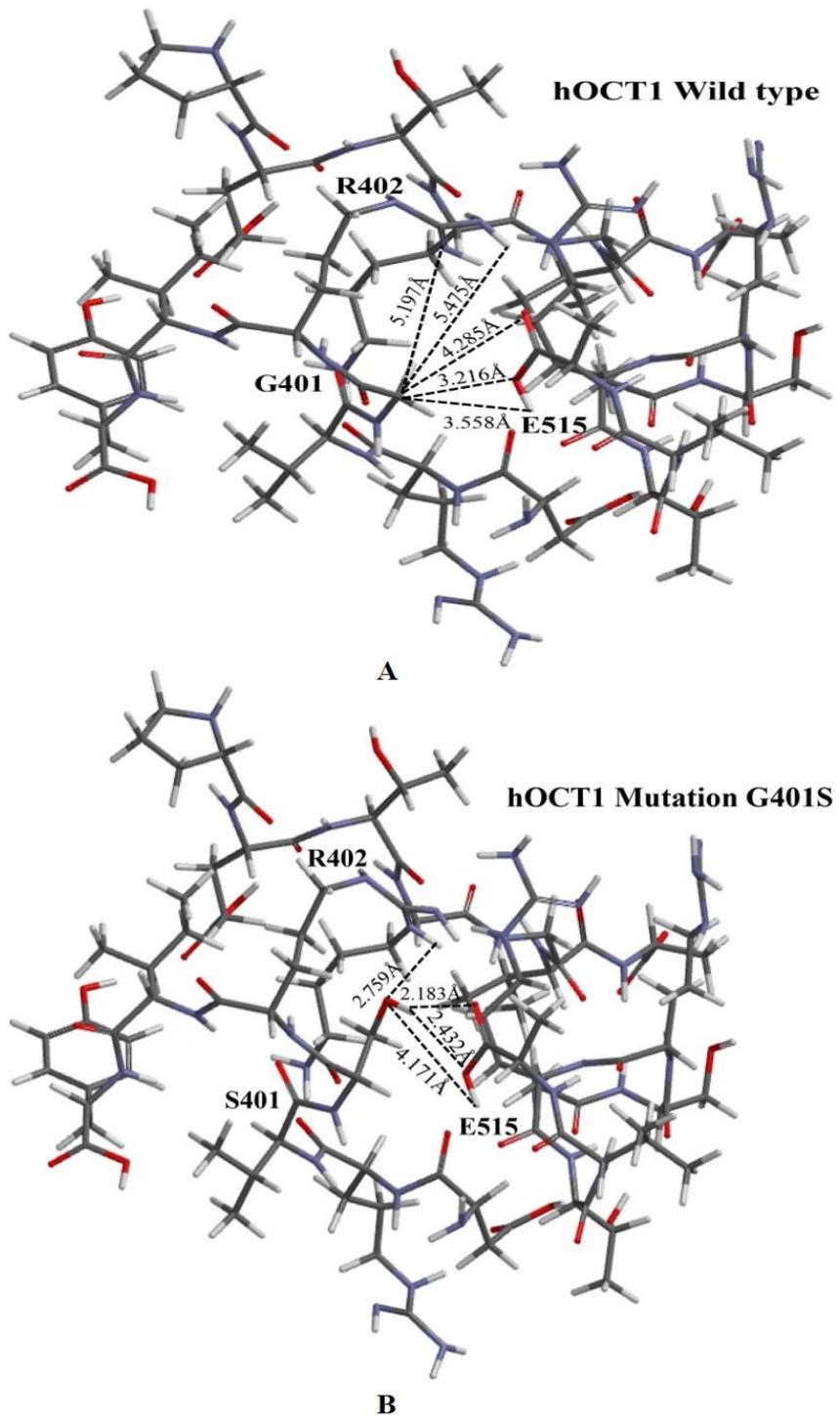


Fig.S3. Stick representation of amino acid structure in the proximity of position 401 in hOCT1: A) Bonding distances for the 401Gly structure; B) Bonding distances for the Ser401 structure

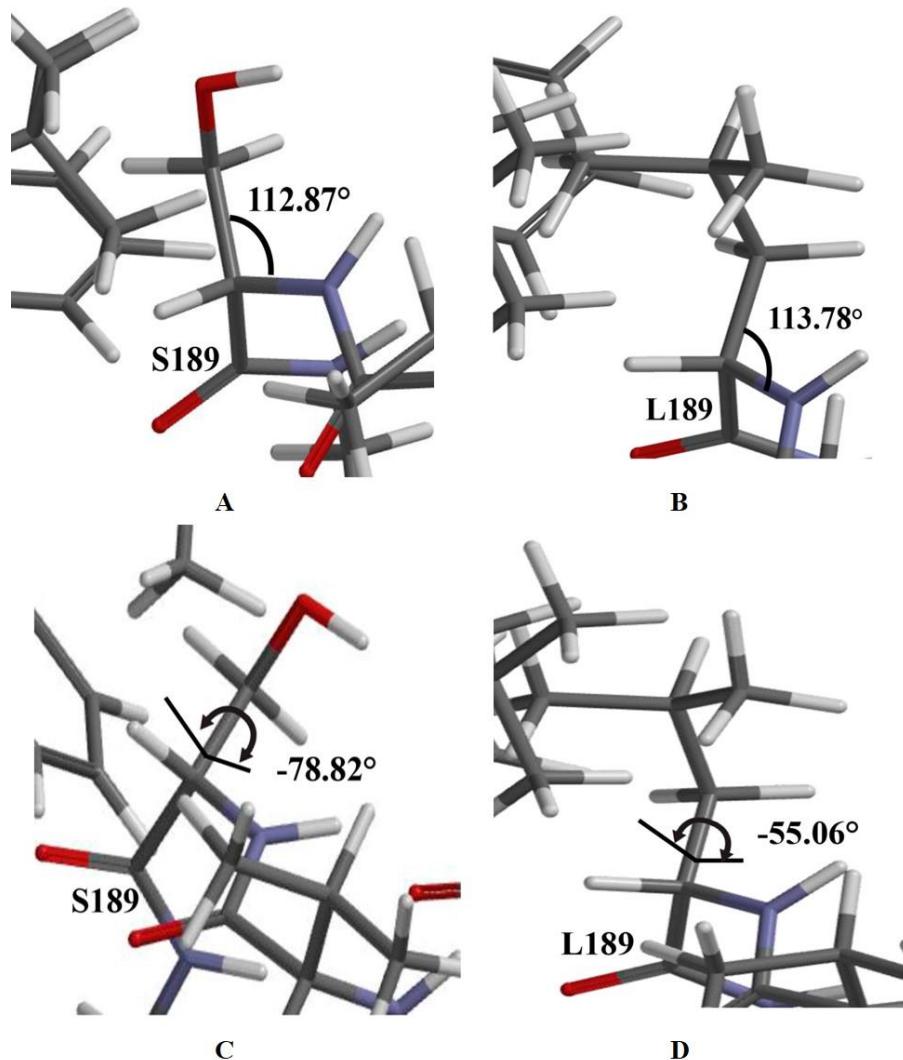


Fig.S4. Structural comparison of the region adjacent to position 189 of the hOCT1 channel: A) 3D visualization of the change in angle of the alpha carbon in the wild type Ser189 channel; B) 3D visualization of the change in angle of the alpha carbon in the wild type Leu189 mutated channel; C) 3D visualization of the change in the dihedral angle between alpha carbon planes in the wild type Ser189 channel; D) 3D visualization of the change in the dihedral angle of the alpha carbon planes Leu189 mutated channel