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Simulations of the pore structures for a M2G1yR derived channel forming peptide in membrane AHLAM N. AL-RAWI, ASMA AL-RAWI, JIANHAN CHEN, ALVARO HERRERA, JOHN TOMICH, Kansas State University, TALAT S. RAHMAN, University of Central Florida — In an effort to develop a peptide-based compound suitable for clinical use as a channel replacement therapeutic for treating channelopathies such as cystic fibrosis, we present a reductionist model that appears to capture many of the biophysical properties of an intact ion channel using short channel-forming peptides. We have developed two anion selective channel-forming peptides with near native and altered properties from the peptides derived from the glycine receptor: NK_4-M2GlyR-p22 WT (KKKKPAR-VGLGITTVLTMTTQS) and NK_4-M2GlyR-p22 S22W (KKKKPARVGLGITTVLTMTTQW), respectively. Starting with the two structures determined by solution multidimensional NMR (800 MHz) in SDS, we used CHARMM and NAMD to perform molecular dynamics simulations on the monomers. Using the existing experimental data, we then built an initial 5- helix assembly by altering the tilted angle, rotational angle and pore radius. We investigated the impact of the single mutation at position 22 on the structure and dynamics of the pore formed in a membrane build in a hydrated POPC lipid bilayer. Probable structures for both assemblies are presented.

Talat S. Rahman
UNIVERSITY OF CENTRAL FLORIDA

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