File name: Supplementary Movie 1

Description: 1-μs molecular dynamics (MD) simulation of GPR34 bound to the various agonists. The MD simulation movie was recorded every 500 ps. Hydrophilic network residues (*e.g.,* K128$^{3.26}$, F205^{ECL2}, R286$^{6.55}$, N309$^{7.35}$, and E310$^{7.36}$) are shown as sticks. The hydrophilic binding sites of GPR34 contain an assembly of charged amino acid residues that can efficiently interact with the charged phosphoserine. Therefore, hydrophilic interactions of the ligand in the binding pocket could be swapped. In fact, in the 1-μs MD simulation of *sn*-1 LysoPS, the *sn*-1-type hydrophilic interaction mode barely switched to the *sn*-3-type, consistent with its low activity. The movies of the five simulations are concatenated as one movie, S3E-LysoPS, M1, S3E-LysoPS-no_amine, *sn*-1 LysoP1, and *sn*-2 LysoPS, in that order.