**Figure S3.** Secondary structure analysis of the WT FSHR and the Gly³ and Ala³ FSHR mutants. All protein structures exhibited stable seven transmembrane α-helices (TM1-TM7) across the lipid bilayer and a helix eight (H8) parallel to the bilayer at the intracellular interface. In all structures, stable β-sheet structures were observed in regions Asp317 to Asp320 and Met 495 to Ile505 in the amino-terminus and the second extracellular loop, respectively. The carboxyl-terminus was highly dynamic in all structures, with sporadic interconversion between α-helices and 3-helices and turns. At the secondary structure level, within ~20 ns of MD simulation, WT and triple mutants displayed similar profiles. A-Helix: α-helix (helix every 4 amino acid residues); 3-Helix (helix every 3 residues); B-Sheet: β-sheet; B-Bridge: β-bridge (single pair β-sheet hydrogen bond formation).