Membrane proteins typically account for 30% of most genomes but their structural stability, dynamics and interactions are ill understood. In this talk I will present our work in each of these areas, with particular emphasis on membrane receptors. In our efforts to develop better mechanistic understanding of membrane protein stability, I will present an analysis of the predicted (un)folding pathways of different alpha-helical membrane protein structures and discuss potential implications for membrane protein misfolding. Our studies on membrane receptor dynamics focus on modulation of activity of G protein coupled receptors. In particular, we try to understand adaptation of the visual receptor rhodopsin to dim light conditions by interaction with chlorophyll-derivatives and the allosteric modulation of metabotropic glutamate receptors. Finally, I will present our combined computational and experimental approach to investigate protein interactions involving membrane receptors, providing a system-wide view of the human membrane receptor interactome.