Membrane proteins and their interactions with lipid bilayers play a key role in a wide range of biological processes. As the number of high resolution structures of membrane proteins increases, there is a need to improve our understanding of how such proteins interact with their lipid bilayer environment. Multiscale molecular dynamics (MD) simulations enable us to combine self-assembly of lipid bilayer/protein complexes by coarse-grained (CG-MD) simulations with refinement of predicted lipid/protein interactions by atomistic MD. This approach has been tested against model peptides, yielding good agreement with solid state NMR data [1]. Application of multiscale simulations to Aqp0 predicts protein/lipid interactions that agree well with those in electron crystallographic structures. Simulations of all aquaporins of known structure suggest that there is conservation of lipid/protein interactions across this family of membrane proteins. Large scale CG-MD simulations may be used to explore the interactions of multiple membrane proteins within a lipid bilayer. The results reveal a complex interplay of protein/protein and protein/lipid interactions in determining whether a membrane protein forms aggregates within a bilayer.