Protein interactions dominate the majority of cellular processes, making their structural characterization an important step in our understanding of cellular homeostasis and disease. In this presentation, I will introduce the concept of integrative modeling, which allows building high-quality structural models of protein interactions with atomic resolution by combining sparse experimental data with computational modeling methods. I will then show how we recently pieced together the complexes of GPCRs with a kinase and a chemokine ligand from existing crystal structures, using NMR and mass spectrometry data together with simulation.