The β2 adrenergic receptor is among the most extensively studied G-protein-coupled receptors (GPCRs), offering a wealth of information for development of new GPCR structure and binding site prediction methods. Since the β2 crystal structure was published in late 2007, the MSC has advanced both structure and binding site prediction procedures using the experimental structure as a guide. The TwoHelix analysis, in addition to its utility as a structure prediction tool, can be used to develop an ensemble of low-energy packings for the β2 crystal structure. With the ensemble docking approach, we can determine which of these packings will bind favorably to a ligand and begin to consider possible activation or deactivation pathways.