Cells have the ability to detect and respond to diverse environmental stimuli by means of biochemical signaling pathways that propagate information from the cell membrane into the cell. In this work, we use computational methods to study a common signaling pathway that exhibits bistability and observe how its dynamical and steady state behavior is affected by various cellularly relevant factors. Bistable networks have two distinct stable steady states and are commonly used in cellular decision-making. In the network studied, a substrate protein can be phosphorylated and dephosphorylated at two residues by kinase and phosphatase proteins. The reaction network is simulated using computational methods based on ordinary differential equations, and the transition from bistable to monostable behavior is characterized by observing the time dependence of the system starting from different initial conditions. We find that confining the system, which leads to increased concentration, promotes bistability while decreasing the rate at which enzymes become activated suppresses bistability. In addition, we consider effects of network topology by including additional reactions with reaction rates proportional to an independent control parameter. The reactions, which mimic the ability of proteins to rapidly rebind when in close spatial proximity, are found to greatly influence the signaling dynamics.