Proton conduction in the M2 protein in the influenza viruses plays a major role in viral replication. Exploring the Protein Data Bank for the AM2 protein, the protein sequence in entry, 3BKD\(^1\), is chosen. According to Stouffer’s work\(^1\), VMD\(^2\) was used to generate four configurations of AM2 protein structures in correspondence to the pH level. Different numbers of protons were added to these structures to explore on how proton influences the widening of the pore channel. Water were then added to these protein systems and modelled using TIP3P\(^5\) in order to resemble the aqueous environment. NAMD\(^3\) was used to perform minimization runs on these protein structures. CHARMM36\(^4\) force field acted as a topology file to determine the applied force on each atom. Energies were collected as a result of 1 million steps of minimization and then 1million steps of MD. Molecular dynamics was performed to find the equilibrium distribution of water molecules within the channels for all protein structures.