The EGR family of transcription factors is activated in cells exposed to growth factors. The overall structure of the family is highly conserved while the amino acid sequence can be quite diverse allowing for a wide array of DNA recognition sequences. Through homology modeling we have found we are able to reproduce the structure of the DNA binding domain of EGR proteins, which consists of three zinc fingers. We have also determined through molecular dynamic simulations that most side chains within the domain reach an equilibrium state. Furthermore, the three recognition residues in each zinc finger are found to have side chain conformations that are optimal for recognition. These studies help to show a possible mechanism for zinc finger recognition of DNA.