Empirical potentials, in both an all-atom form and in a simplified united-residue form, are used, together with global optimization procedures, to predict the three-dimensional structures of globular proteins from the amino acid sequence without using knowledge-based information in the global search of the multi-dimensional conformational space. The procedures used will be described, and the results of such computations in successive biannual blind tests [CASP - Critical Assessment of Protein Structure Prediction] will be presented. In addition, initial attempts to predict protein folding pathways will be described.