A protein can potentially assume an exceeding large number of conformations. Under physiological conditions, a protein usually folds properly and adopts the native structure with a well defined three dimensional conformation. Unlike the native protein, a denatured protein consists of a collection of conformational isomers that typically exist in a state of equilibrium. Conformational isomers of denatured proteins are rich in number and varied in shape. They represent an opulent resource of biological molecules that have remained untapped for their potential applications in the prevention, diagnosis and treatment of human diseases. A major obstacle in utilizing this untapped resource is that isomers of denatured proteins are notoriously heterogeneous. They are inherently difficult to isolate and characterize due to their instability and rapid inter-conversion. In order to exploit applications of diverse isomers of denatured proteins, methods that are able to generate significant concentration of desired isomers in purified and stable form are required. During the past years, our laboratory has developed an useful method for design, production and isolation of stabilized conformational isomers of denatured proteins. The application of this method in characterizing the protein stability, in elucidating the pathways of protein folding/unfolding, and in producing the isomers of disease-associated proteins will be presented.