of all polypeptides synthesized may be destroyed because they do not fold correctly. In some cases, the misfolding causes or contributes to the development of serious disease. Many conditions, including type-2 diabetes, Alzheimer's disease, Huntington's disease, and Parkinson's disease, arise from a common misfolding mechanism. In most cases, a soluble protein that is normally secreted from the cell is secreted in a misfolded state and converted into an insoluble extracellular amyloid fiber. The diseases are collectively referred to as amyloidoses.

Protein Denaturation: Protein structures have evolved to function in particular cellular environments. Conditions different from those in the cell can result in protein structural changes, large and small. A loss of 3-D structure sufficient to cause loss of function is called denaturation. The denatured state does not necessarily equate with complete unfolding of the protein and randomization of conformation. Under most conditions, denatured proteins exist in a set of partially folded states, which as yet are poorly understood. Most proteins can be denatured by heat, which has complex effects on the weak interactions in a protein (primarily hydrogen bonds). Proteins can also be denatured by extremes of pH, certain miscible organic solvents such as alcohol or acetone, certain solutes such as urea and guanidine hydrochloride, or by detergents. Each of these denaturing agents represents a relatively mild treatment in the sense that no covalent bonds in the polypeptide chain are broken. Organic solvents, urea, and detergents act primarily by disrupting the hydrophobic interactions; extremes of pH alter the net charge on the protein, causing electrostatic repulsion and the disruption of some hydrogen bonding.

Protein separation and Analysis: A pure preparation is essential before a protein's properties and activities can be determined. Classical methods for separating proteins take advantage of properties that vary from one protein to the next, including size, charge, and binding properties. Some of the common procedures used for the purification and analysis of proteins include Fractionation, Dialysis, Polyacrylamide gel electrophoresis (PAGE), Chromatography, Mass-spectrometry, NMR etc.