Abstract

The conformational changes occurring in proteins under the influence of various environmental factors are an important phenomenon, allowing for the exploration and understanding of many fundamental molecular processes taking place in living organisms. One such factor is the presence of various chemical compounds or macromolecules, which, when added to a solution containing a protein, affect its structure — including its secondary, tertiary, and even quaternary structure. An example of such a compound is the anionic surfactant sodium dodecyl sulfate (SDS), which induces conformational changes in proteins.

Sodium dodecyl sulfate influences both the secondary and tertiary structures of all five tested proteins: α-chymotrypsin, α-chymotrypsinogen, albumin, lysozyme, and α-lactalbumin. However, there is no single, universal pathway for these changes. It is evident that SDS affects protein conformational changes at millimolar concentrations, and these changes are visible both below and above the critical micelle concentration (CMC). Nevertheless, depending on the concentration value, the pathways of these changes differ, indicating that the proteins tested interact with both individual surfactant molecules and micelles. This, in turn, suggests that interactions with both micelles and monomeric SDS molecules play a significant role in protein conformational transitions.

The structure a protein adopts after binding to SDS may, but does not necessarily, represent its final stable conformation. The changes induced by SDS in the secondary and tertiary structures can proceed at different rates, and the measurement of various physical parameters — such as fluorescence or circular dichroism — reveals different aspects of these transitions, each linked to specific structural characteristics of the protein.

An important factor in studies of the protein–SDS system is the sample preparation procedure — specifically, whether the initial protein solution contained a certain amount of surfactant before reaching the final SDS concentration. It turns out that in the case of structural changes in the secondary and tertiary structures of lysozyme and albumin, these changes are independent of the procedure used to achieve the final SDS concentration in the solution. However, this is not the case for α-chymotrypsin and α-lactalbumin. For α-chymotrypsin, the procedure affects both secondary and tertiary structure changes, while for α-lactalbumin, it influences only the tertiary structure alterations.

Another crucial factor influencing structural changes in proteins exposed to SDS is the ionic strength of the solution. This is evident in both steady-state and kinetic measurements

involving circular dichroism and fluorescence. However, there is no single, universal pathway for these changes. Additionally, ionic strength affects the rate of this process as well as its sequential progression.

A particularly interesting phenomenon observed during studies of the α-chymotrypsin–SDS system is the fact that the contribution of fluorescence emitted by individual tryptophan residues to the total recorded protein fluorescence depends on the excitation wavelength. This is not because the fluorescence of tryptophans themselves depends on this excitation energy, but rather because the non-radiative energy dissipation pathways of the tryptophans occur with different probabilities.

In summary, the structural changes occurring in proteins under the influence of sodium dodecyl sulfate are an exceptionally interesting phenomenon, often yielding unpredictable results. The number of factors that can influence conformational changes in both secondary and tertiary structures is undoubtedly large and, to a great extent, depends on the specific protein being studied.