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Protein Secondary Structure

Protein secondary structure is an important consideration when studying protein folding, protein stability, or enzyme activity.

Circular Dichroism: A powerful tool used to monitor secondary structure is circular dichroism (CD), which is the differential absorbance of left and right circularly polarized light. Since proteins consist of chiral amino acids, they are CD active and exhibit distinct CD spectra that are sensitive to the protein's secondary structure. This spectrum can provide a qualitative snapshot of the protein structure or the secondary structure composition of a protein can be estimated from the far UV CD spectrum using a number of algorithms, several of which are made available in Olis [GlobalWorks](#) software.

Protein secondary structure can also be used to monitor protein folding and unfolding. An equilibrium study consists of collection of CD spectra as a function of increasing temperature or chemical denaturant. As the protein unfolds, the CD spectrum reflects this. Fitting data at a single wavelength or the full spectral scans during this denaturation progress provides thermodynamic information such as the melting temperature and the enthalpy of unfolding. Both these parameters provide important information about the stability of the protein under study.

The [DSM 17](#), [DSM 20](#), [DSM 1000](#), and the [Multiscan](#) support protein secondary structural studies. Accessories such as the [CD 250 Peltier cell holder](#) provide a convenient method for conducting these experiments.

Stopped Flow: The kinetics of protein folding and unfolding can be monitored by the use of a [stopped flow](#) accessory. Millisecond changes to protein structure can be studied by observing the CD signal at an informative wavelength during the course of a stopped flow reaction. [GlobalWorks](#) also supports the kinetic analysis of these kinetic traces.

Second Derivative Absorbance: A second, less common, method of protein secondary structure determination is that of second derivative absorbance spectra. This technique takes advantage of subtle changes in the UV absorbance spectra of proteins as they undergo folding and unfolding.

This technique is supported in the [Multiscan](#).

Links to client publications:

Download a PDF of client publications related to Protein Secondary Structure [here](#).