New perspectives in CD spectroscopy for the study of protein structure

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Circular dichroism spectroscopy is a widely used technique for the study of the secondary structure of proteins. However, previous algorithms analyzing the CD spectra provided insufficient reliability on β-sheet rich proteins and amyloid fibrils. We showed that the large spectral diversity of β-structures is a result of the parallel/antiparallel orientation and the twisting of the beta-sheets. We have developed a new method that takes into account the twist of the β-sheets for the accurate secondary structure estimation for a broad range of proteins. Moreover, the method is capable of predicting the protein fold. In the presentation, the use of protein CD spectroscopy will be overviewed from the basics to the applications including practical tips.

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