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Nanotechnologies — Assessment of protein secondary structure during an interaction with nanomaterials using ultraviolet circular dichroism

Nanotechnologies — Évaluation de la structure secondaire des protéines durant une interaction avec des nanomatériaux à l'aide du dichroïsme circulaire ultraviolet

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ISO copyright office
CP 401 • Ch. de Blandonnet 8
CH-1214 Vernier, Geneva
Phone: +41 22 749 01 11
Email: copyright@iso.org
Website: www.iso.org

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Foreword

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Introduction

Nano-objects and their aggregates and agglomerates (NOAA) are currently produced in large mass quantities globally and used in a variety of applications. However, there is concern about their interaction with biological systems, including proteins, which could lead to reversible or irreversible alterations in their secondary structure. The latter could affect the functionality and conformation of protein, which in turn might affect the overall bio-reactivity of the proteins. The monitoring of the occurrence of such alterations could thus provide important information on the interaction of NOAAs with biological systems.

The process of folding of polypeptides in biological media produces the secondary structure of proteins which determines their bioactivity. The important features of this structure include hydrogen bonds between the amine hydrogen and carbonyl oxygen atoms in the peptide backbone and disulfide bonds between two cysteine residues.

The protein secondary structure could be affected by exposing it to certain metallic ions and bioactive compounds. Furthermore, it is also influenced by different buffer ionic strength, pH values, and temperature[1]. Alterations in the functionality and conformation of proteins can be attributed to reorganization (so-called misfolding) and changes of the overall molecular dimension that accompany the folding process. Some diseases, such as amyotrophic lateral sclerosis (ALS), Alzheimer's and Parkinson's, are a consequence of misfolded proteins[2].

There are several standard techniques for determining the molecular structures/conformations and folding process of proteins and upon their interaction with NOAAs. These include high-field nuclear magnetic resonance (NMR), Fourier-transform infrared (FT-IR), Raman spectroscopy and ultraviolet circular dichroism (UV-CD) spectroscopies[3][4][5][6]. In addition, a novel technique synchrotron radiation circular dichroism (SRCD) spectroscopy is a sensitive method to provide information on protein secondary structures and folding[7].