SRCD/OCD at DISCO overview and highlights

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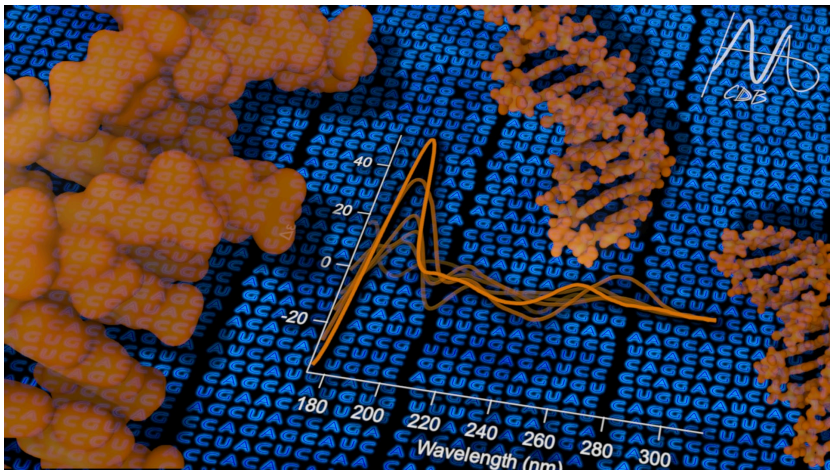

Synchrotron Radiation Circular Dichroism and Orientated Circular Dichorism spectroscopy at DISCO beamline (Synchrotron SOLEIL) measures the differential absorption of circular right and left polarized light in the Ultra-Violet range by chiral molecules, like nucleic acids and proteins for instance. In the spectral range between 7 and 4 eV, electronic transitions (n-π*, π -π* and charge transfer) are at the origin of the UV-light absorption. Characteristic absorption bands of circular (right or left) polarized UV light allow to distinguish different types of folding of these complex biological macromolecules. Their spatial arrangement correlates with the CD spectra and ultimately aids to determine the folding of proteins, nucleic acids and their complexes.
For the past two decades biologists have collected, deposited and screened CD spectra obtained from proteins (Ref. **PCDDB**) permitting them to successfully determine secondary structure content (alpha helices, beta sheets and random coils) for amyloids, membrane proteins and protein-protein complexes notably. Reference (Ref. **BeStSel**)

For Nucleic acids, scientists have published spectra dating back as far as the late 50's. Our first goal has been achieved now by systematically digitalizing nucleic acid CD spectra from the literature. In addition, data collected recently at the DISCO beamline at SOLEIL Synchrotron have been added including hundreds of Synchrotron Radiation Circular Dichroism (SRCD) spectra. All these spectra have now been deposited in a public repository (Ref. **NACDDB**), which archives and freely distributes the experimental data including metadata (sample conditions like pH, salinity and temperature), structural models and links to the corresponding references, extending the CD spectroscopy and structure information publicly accessible through the internet in contrast to time consuming literature research and visual comparison. It is our aim to create an algorithm allowing to determine the folding of nucleic acids (RNA and DNA) similar to BeStSel for proteins.

PCDDB: Ramalli SG et al. J Mol Biol 167441 (2022)

BeStSel: Micsonai A et al. Nucleic Acids Res. gkac345 (2022)

NACDDB: Cappannini A, et al. Nucleic Acids Res. gkac829 (2023)