Analysis on CD spectrometer

First and last name:

Phone number:

No of project and name of project leader:

Institution:

Name of the sample:

Signature:

Sample description

1. Proteins 2. DNA/RNA 3. Chiral molecules

Concetration of sample (proteins, DNA/RNA- in mol/L):

Buffer (in mol/L): Salts:

Interfering reagents (detergents and similar):

Parameters:

1. far UV spectra (200 µl ;1mg/ml) 2. near UV spectra (2 ml;1mg/ml)

Start point wavelegnth (nm): End point wavelength (nm):

Scan speed (od 20-100 nm/min):

Number of accumulation (1-5):

Spectra processing

Smoothing: 1. Means-Movement 2. Adaptive smoothing 3. Binomial

Smooting range (5-25):

Spectra expressed as: 1. Molar elipticity

2. Specif. elipticity

3. Molar elipticity of amino acid residue*

* Number of amino acids

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Notes for sample preparation:

Blank buffer required. Buufer with low amount of salts. All samples must be centrifuged and filtrated.