

CD

ADVANTAGES

Quick method for determining if a protein is folded

Quick method for determining the effects of pH and buffer conditions

Quick method for determining effects of binding partners

Recovery of your sample

Very small amount of protein is need – 20 μ M at 200 μ L for far-UV and 20 μ M at 800 μ L for near-UV

DISADVANTAGES

CD cannot, in general, say where the alpha helices or beta strands that are detected are located within the molecule.

CD cannot, in general, completely predict how many there are.

FLUORESCENCE

LIMITATIONS

What about proteins with TYR, TRP and PHE residues?

Trp fluorescence can be selectively excited at 295-305 nm. (to avoid excitation of Tyr)

What about proteins without TYR, TRP and PHE residues?

Organic molecules to “end-label” your proteins and have fluorescence characteristics

Local structural changes ONLY

ADVANTAGES

Recovery of your sample

Limited amount needed – 20mL and 1mL

Quick method