Università degli Studi del Sannio

*Dipartimento di Scienze e Tecnologie*

**ANNO ACCADEMICO 2017/2018**

**CORSO DI LAUREA MAGISTRALE**
**IN**
**SCIENZE E TECNOLOGIE GENETICHE**

**INSEGNAMENTO in SCIENZE E TECNOLOGIE OMICHE - PROTEOMICA E METABOLOMICA**
**(Modulo di Protreomica)**

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# PROGRAM

### INTRODUCTION TO PROTEOMICS
From proteins to proteomics

### ELECTROPHORETIC TECHNIQUES IN PROTEOMICS
Protocols for sample preparation
Mono and two dimensional electrophoresis
Image analysis of 2-DE maps
Differential gel electrophoresis (DIGE)

### MASS SPECTROMETRY
Introduction to mass spectrometry.
Ion sources used for protein and peptide analyses: MALDI and ESI ion sources
Mass analyzers: Quadrupole, TOF, Ion Trap mass analyzers. The hybrid instruments.
Tandem mass spectrometry: interpretation of fragmentation spectra
Mass spectrometry for the structural characterization of proteins: analysis of intact proteins; mass mapping approaches for the control of the primary structure of proteins; assignment of protein post-translational modifications.

## CHROMATOGRAPHIC TECHNIQUES IN PROTEOMICS

Liquid chromatography: ion exchange chromatography, gel permeation chromatography, affinity chromatography, reversed phase chromatography
Two dimensional chromatography and LC-MS instruments

## PROTEIN IDENTIFICATION

Analytical strategies for protein identification: peptide mass fingerprinting (PMF), Sequence Query and MS/MS Ion Search approaches

## QUANTITATIVE PROTEOMICS AND FUNCTIONAL PROTEOMICS

Analytical approaches in differential and quantitative proteomics: label-based (ICAT, SILAC, iTRAQ, 18O) and label-free (spectral counts) proteomic approaches
Targeted and un-targeted proteomics
Function proteomics