

THE COURSE

LEARNING OUTCOMES

- Sample treatment of complex proteomes
- Protein identification and protein quantification of complex proteomes
- Mass spectrometry-based diagnostic & prognostic
- Bioinformatics I: Protein identification and data normalization (MaxQuant & Perseus)
- Bioinformatics II: Cytoscape – pathways analysis
- Bioinformatics III: Differential Personalized Pathway Index (dPPi) & Total Protein Approach (TPA)

COURSE OUTLINE

Sample treatment & Protein identification

- Sample treatment and protein quantification
- Proteomic sample preparation: Filter Aided Sample Preparation (FASP)

Proteomics & Diagnosis and Prognosis

- Protein identification by Mass Spectrometry: MaxQuant
- Label-free quantification by MS: Total Protein Approach (TPA)
- Bioinformatics: MaxQuant, Perseus & Cytoscape (different datasets)
- Differential Personalized Pathway Index (dPPi) for diagnosis and prognosis