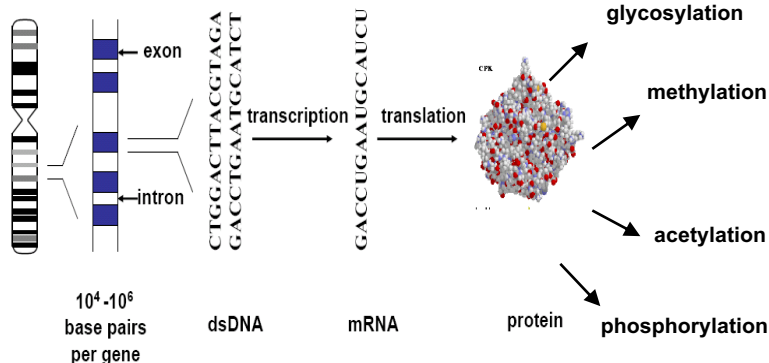


Overview:

- Introduce students to a variety of methods for identifying, quantifying and characterizing proteins by modern mass spectrometry.
- Using a cell culture, students will perform a total protein digestion for downstream reverse phase separation using nano ultra high pressure liquid chromatography and quantification with the Q Exactive High Field X mass spectrometer. CE-MS for Amino Acid Analysis is explored, along with strategies for Protein Quantification.



Lectures:

1. From Genomics to Proteomics
2. Basic Genetics & Intro to Mass Spectrometry
3. Quantitative Proteomics Overview
4. Relative Protein Quantification
5. Absolute Protein Quantification
6. -OMICS Research: Contemporary Directions

Labs:

1. Protein Extraction and Quantification, 1D-SDS-PAGE
2. Filter-Aided Sample Preparation (FASP) – Protein Digestion
3. Fe-NTA Phospho-peptide enrichment & Protein Hydrolysis
4. Linear Quadrupole Orbitrap (QE HFX) for Amino Acid Profiling using CE-MS
5. Bioinformatic Analysis of Data
6. SRM/MRM/PRM for Protein Quantification