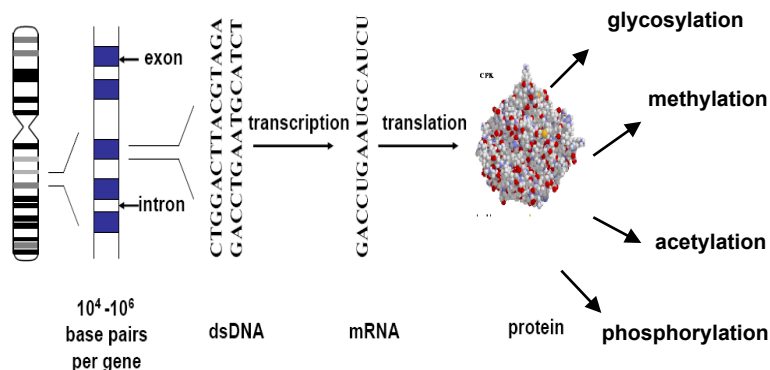


Overview:

- Introduce students to a variety of methods for identifying, quantifying, and characterizing proteins by mass spectrometry.
- Students will grow up yeast cultures, and a total protein digestion will be performed for downstream reverse phase separation using nano ultra high pressure liquid chromatography and quantification with the Q Exactive High Field. Absolute protein quantification will be accomplished using Triple Quad MS.



Lectures:

1. From Genomics to Proteomics
2. Yeast: Statistics, Proteome, ORFs
3. Tools of Proteomics: Enzymes, Separation, Mass Spectrometry
4. Protein Identification and Analysis of Protein Sequences
5. Bioinformatics: Relative and Absolute Quantification
6. Protein Modifications

Labs:

1. Culture Yeast, Protein Extraction and Quantification, 1D gels
2. Fe-NTA Phospho-peptide enrichment
3. Hands on experience with Linear Quadrupole Ion Trap Transform MS/MS and Triple Quadrupole MS/MS for Protein Identification and Quantification