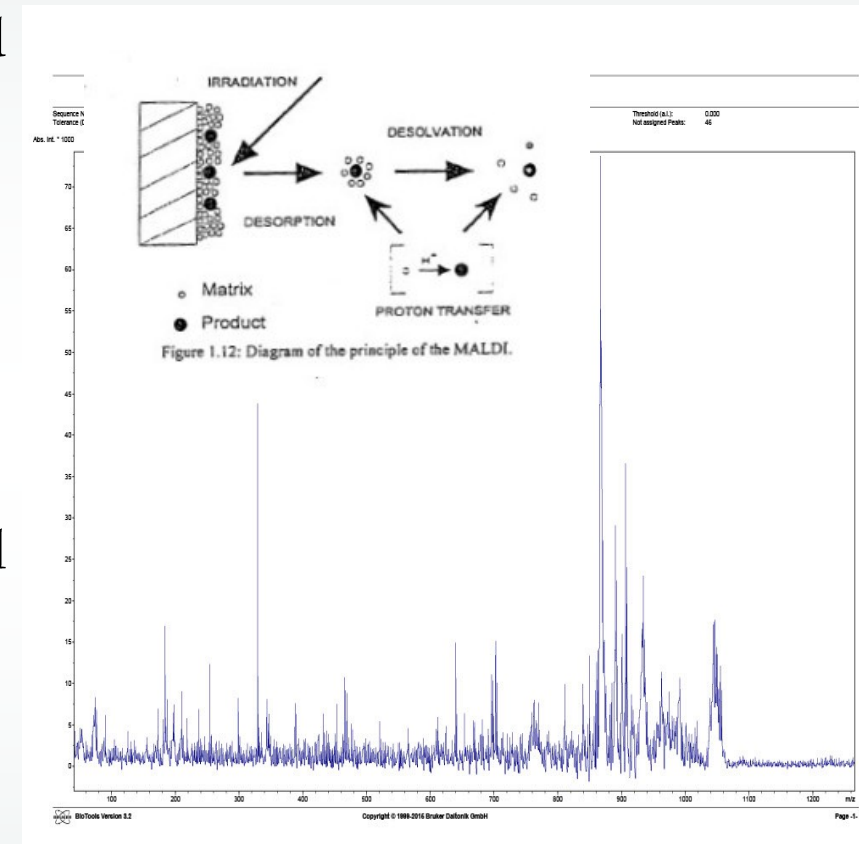


# PROTEOMICS IN A MASS SPECTROMETRY ERA:

## Identifying Proteins Using Matrix Assisted Laser Desorption Ionization Mass Spectrometry (MALDI)

### Chemistry Distinction Webinar

Proteins are at the center of major biological processes and biological mishaps, which often lead to serious diseases like Alzheimer's disease, Cystic Fibrosis, and a variety of cancers. One important aspect of this research is the ability to identify and sequence the proteins. Previous protein identification methods, such as Edman degradation, could not sequence larger peptides (more than 50 amino acids) efficiently and would potentially take days to complete. Modern mass spectrometry techniques, such as electrospray ionization (ESI) and matrix assisted laser desorption ionization (MALDI) have overcome these issues, allowing a more comprehensive study of proteins in a fraction of the time. By using MALDI with a time-of-flight time-of-flight mass spectrometer (MALDI-TOF/TOF) paired with the Mascot database software, the successful sequencing and identification of gel separated *Tetrahymena thermophila* (*T. thermophila*) proteins via tryptic digestion and extraction will be presented.

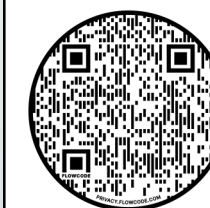


*Henry Wisniewski*

Henry is a Chemistry and Mathematics double major from Nashville, Tennessee with an interest in analytical/bioanalytical chemistry. Henry has previously worked in Professor Douglas Beussman's lab on the Human Scent Project, which involves the investigation of the connection between skin scent molecules and an individual's demographics. Henry has also worked for the Chemistry Department, being a Laboratory Teaching Assistant for the last three years. For the upcoming Fall Semester, Henry will begin pursuing a Ph.D. in chemistry at Rutgers University Newark.

**Wednesday, April 28**

**3:30-4:30 pm**



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