Agilent Ion-Trap Mass Spectrometer (HPLC-MS/MS)

Brief description:
Mass spectrometry is an important method used for the characterization of proteins. It is an analytical device that determines the molecular weight of chemical compounds, according to their mass-to-charge ratio (m/z). Tandem Mass Spectrometry (MSn) allows one to induce fragmentation and therefore analyze the mass of the fragment ions.

Proteins are being separated by electrophoresis or other method (such as size exclusion) and then subjected to enzymatically digestion (most often Trypsin). Subsequently these peptides are further separated by HPLC coupled to mass spectrometer. The results are analyzed via proteomics software to detriment the identity of the proteins in the samples, as well observation of basic post translational, modification.

Our instrument is best suited for peptide identification with mass range of 150kDa to 2100kDa.

Location:
Bldg. 100, room E4-230

Main contact:
Orr Sharpe
Bldg. 101 C4-191
Extension: 63388
sharpe@stanford.edu

Access:
Open for all VA appointed researchers and VA R&D approved projects, but the laboratory requires that users will provide peptides mix in either 96w format, or in tubes.

Cost to use:
None at this time.

Other information:
We recommend that research use pre-cast gels, and use HPLC grade reagent. Please contact Orr Sharpe with questions on how to digest the