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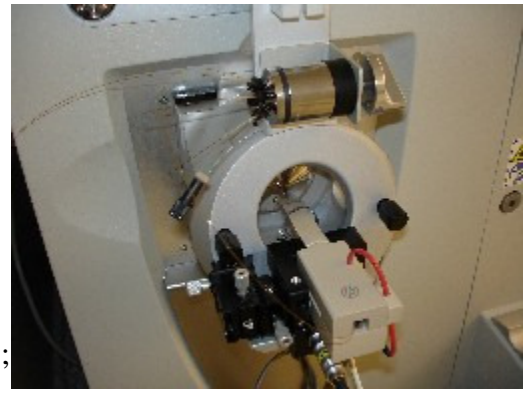
LTQ-FT (ThermoElectron)

The LTQ-FT instrument is a linear ion-trap/FTMS hybrid mass spectrometer. It is an extremely powerful instrument that is one of the highest-performance mass spectrometers in the world for proteomics research.

The combination of very fast MS/MS scanning in the linear ion-trap, high resolution and high mass accuracy measurements in the FTMS, and very high sensitivity, make this instrument ideal for analysis of complex protein digests for protein ID and characterization of post-translational modifications. This instrument provides ultimate sensitivity and confidence in protein ID, in which proteins can be identified from a Mascot database search with as few as one or two peptides identified from attomole-level of digest injected on column.

LTQ-FT Performance and Capabilities



- **Nano-LC/MS/MS**
  - splitless gradients as low as 20 nl/min;
    75um ID C18 column; typical run at 400nL/min; peak widths 3sec wide at half height
- **AP Maldi/MS/MS**
  - femtomole sensitivity for peptides; < 4000 MW limitation due to linear ion-trap
- > 500,000 resolution at m/z 400
- < 2ppm mass error with FTMS (external standard calibration)
- < 1ppm mass error with FTMS (internal standard calibration)
- **Attomole-range sensitivity for protein ID**
  - (e.g. 500 attomoles BSA digest injected on column yields 10 peptides identified with less than 2 ppm mass error)
  - (e.g. 200 attomoles BSA digest injected on column yields 8 peptides identified with less than 2ppm mass error)
- **MS/MS fragmentation techniques for peptide sequencing and structure elucidation:**
  - Electron-capture dissociation (ECD) in the FTMS
  - Infrared multiphoton dissociation (IRMPD) in the FTMS
  - Collision-induced dissociation (CID) in the linear ion-trap

- ECD for analysis of labile protein modifications (e.g. phosphorylation, GlcNAc)
- ECD for "Top-down" analysis of intact proteins (generally < 30k Da MW)
- Very fast MS/MS scanning for complex protein digests (e.g. "mudpit")
- **Resolution of 13-C and 34-S isotopes in peptides**
    - Demonstrate if unknown peptides contain cysteine or methionine (peptides <1000 MW)
- **Accurate MW measurement of intact proteins and other**
    - (e.g. <0.2 Da mass error for small proteins isotope-resolved; <3 Da for large proteins)
- **Accurate mass measurements for structure elucidation (<1ppm with int. std.)**