10.8 HIGH RESOLUTION REFLECTRON TIME-OF-FLIGHT MASS SPECTROMETER

The spectrometer consists of a broad high current (mA) ion source (Kauffmann type) that works on the principle of magnetron wherein the electrons are trapped in a specific volume within a steady magnetic field effecting multiple collision ionization of gaseous and/or low vapor pressure liquid/solid samples. The ions in the plasma within the volume are then extracted by applying opposite potentials and then channeled into the special ion optics to accelerate them perpendicularly into the drift space and subsequently to the reflectron through a symmetric lens system.

The reflectron has a gridless design. Ions are detected using a hybrid ion detector consisting of a combination of chevron with scintillator and PMT enabling the detection of very large mass ions, which produce very few secondary electrons. Ions up to certain masses can also be detected by a large cone channeltron positioned behind the reflectron and hence allowing the linear mode operation of the spectrometer.

The ionization volume is located at the center of the optics and is confined to within 2 mm³, from which the ions are accelerated. Because of the gridless design there are no transmission losses leading to enhancement of both sensitivity and dynamic range. This reflectron takes care of the KE differences of isomass ions and hence enables a higher resolution of the spectrometer. The machine also has the provision of coupling a quadrupole ion trap just by replacing the ion optics, in order to operate it in IT-TOF mode that is required for a low repetition rate measurements e.g. processes like associative collision, melting of clusters having large inherent interaction times.

TOF mass spectrometry is sensitive to femtomole amount of a sample. Apart from its use in basic research in nanoscience e.g. studies of molecular beam of atomic clusters, it can also be used for rapid sampling of mixtures of large masses like in petroleum industry and pharmaceutical industry and for fingerprinting of proteins.