Discovery and identification of biomarkers by the mean of Mass Spectrometry.

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Mass spectrometry is an analytical tool used for measuring the molecular mass of a sample. For large samples such as biomolecules, molecular masses can be measured to within an accuracy of 0.01% of the total molecular mass of the sample i.e. within a 4 Daltons (Da) error for a sample of 40,000 Da. This is sufficient to allow minor mass changes to be detected, e.g. the substitution of one amino acid for another, or a post-translational modification. For small organic molecules the molecular mass can be measured to within an accuracy of 5 ppm or less, which is often sufficient to confirm the molecular formula of a compound, and is also a standard requirement for publication in a chemical journal.

Also structural information can be generated using certain types of mass spectrometers, usually those with multiple analyzers which are known as tandem mass spectrometers. This is achieved by fragmenting the sample inside the instrument and analyzing the products generated. This procedure is useful for the structural elucidation of organic compounds and for peptide or oligonucleotide sequencing.

Mass spectrometers can be divided into three fundamental parts, namely the ionization source, the analyzer, and the detector. The analyzer and detector of the mass spectrometer, and often the ionization source too, are maintained under high vacuum to give the ions a reasonable chance of traveling from one end of the instrument to the other without any hindrance from air molecules. The entire operation of the mass spectrometer, and often the sample introduction process also, is under complete data system control on modern mass spectrometers.
The detector monitors the ion current, amplifies it and the signal is then transmitted to the data system where it is recorded in the form of mass spectra. The m/z values of the ions are plotted against their intensities to show the number of components in the sample, the molecular mass of each component, and the relative abundance of the various components in the sample.

The aim of my internship during my doctorate studies, is learning to use mass spectrometry instruments, in combination with classical protein methods discovering and sorting (like 2D-E and chromatography) to identify known and unknown biological markers in clinical and research fields, like looking for disease-related biomarkers in human samples like urine, blood, sweat, tears, for an early identification of a disease process, or the effectiveness of purification methods in clinical treatments like dialysis, or for any other purpose that can be developed during my studies.