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Mass Spectrometry & Purification Techniques

Perspective

Brief Note on Mass Spectrometer

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DESCRIPTION

The mass-to-charge ratio of charged particles is measured by using a Mass Spectrometer (MS). It can be used to determine the number of particles as well as the basic chemical structures of molecules such as peptides and other chemical compounds. Mass spectrometry, on the other hand, is a strong analytical tool for quantifying known materials, identifying novel compounds within a sample, and elucidating the structure and chemical characteristics of various molecules. The entire procedure entails converting the material into gaseous ions, which are subsequently characterized by their mass to charge ratios (m/z) and relative abundances, with or without fragmentation.

Principle of mass spectrometer

A mass spectrometer produces several ions from the sample under investigation, separates them based on their mass-to-charge ratio (m/z), and then records the relative abundance of each ion type. The creation of gas phase ions of the compound, primarily by electron ionization, is the first step in mass spectrometric analysis of substances. The fragmentation of this molecular ion occurs. After that, each primary product ion formed from the molecular ion fragments, and so forth. In the mass spectrometer, the ions are separated by their mass-to-charge ratio and detected in proportion to their abundance. As a result, a molecule's mass spectrum is generated. It plots the ion abundance against the mass-to-charge ratio to show the outcome. Ions are the building blocks of life information about the structure and nature of their precursor molecule. The molecular ion, if present, appears at the highest m/z value in a pure compound's spectrum (followed by ions carrying heavier isotopes) and indicates the compound's molecular mass.

Types of mass spectrometer

Matrix-assisted laser desorption/ionization-time of flight (MALDI-TOF): In the case of MALDI-TOF the molecule which fly through the time-of-flight tube or "drift" section to the detector is used to distinguish molecules in MALDI-TOF. The molecules are separated by their journey through the drift area.

MALDI-TOF mass spectrometer, which is having a considerable impact on clinical microbiology, may produce results and positive identifications astonishingly very fast. It has a traditional methods for identifying bacteria in the clinical laboratory are being replaced by matrix-assisted laser desorption-ionization time of flight mass spectrometer (MALDI-TOF MS). Many of the obstacles of recognizing bacteria and fungi are overcome with this relatively easy procedure. MALDI-TOF MS has become a crucial tool for clinical microbiology laboratories over the last decade. The quickness with which a person can be identified. This technology is characterized by accuracy, cheap cost, and waste minimization. It helps in analyzing Antibiotic Susceptibility Testing (AST) and subspecies also has a lot of promise.

Inductively coupled plasma mass spectrometer (ICP-MS): Although quadrupole mass analyzers were initially used, the majority of ICP-MS systems were now used as ToF mass analyzers. The main advantage here is that the entire mass spectrum is generated much faster and with much higher mass resolution than in quadrupole-based systems. A few specialized systems employ magnetic sector instruments, which are frequently used in conjunction with multi collector detection systems for high precision isotope ratio measurements. Furthermore, by combining the technique with a laser beam to form laser ablation (LA)-ICP-MS, the technique can be adapted to generate images based on the mass analysis of the ablated material. Because this is a destructive technique and the material can only be analyzed once, the ability to mine and process the ToF data retrospectively is a significant advantage. ToF imaging stores the entire mass spectrum in each (x,y) pixel location of the resulting image, allowing new ion images to be easily generated post-analysis.

Direct analysis in real time mass spectrometer (DART-MS): DART-MS also employs a ToF mass analyzer for the reasons stated previously. However, it is an ambient pressure technique, which is critical to pay attention to the interface between the source (ambient) and the mass spectrometer (vacuum). Analyze ions are directed to the mass analyzer *via* a pair of orifices with a slight potential difference between them in the original design.

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The two orifices are staggered in order to trap neutral contamination and protect the high-vacuum region. Ions are guided to the second orifice *via* an intermediate cylindrical electrode, but neutral molecules follow a straight path and are thus prevented from entering the mass analyzer and are removed by a vacuum pump.