Virtual Models of Mass Spectrometers as Teaching Tools for Graduate Students.

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Mass spectrometry is an analytical powerful technique for identifying unknowns, quantitating knowns and discovering chemicals properties and molecular structures. The mass spectrometry concept is very simple: The sample becomes an ion through an ionization method. Ions are selected by mass to charge ratio (m/z) based upon the motion in a magnetic field and each one is register under a spectrum. To access the basic of these techniques by using appropriate literature, videos, virtual models and simulations for this machines behavior is today's exclusiveness for researchers through manufacturer handbooks. This reality becomes the science popularization and knowledge diffusion about proteomic analysis something plenty arduous for the portion or part of graduate students. The work objectives were making a multimedia school-book showing biochemical techniques for proteomic analysis using mass spectrometry. The material was make with specific software for building 3D models and animation of different ionizations methods: Electron Ionization (EI), Electro spray Ionization (ESI), Atmospheric Pressure Chemical Ionization (APCI), Matrix Assisted Laser Desorption/Ionization (MALD) and mass analyzers: *Time of Flight* (TOF), Quadrupole and Ion Trap.

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Mass analyzer

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