

BUSTA 1

- 1) Descrivere le principali operazioni di manutenzione ordinaria di spettrometri di massa ad alta risoluzione.
- 2) Descrivere i parametri più importanti da impostare nei motori di ricerca per analisi proteomiche qualitative.
- 3) Descrivere i principali passaggi di estrazione di peptidi endogeni dal latte.

Please, read and translate...

Mass spectrometry is a central analytical technique for protein research and for the study of biomolecules in general. Driven by the need to identify, characterize, and quantify proteins at ever increasing sensitivity and in ever more complex samples, a wide range of new mass spectrometry-based analytical platforms and experimental strategies have emerged. Here we review recent advances in mass spectrometry instrumentation in the context of current and emerging research strategies in protein science.

BUSTA 2

- 1) Descrivere le principali operazioni di manutenzione ordinaria di cromatografi a nano-flussi accoppiati a spettrometri di massa.
- 2) Descrivere i parametri più importanti da impostare nei motori di ricerca per analisi proteomiche quantitative.
- 3) Descrivere i principali passaggi di estrazione di peptidi endogeni da prodotti caseari freschi.

Please, read and translate...

Recent successes illustrate the role of mass spectrometry-based proteomics as an indispensable tool for molecular and cellular biology and for the emerging field of systems biology. These include the study of protein-protein interactions via affinity-based isolations on a small and proteome-wide scale, the mapping of numerous organelles, the concurrent description of the malaria parasite genome and proteome, and the generation of quantitative protein profiles from diverse species. The ability of mass spectrometry to identify and, increasingly, to precisely quantify thousands of proteins from complex samples can be expected to impact broadly on biology and medicine.