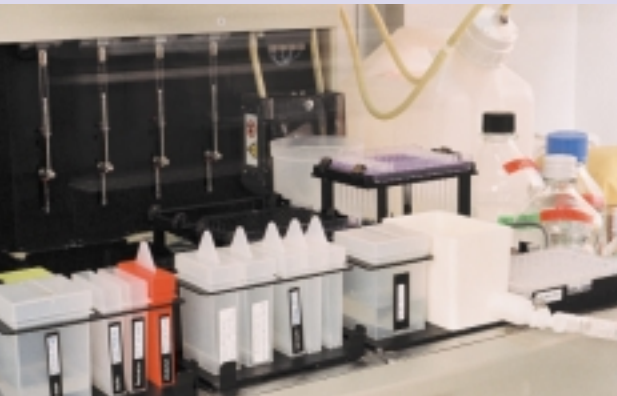


Proteomics technological platform

A CEA laboratory was established to set up in the same place all the up-to-date technologies for protein microanalyses. This laboratory has two main objectives

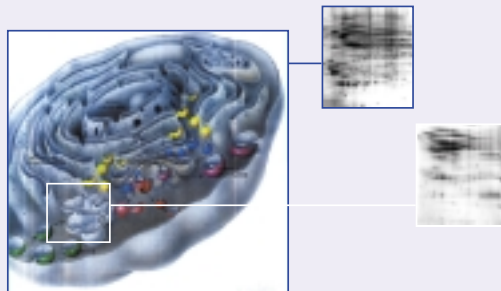
- **To develop the most performant and complete methodological platform to analyze proteins** while using the latest technologies for the identification of proteins, such as the coupling of 2D-PAGE with mass spectrometric analysis of proteins. With MALDI-TOF mass spectrometry, peptide mass maps can be constructed. They allow the identification of proteins present in protein databases. When proteins are absent from protein databases, MS/MS sequencing is essential for genome mining.



- **To carry out research program in cell biology.** Lysosomes and phago-lysosomes are analyzed. Using proteomic approaches. Our main objectives are : 1) to identify new lysosomal proteins and to characterize their function, and 2) to identify the molecular determinants and understand the fine mechanisms governing phagosome function in macrophages.

Equipment / Technology

- One mass spectrometer of the MALDI-TOF type;
- Two Q-TOF tandem mass spectrometers coupled to nano-flow liquid chromatography;
- One robot for automated sample preparation.



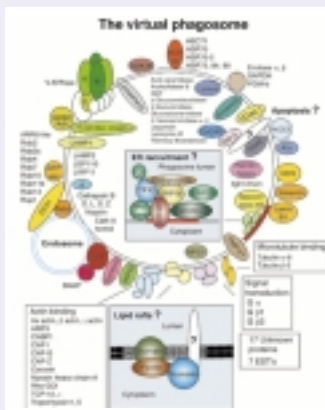
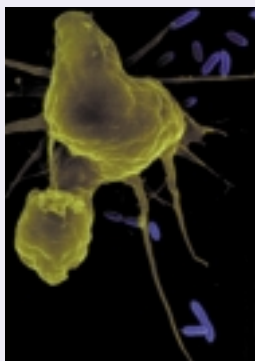
R&D set of themes

The strategy is:

- to combine newly developed bioinformatics programs with the extensive use of nanoLC-MS/MS for analysis of complex protein mixture.
- to develop procedures dedicated for quantitative analysis of hydrophobic proteins, since no methods are presently available for this.

Bioinformatics. To date, mass spectrometric protein identification relies on protein sequence and expressed sequence tag (EST) databases. In collaboration with INRIA and Genome Express, new bioinformatic tools dedicated to proteomic studies are developed that will make it possible to mine mammalian genomes.

NanoLC-MS/MS. In order to identify more rapidly all the protein components of a complex sample, a strategy of mixture analysis is implemented. One advantage of this approach is the simplicity of establishing it as a high-throughput method by incorporating autosampler in front of the nanoLC system.



Features

Number of people in 2002 : 8 (Proteomic platform and methodological developments)

Location: Grenoble (CEA-Grenoble)



Partners:

CEA, INSERM, Génopole Rhone Alpes, INRIA, CNRS, Genome Express, Génoplante

Contact:

Jérôme GARIN (CEA Grenoble)