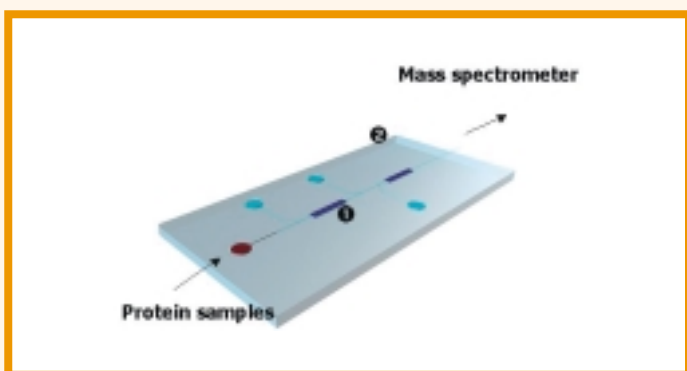


ProteoLab and BioChipLab: Integrated microsystems for preparation of protein sample for mass spectrometry identification

Aim

ProteoLab and BioChipLab are innovative microsystem interfaces designed to increase sensitivity of protein identification by mass spectrometry. They offer 3 major advantages

- higher yields and faster kinetics of protein digestion
- low sample volumes
- direct interfacing with the mass spectrometer with no dead volumes or sample loss



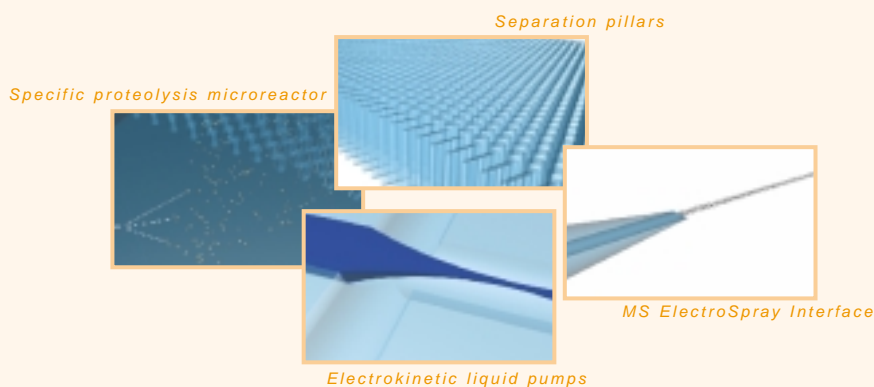
Principle

Sample preparation is carried out in 2 steps:

- 1 Proteins (isolated from a 2D gel separation) are digested by trypsin (ie cut into smaller peptides), grafted to the surface of the microreactor.
- 2 Peptides are separated by on chip chromatography and sent to the mass spectrometer for identification.

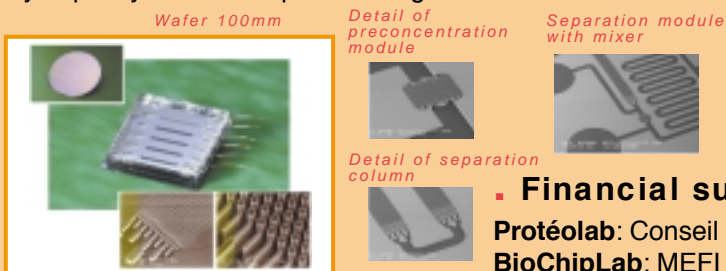
A modular architecture

The proteolysis and separation modules are designed for optimum fluid flow profiles and maximum surface to volume ratios. Fluid transport is controlled by electro-osmotic flow. Interface with the mass spectrometer is achieved by electrospray injection.



First prototypes

First prototypes were microfabricated by the CEA/Leti on silicon. The Trypsin protease was immobilized on the pillars of the first module. Sample injection and recovery is done by capillary inlet/outlet ports through the elastomer cover.



Wafer 100mm

Detail of preconcentration module

Separation module with mixer

Detail of separation column

Pillar diameter: 15 μ

Partners

CEA: Microtechnology and Electrokinetics
Biological and Chemical Integration
Research Models and Biological Validation

USTL and CNRS:
Microtechnology and Electro spray Output Interface In situ Polymer Chemistry

Osmooze: Droplet Electrotransport

Sanofi-Synthélabo: Industrial Models and Validation

Financial support

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BioChipLab: MEFI - Ministère de l'Economie, des Finances et de l'Industrie.

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