



## Proteomics Analysis

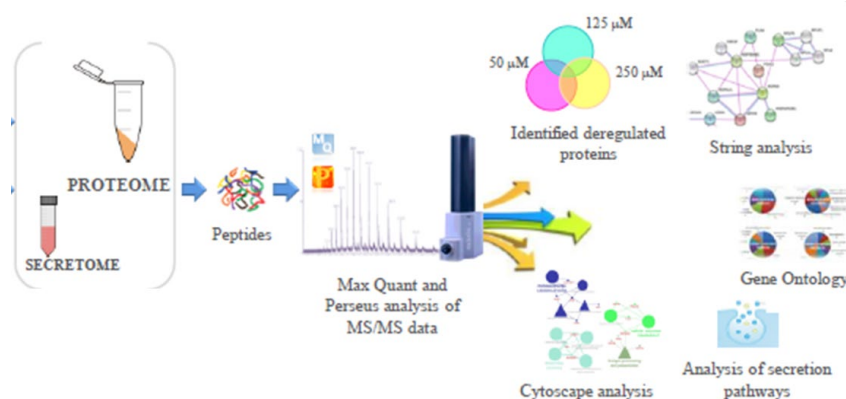
LC – MS (/MS) analysis is the method of choice for proteomics. We use high resolution mass spectrometers to identify and relatively quantify thousands of proteins and their modification(s) and then perform statistic and bioinformatic analyses to determine differentially regulated proteins and pathways.

### BACKGROUND

The host proteome reflects critical cellular pathways involved in recombinant protein production including protein synthesis, the secretory pathway, protein degradation pathways, metabolic and cellular stress pathways. Its analysis can thus support host development, expression system choice and optimisation and fermentation condition optimisation.

### TECHNOLOGY

We routinely perform 4D proteomics experiments by combining nano-HPLC, gas phase ion mobility and high-resolution tandem mass spectrometry data dependent or independent parallel accumulation–serial fragmentation. Proteins are identified by database search, quantified across groups (e.g. genotype and/or condition) and annotated employing public databases and bioinformatic tools. Our expertise has already been proven many times in external projects.



### OFFER

We professionally assist you with proteomics analysis taking CDA/NDA for granted. IP developed in such a project would fully belong to our investor/industrial partner.

### EXPERT:

Ruth Birner-Gruenberger, Ph.D.

### AVAILABLE FOR:

- Investments
- Joint Research Projects
- Contract Research

### DEVELOPMENT STATUS:

Technology Readiness Level 6  
(Demonstrated in relevant environment)

### IPR:

Can be generated for our industrial partners / investors

### KEYWORDS:

LC-MS/MS analysis  
Proteomics  
Posttranslational protein modifications

### CONTACT

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