

# PROTEOMICS IN BIOMEDICAL RESEARCH

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|-----------------------|-------------------------------------------------------|
| <b>Vakcode:</b>       | M_CPROTBI09                                           |
| <b>Periode:</b>       | Ac. Jaar (september), Periode 3+4+5 (jan/ feb. 2018)  |
| <b>Credits:</b>       | 3.0                                                   |
| <b>Voertaal:</b>      | Engels                                                |
| <b>Faculteit:</b>     | V Umc                                                 |
| <b>Coördinator:</b>   | prof. dr. C.R. Jimenez                                |
| <b>Examinator:</b>    | prof. dr. C.R. Jimenez                                |
| <b>Lesmethode(n):</b> | Lectures, Laboratory project, Literature presentation |
| <b>Niveau:</b>        | 500                                                   |

## GOAL COURSE

Function and structure of cells depend on the composition of proteins. During pathological conditions the expression of proteins is altered leading to impaired function/structure of cells. Apart from changes in expression level, post-translational protein changes occur as a result of altered signaling pathways. The large-scale analysis of proteins and their quantitative changes in health and disease, a research field called proteomics, may provide candidate biomarkers and targets for therapeutic interventions.

This proteomics course consists of one week of theory ("hoorcollege" and literature study) and one week of practice in the lab. Together this will provide a solid basis for understanding of what proteomics is about, how its central technique, mass spectrometry, can be used for global protein identification and quantification, and what biomedical/clinical questions can be answered using appropriate experimental design. In the second week, students will get hands-on experience with a real proteomics experiment and the generated data will be used to illustrate what

bioinformatics analyses can be done to enable biological insight of large scale data.

## **COURSE CONTENT**

- Insight into the nuts and bolts of modern day biomedical proteome research by mass spectrometry-based proteomics
- The theory behind protein identification and quantification by tandem mass spectrometry and database searching
- Sample preparation for mass spectrometry after gel electrophoresis
- Data mining: placing large scale protein expression data in a biological context by gene ontology mining and protein network analysis

## **LITERATURE**

Syllabus including relevant articles

## **HOW TO SIGN UP**

Students can register for this course and examinations via [vunet.vu.nl](http://vunet.vu.nl) (under My study, register for courses and exams). The general VU registration rules apply. Information on registration deadlines can be found in VUnet. Please note that the general VU rules are strict, both for booking of the classes and (resit-)exams.

## **OTHER INFORMATION**

Minimum number of participants: 5, maximum: 12

For optimal participation, basic knowledge of molecular and cellular biology is needed.

Contact:

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