



## COURSE DESCRIPTION CARD - SYLLABUS

Course name

Proteomics [S1Bioinf1>PROT]

### Course

Field of study

Bioinformatics

Year/Semester

3/5

Area of study (specialization)

–

Profile of study

general academic

Level of study

first-cycle

Course offered in

Polish

Form of study

full-time

Requirements

compulsory

### Number of hours

Lecture

0

Laboratory classes

0

Other (e.g. online)

0

Tutorials

30

Projects/seminars

0

### Number of credit points

2,00

### Coordinators

Łukasz Marczak

lukasz.marczak@put.poznan.pl

### Lecturers

### Prerequisites

A student starting this course should have basic knowledge about the role of proteins in organisms. She/he should have the ability of solving basic problems related to vacuum and physics of ions.

### Course objective

1. Passing basic knowledge about qualitative (identification) and quantitative analysis of proteins and possibilities of protein profiling. 2. Introduction to physicochemical methods applied for protein separation and identification – mass spectrometry. 3. Explication and learning basic methods of correlation data from protein level with data obtained on other molecular levels, for example: transcriptome, metabolome. 4. Awareness of necessity for utilization bioinformatics and statistical methods for interpretation data obtained from mass spectrometric analyses. 5. Practical demonstration of mass spectrometry laboratory and proteomic analysis of biological material.

### Course-related learning outcomes

Knowledge:

Upon completion of the course the student:

- understands basic biological processes related to proteins, interprets biological phenomenon on the

basis of experimental data and mathematical methods,

- knows structures and properties of different kinds of biopolymers and their components,
- knows basic biochemical metabolic pathways,
- knows selected methods and techniques used in research on proteins, including methods utilizing high-throughput technologies,
- knows approaches to structural analysis of biopolymers.

Skills:

Upon completion of the course the student:

- can integrate information from proteome and metabolome level, is able to conclude about interactions between proteome and metabolome,
- makes simple laboratory experiments and measurements concerning techniques of proteomic and metabolomic analysis, is able to interpret their results,
- applies analytical methods for qualitative and quantitative analysis of proteins, is able to evaluate their usefulness,
- sees systemic and other than technical aspects of realized bioinformatic tasks.

Social competences:

Upon completion of the course the student:

- understands necessity of learning during whole life time and lifting her/his competences,
- can act within a group, taking various roles.

### Methods for verifying learning outcomes and assessment criteria

Learning outcomes presented above are verified as follows:

Learning outcomes presented above are verified as follows:

Evaluation of gained knowledge and skills connected to performing and interpretation of mass spectral data and evaluation of developed protein electrophoretograms. Verification of the knowledge will be realized on the basis of a test; the test will be done after realization of the program directed to rules of mass spectra registration. Evaluation of oral answers to questions formulated during tutorials.

Knowledge of students after the course will be evaluated on the basis of a final test. Juxtaposition of the notes obtained during the course will be given as the weighted average: participation in discussion – 20%, result of the partial test – 25%, result of the final test – 55%.

### Programme content

1. Mass spectrometric techniques applied to analysis of biopolymers (peptides, proteins, nucleic acids, oligosugars) in biological material (6 hours):

- Ionization methods
- Hyphenation of mass spectrometric instruments with chromatographic apparatus
- Tandem mass spectrometry

2. Application of desorption methods of ionization (ESI, APCI, MALDI) utilized with tandem mass spectrometric analysis (7 hours):

- Bottom-up proteomics
- Top-down proteomics
- Shotgun proteomics
- Protein quantitative analysis with mass spectrometric methods.

3. Examples of practical applications of mass spectrometric techniques in projects directed to identification and estimation of role and function of natural products and biopolymers. Utilization of separation techniques (liquid and gas chromatography hyphenated to mass spectrometers) for analysis of complicated mixture originating from biological material.

Additionally in the course, practical exercises in mass spectrometric laboratory will take place, directed to performance of mass spectra of proteins and interpretation of registered spectra.

### Course topics

none

### Teaching methods

Tutorials: multimedia presentation, practical exercises in mass spectrometry laboratory, teamwork,

demonstrations.

## Bibliography

### Basic

1. Spektrometria mas – podręcznik dla chemików i biochemików, R.A.W. Johnstone i M.E. Rose, PWN 2001.
2. Spektrometria mas, E. De Hoffmann, J. Charette, V. Stroobant, Wydawnictwo Naukowo Techniczne 1998.
3. Spektrometria mas, P. Suder, J. Silberring red., Wydawnictwo Uniwersytetu Jagiellońskiego, 2006.
4. Proteomika, J.Silberring red., Wydawnictwo Uniwersytetu Jagiellońskiego, 2008.
5. Proteomika i metabolomika, J. Silberring, A. Drabik, A. Kraj, Wydawnictwa Uniwersytetu Warszawskiego 2011.

### Additional

1. Handbook of Proteomic Methods, P.M. Conn Ed., Humana Press 2003.
2. Introduction to mass spectrometry, 4th Edition, J.T Watson i O.D. Sparkman, Wiley 2008.

## Breakdown of average student's workload

	Hours	ECTS
Total workload	50	2,00
Classes requiring direct contact with the teacher	30	1,50
Student's own work (literature studies, preparation for laboratory classes/ tutorials, preparation for tests/exam, project preparation)	20	0,50