Module Number	Title:
2b	**High-Throughput Analysis: Genomics and Proteomics**

Module type: compulsory elective	Language: English	Group Size: 8 students

Study semester: 1	Availability: Each winter semester	Duration: 1 semester

Workload: 180 hrs	Credits: 6 CP	Contact time: 45 hrs	Independent Study: 135 hrs

1	**Courses**
	   a) Lecture: 1 PPW
	   b) Practical course: 3 PPW
	   c) Seminar: 1 PPW

2	**Intended Learning Outcomes** This module consists of a genomics and a proteomics part. Upon completion of the genomics part, the students will be able to describe the various gene regulation mechanisms on the DNA and RNA level and all necessary analytical tools to analyse genes, genomes, and gene expression. The students will be able to perform basic DNA and RNA analyses and they will be capable to describe and explain genome-wide, high-throughput DNA and RNA analyses in order to detect genomic variations and changes in gene expression. After completion of the proteomics part, the students will be able to describe and to apply state-of-the-art proteomic approach facilitating protein mass spectrometry (MS) and will be capable to describe the function of MS. They will be able to describe and apply data analysis for protein identification and quantification. The students will be able to discuss critically the obtained results and present basic aspects of genomics and proteomics in an oral presentation.

3	**Content**
	The lecture about genomics will cover basic aspects of eukaryotic gene expression and regulation. The theoretical background of PCR, classical Sanger sequencing, DNA microarray analysis, and next generation DNA and RNA Seq analyses will be described. The students will discuss the obtained results in a seminar.
	The practical course will include:
	   - Isolation and purification of DNA and RNA
	   - Quantitative and qualitative nucleic acid measurements
	   - PCR
	   - DNA Sanger sequencing (detection of genetic variations)
	   - DNA microarray / NGS sequencing analyses (changes in gene expression)
	
	In the practical course about proteomics the students will perform all steps for protein identification and quantification comprising:
	   - Sample preparation (lysis, homogenisation, digestion etc.)
	   - Peptide separation by UPLC
	   - Peptide analysis using LC-ESI-MS/MS
	   - Protein identification using data base searches
	   - Protein quantification
	
	In the theoretical part the students will get insight into the set-up and function of mass spectrometers and the analysis of quantitative mass spectrometric data.

4	**Teaching methods** Combination of lecture, hands-on practical course and seminar
5	**Prerequisites** **Formal:** Proficiency in English level B2 of Common European Framework of Reference for Languages (CEFR) **With regards to content:**

6	**Examination types** Oral presentation
7	**Requirements for award of credit points** Regular and active participation in the practical course; written summary of the practical course; passing the final examination.
8	**Module applicability (in other study courses)** Master Biology
9	**Assessment** The mark given will contribute to the final grade in proper relation to its credits.
10	**<u>Module convenor</u> and main lecturers** <u>Prof. Dr. Karl Köhrer</u>, Prof. Dr. Kai Stühler, Dr. Gereon Poschmann, Dr. Nina Overbeck, Dr. Patrick Petzsch
11	**Further information** The regular participation in the lecture is strongly recommended. The content of the lectures is a prerequisite for the practical.