BB2250 Applied Gene Technology 6.0 credits

Tillämpad genteknologi

This is a translation of the Swedish, legally binding, course syllabus.

If the course is discontinued, students may request to be examined during the following two academic years

Establishment

Course syllabus for BB2250 valid from Autumn 2007

Grading scale

A, B, C, D, E, FX, F

Education cycle

Second cycle

Main field of study

Biotechnology

Specific prerequisites

Language of instruction

The language of instruction is specified in the course offering information in the course catalogue.

Intended learning outcomes

The course Applied Gene Technology aims to give detailed insight into the techniques and technological trends in the fields of genomics and transcriptomics, building up the necessary foundations for further research in association studies, population genetics, diagnostics, medicine and drug development. The course includes a short introduction to conventional assays used in molecular biotechnology, description of different methods for typing of genetic variations, a variety of techniques for multiplex amplification, advanced techniques and technological platforms for DNA sequencing and whole genome sequencing and different techniques for transcript and protein profiling.

In addition, the course involves a literature workshop of selected articles, which will be performed in groups. Each group presents one article and will oppose two other group's articles. This project aims to learn critical reading, interpretation and comparison of the most advanced techniques and platforms in the fields of whole genome sequencing, massive parallel genotyping and transcript profiling.

Following completion and passing the course the student should be able to describe:

- the objectives of genome projects and how genome sequencing and annotations are performed.
- conventional methods and platforms for discovery and typing of single nucleotide polymorphisms (SNPs).
- obstacles with multiplex PCR amplification.
- different techniques and platforms enabling multiplex PCR amplification.
- different techniques and platforms enabling whole genome SNP genotyping.
- conventional methods for DNA sequencing and also be able to understand limitations with these techniques
- most recent developed techniques and platforms for whole genome sequencing and future trends in the field.
- different microarray-based techniques for parallel analysis of gene expression and also be able to describe experimental design and difficulties with microarray-based approaches.
- alternative techniques and platforms for analysis of gene expression.
- techniques involved in proteomics.

In addition to be able to describe these techniques, the student should know the application area(s) of each specific approach and should have understanding for advantages and disadvantages of each technique and also be able to compare and discuss usefulness of the techniques in each field.

Course contents

The course is based on the knowledge and technologies in Molecular Biotechnologies and the present course aims to cover the recent advanced technologies in the fields of genomics, transcriptomics and proteomics followed by literature projects including report, presentation and opposition. A brief introduction to methods in functional genomics will be included.

Course literature

Distributed review articles.

Examination

- PRO1 - Project, 1.5 credits, grading scale: P, F
- TEN1 - Examination, 4.5 credits, grading scale: A, B, C, D, E, FX, F

Based on recommendation from KTH's coordinator for disabilities, the examiner will decide how to adapt an examination for students with documented disability.

The examiner may apply another examination format when re-examining individual students.

Other requirements for final grade

Written Exam (TEN1; 4.5 credits, grading scale A-F), literature study with report, presentation and opposition seminar (PRO1, 1.5 credits, grading scale Pass/Fail).

Ethical approach

- All members of a group are responsible for the group's work.
- In any assessment, every student shall honestly disclose any help received and sources used.
- In an oral assessment, every student shall be able to present and answer questions about the entire assignment and solution.