

Gene Technology and Molecular Diagnostics (I002522)

Course size *(nominal values; actual values may depend on programme)*

Credits 6.0

Study time 180 h

Course offerings and teaching methods in academic year 2024-2025

A (semester 1)	English	Gent	practical lecture seminar
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Lecturers in academic year 2024-2025

Kyndt, Tina	LA25	lecturer-in-charge
De Mey, Marjan	LA25	co-lecturer
Van Damme, Els	LA25	co-lecturer

Offered in the following programmes in 2024-2025

	crdts	offering
Bachelor of Science in Bioscience Engineering	6	A

Teaching languages

English

Keywords

Cloning techniques, expression vectors, cDNA- and genomic libraries, DNA-, RNA- and protein-analysis techniques, PCR applications, molecular markers, gene isolation, gene- and genome analysis

Position of the course

Molecular biotechnology is being used to specifically alter organisms and therefore the DNA sequence must first be cloned. On the other hand a variety of molecular techniques is being used to study living organisms or to identify individuals or specific characteristics. A plethora of molecular methods have been optimised and others are being developed constantly. This course will describe and discuss a variety of molecular techniques explaining the basic concepts but also following the latest trends.

Contents

Content

- I INTRODUCTION
 - I.1 Genome
 - I.2 Transcriptome
 - I.3 Gene expression
 - I.4 Basic techniques for DNA-analysis
 - I.5 Basic principles recombinant DNA
- II DNA HYBRIDISATION
 - II.1 General principles of hybridisation
 - II.2 What to use as probe?
 - II.3 Allele-specific probes for SNP detection
 - II.4 Array or chip technology
 - II.5 Labels and detection
- III PCR & Q-PCR
 - III.1 Basic principles PCR
 - III.2 Specificity, accuracy and contamination in the context of PCR
 - III.3 Technical variants of PCR
 - III.4 Non-PCR-based amplification methods
 - III.5 Semi-quantitative PCR, Q-PCR and droplet digital PCR (ddPCR)
 - III.6 Colony PCR

- III.7 PCR for diagnostics
- IV HIGH THROUGHPUT SEQUENCING
 - IV.1 NGS or 2nd generation sequencing: based on amplified single molecule sequencing
 - IV.2 Next Next generation Sequencing or Third generation sequencing: single molecule sequencing
 - IV.3 Comparing different sequencing methods
 - IV.4 Applications of high throughput sequencing
- V ANALYSING GENETIC VARIATION BY STUDYING DNA POLYMORPHISMS
 - V.1 MOLECULAR MARKERS AND POLYMORPHISMS
 - V.2 Protein markers
 - V.3 DNA markers
 - V.4 Typical target regions used for diagnostics
 - V.5 Applications of molecular marker techniques
- VI RECOMBINANT DNA
 - VI.1 Restriction enzymes
 - VI.2 Other enzymes: ligases, kinases and phosphatases, nucleases, polymerases,
 - VI.3 Ligation and transformation
 - VI.4 cDNA and cDNA libraries
 - VI.5 Genomic libraries
 - VI.6 Clone analysis
- VII DNA ASSEMBLY METHODS
 - VII.1 The challenge in DNA assembly
 - VII.2 The traditional multiple cloning site approach
 - VII.3 Modern DNA assembly methods based on restriction enzymes
 - VII.4 Modern DNA assembly methods based on homology
- VIII CLONING VECTORS AND THEIR APPLICATIONS
 - VIII.1 Basic vectors and vectors for special applications
 - VIII.2 Modern cloning techniques
 - VIII.3 Expression vectors for the production of proteins
 - VIII.4 Expression vectors for the production of metabolites
- IX ANALYSIS OF PROTEINS
 - IX.1 Extraction and purification of proteins
 - IX.2 Protein electrophoresis
 - IX.3 Detection and quantitative determination of proteins with the help of antibodies
 - IX.4 Yeast two-hybrid
 - IX.5 Tandem affinity purification
 - IX.6 In vitro transcription and translation systems
 - IX.7 Proteomics and mass spectrometry
- X GENOME EDITING
 - X.1 Genome editing using homology-directed recombination
 - X.2 Genome editing using CRISPR/Cas
- XI FUNCTIONAL GENETICS
 - XI.1 Libraries and cloning
 - XI.2 Picking up a gene based on sequence similarity
 - XI.3 Finding interesting genes based on expression pattern or protein characteristics
 - XI.4 Starting from an interesting mutant: forward genetics
 - XI.5 Genome sequences and their annotation
 - XI.6 Reverse genetics
 - XI.7 Analyses on protein level
- XII GENE EXPRESSION ANALYSES
 - XII.1 Run-on or Run-off analysis of RNA
 - XII.2 Steady state analyses: RNA-extraction
 - XII.3 Analyzing transcripts through hybridisation
 - XII.4 Transcriptome analysis through sequencing
 - XII.5 RT-qPCR
 - XII.6 Analyzing gene expression in an organism
 - XII.7 Reporter genes
 - XII.8 Protein analysis

Exercises:

- 1 PC-practicum
- 2 PCR, RT-PCR and Q-PCR, reporter genes

Initial competences

(Approved)

Gene Technology and Molecular Diagnostics builds on certain learning outcomes of course unit Biochemistry and Molecular Biology ; or the learning outcomes have been achieved differently

Final competences

- 1 to have knowledge on genome structure and genetic diversity at the molecular level
- 2 to utilise techniques for analysis of DNA, RNA and proteins with interpretation of the results
- 3 to have insight in genome structure, gene structure, gene expression and regulation of gene expression
- 4 to know the techniques for expression and inactivation of genes
- 5 to search and analyse DNA sequences in data bases, to search for data in other scientific data bases
- 6 to execute tasks on DNA and RNA analysis in the frame of a scientific problem
- 7 to be able to select the best analytical molecular technique for the analysis of a problem
- 8 to be able to recognise the most important elements on a DNA-vector and to understand the function of it
- 9 to work accurately in molecular lab experiments and to critically analyse the results
- 10 to be able to critically compare the advantages and disadvantages of different molecular analysis techniques
- 11 to know correct terminology in molecular genetics and recombinant DNA
- 12 to ethically reflect on opportunities and problems associated with DNA analysis
- 13 to be aware of possibilities of molecular techniques and the importance of communication to society
- 14 to have an idea about the possible job profiles for bio-engineers in cell and gene biotechnology
- 15 to be able to understand and compare the high throughput sequencing techniques
- 16 work in a team for experimental work and reporting

Conditions for credit contract

Access to this course unit via a credit contract is determined after successful competences assessment

Conditions for exam contract

This course unit cannot be taken via an exam contract

Teaching methods

Seminar, Lecture, Practical

Extra information on the teaching methods

The course notes can be bought at VLK. The slides are distributed for free via UFORA.

Study material

None

References

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Course content-related study coaching

Additional information or explanation can be obtained by personal contact or by email or the electronic learning platform and during the exercises.

Assessment moments

end-of-term and continuous assessment

Examination methods in case of periodic assessment during the first examination period

Oral assessment, Written assessment with open-ended questions

Examination methods in case of periodic assessment during the second examination period

Oral assessment, Written assessment with open-ended questions

Examination methods in case of permanent assessment

Participation, Assignment

Possibilities of retake in case of permanent assessment

examination during the second examination period is possible in modified form

Calculation of the examination mark

Theory: period aligned evaluation: 80%

Exercises: non-period aligned evaluation: 20%

Students who eschew period aligned and/or non-period aligned evaluations for this course unit

may be failed by the examiner.

Students that are legally absent for some practical exercises do not have to catch this up later, but can get some theoretical questions to be answered. Illegal absence to the practical exercises will lead to a total score (theorie+exercises) of maximum 9/20, regardless of the score for the theory.

If less than 9/20 is scored for one of the 3 parts (2 theory parts and 1 practical), one cannot pass this course anymore. If the total score would be more than 10/20, this score will be reduced to the highest non-pass score.