

Lecture

Principles of Epigenetics WS2022/2023

The lecture series comprises 9 lectures introducing into the basic mechanisms of epigenetics and the use of modern epigenomic methods in human biology and biomedicine. All lectures will be held live and streamed via MS Teams. The slides can be downloaded (password protected) from our homepage.

The lectures will be held jointly with ADVI course for the Biology Master students and is open for Students of Biotechnology, Biophysics and Bioinformatics.

The lecture series finishes with an examen at on 10th of January 2023, 8:30 - 10:00 am, buildg. A4.3, microscopy room.

A successful passing of this examen is obligatory for receiving credit points and to get a preference to participate in the second lecture/course series in SS 2023 "Analysis of functional genomics data".

Lecturers: Jörn Walter (JW), Konstantin Lepikhov (KL) Gilles Gasparoni (GG), Kathrin Kattler (KK)

Venue: Building A4.3, seminar room, ground floor. For presence the registration via staysio app is obligatory (3G rules). The lecture will be streamed via MS Teams. Please confirm via the excel list in the teams channel (MS-Teams code: Kycwk9v) if and how you would like to participate in person or online. Participation in the lecture room will require the wearing of a mask.

Part I

Lecture 1:

11.11. 2022 8:30 – 10:00

Introduction (JW)

- Definition of Epigenetics,
- Impact for developmental biology, cell biology, genetics, functional genomics and biomedical research.
- Short introduction into the various types of epigenetic modifications and their interrelation

Lecture 2:

14.11. 2022 8:30-10:00

Chromatin based epigenetic control I (JW)

- Principles of chromatin organisation: Nucleosomes, histones and histone variants.
- Chromatin and chromosomes, chromatin dynamics during cell replication & cell division.
- Chromosome folding and looping. Approaches to analyse chromatin structures and states „*in vivo*“.
- Introduction into chromatin modifications and their nomenclature.
- Introduction into the reactions of chromatin modifying enzymes,
- Concept of epigenetic reversibility and molecular function: introduction into writers (establishing enzymes), readers (binders) and erasers (demodifying enzymes).
- Model for the mechanisms of “epigenetic inheritance”,

Lecture 3:

15.11.2022 8:30 – 10:00

Chromatin based epigenetic control II (JW)

- Role and function of key histone modifications
- Methods to analyse histone modifications in chromatin (ChIP, IF, MassSpec),
- Histone modifications and gene regulation: classification of regulatory regions, link to silent “heterochromatin”.
- Interplay with RNAi and DNA-methylation,

Lecture 4:

16.11. 2022 8:30 – 10:00

Non-coding long and small RNAs in epigenetic control (JW)

- Basic mechanisms of RNA-interference: enzymes and reactions.
- Concept of transcriptional and posttranscriptional control.
- Definition of small RNA classes and their function.
- RNAi mediated control of chromatin/DNA- modifications
- The role of small RNAs in development and disease.
- Classes and functions of lncRNAs for epigenetic control in mammals.

Lecture 5:

17.11.2022 8:30 – 10:00

Mechanisms of epigenetic control during development (KL)

- Epigenetic control of development.
- Epigenetic programs of cell identity.
- Mechanisms of reprogramming in stem cells.
- Molecular control of X-chromosome inactivation.
Genomic imprinting as a principle of epigenetic inheritance.

Lecture 6:

21.11.2022 8:30–10:00

DNA-methylation and epigenetic control (KK)

- Evolution of DNA-methylation: from viral defense to gene regulation
- Introduction into DNA-methylation reactions: the general principles and diversities of DNA-base modifications
- Basic methods to measure DNA-methylation in DNA
- DNA-methylation in mammals: Concept of establishment, maintenance (inheritance) and erasure of DNA-methylation.
- Function of DNA-methylation in mammals: genome wide distribution, changes during development and disease impact on gene regulation and on the transcriptional control of transposable elements.
- in development and disease.

Lecture 7:

22.11.2022 08:30-10:00

Epigenetics and human diseases (JW)

- Interplay between genetic and epigenetic changes in human cancer.
- Epigenetic/genetic origin of Imprinting disorders.
- Epigenetic in Human clinical diagnostics: identification and use of biomarkers for biomedical research:

- The influence of environment on epigenetic control – effects on long and short term memory.
- Epigenetics and aging.
- Epigenetics and disease therapies.

Lecture 8:

23.11.2022 8:30–10:00

Epigenomics I (GG)

Sample preparation for epigenome analyses:

- Sample collection and preparation (isolation, fixation, sorting, tissues vs. cells, etc.),
- primary cells vs. cell culture

Principles and methods for genome wide DNA-methylation analyses

- Introduction into the bisulfite reaction
- Basic principles of array and sequencing based analyses
- (EPIC arrays, Whole genome bisulfite-Seq)

Lecture 9:

24.11.2022 8:30-10:00

Epigenomics II (KK)

Methods for genome wide Chromatin analyses

- Introduction into Immunoprecipitation (ChIP-seq) and ChIP-Seq analysis

Methods to analyse open chromatin states:

- ATAC-Seq, MNase-Seq, NOMe-Seq, DNaseI seq and data analysis

Methods to analyse nuclear chromatin:

- Introduction into 3D and 4D Nucleome methods (Hi-C, 4C, GAM, ...)

Test/Examen: January 10th, microscopy room, building A4.3, 8.30 to 10.00.

Lecture "Analysis of functional genomics data" SS 2023

Lecture I: **to be determined 16:30 - 18:00**

Epigenomics: Experimental protocols for DNA-methylome analysis (GG)

- EPIC array data,
- ii) WGBSeq and RRBSeq data.
- Hairpin-Bisulfite-Seq,
- iv) Methods to detect oxidative modifications (Ox-BS, fCAB, ...)
- v) „3rd“ generation pore sequencing (minion, ...)

Experimental protocols for chromatin analysis:

- ChIP seq data
- ii) Open chromatin (ATAC-Seq, MNase-Seq, NOMe-Seq, DNaseI seq)
- Hi-C /GAM data,

Protocols and perspectives of single cell epigenomics

Lecture II-2: **to be determined 16:00 - 17:30**

Epigenomics: Data analysis (FM, KK)

- Data retrieval (from NGS machines),
- Quality control, data trimming and decomposition,
- Primary data processing (alignment)
- First data analysis (DNA-methylation, ChIP peak calling, RNA-Seq analysis (SamTools),

Data processing (own data)

- Sources and data retrieval of epigenomic data:
- data formats, download and use of major data resources (IHEC, BLUEPRINT, DEEP; ENCODE, ROADMAP)
- Steps for data deposition,
- Use and importance of technical and biological/medical metadata,

Lecture II-3: Epigenomic data analysis II to be determined 16:30 - 18:00 (FM, KK)

Epigenomics: Data interpretation

- Examples and use of data interpretation tools/software packages.
- Analysis of DNA-methylation data (RNBeads),
- Chromatin data (ChromHMM, DeepTools),
- Open Chromatin data (Macs2, NomeHMM).
- RNA-Seq data (mirBase, EdgeR),

Test/Examen: to be determined, room 0.33, building A 2.4, 4pm