

Course name: Fundamentals of gene regulation (JBL219)

Credit: 4

Objective of the course:

This major aim of this course is to make students grasp the fundamental regulatory mechanisms of gene expression. The course will cover two major facets of gene regulation- transcriptional and post-transcriptional. This course will encompass both established as well as emerging concepts in the field of gene expression and its regulation. Students will also be briefly introduced to latest methodologies in the field which will help them to broaden their learning horizon. This course should be an effective exercise for the MSc, Integrated PhD and PhD students aiming to pursue their career at the liaison of molecular biology and other specialized themes such as immunology, oncology etc.

Syllabus:

A) Concepts of gene expression

- DNA structure
- Nucleosomes and histones
- RNA Polymerases and their function (brief)
- RNA-PolII pausing
- Capping and termination

B) Role of epigenetic mechanisms in regulation of gene expression

- *Cis*-regulatory elements
- Concept of promoter and conventional enhancers
- Latent enhancers
- Super-enhancers in gene regulation
- Silencers
- Insulators
- Open chromatin regions (OCRs)
- DNA-methylation in regulation of gene expression

C) Genome organization and gene regulation

- Role of Mediator, Cohesins and CTCF in genome organization and gene regulation
- Phase separation and gene regulation

D) Post transcriptional regulation of eukaryotic gene expression

- Small non-coding RNAs such as miRNA in gene regulation
- Long non-coding RNAs
- Basics of RNA editing

E) Gene regulation and diseases

- Dysregulation of gene expression in diseases and it's reversal by drug treatment

F) Emerging methodologies to evaluate the gene expression and its regulation

- Introduction to high-throughput sequencing methodologies to evaluate gene expression – Bulk RNA-seq, Single cell RNA-seq: How and why?
- Methods to evaluate chromatin state- ChIP-seq, Assay for transposase accessible chromatin (ATAC)-seq
- Method to analyze DNA methylation- Reduced representation bi-sulfite sequencing (RRBS)
- Chromatin architecture- Hi-C, HiChIP

Book: Genes VII by Benjamin Lewin, Research articles shared in the course work.