Course name: Fundamentals of gene regulation

Credit: 3

Objective of the course:

This major aim of this course is to make students understand 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 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

- Genes and genomes
- RNA Polymerases and their function
- RNA-PolII pausing
- Transcription factors
- Regulatory elements

B) Role of epigenetic mechanisms in regulation of gene expression

- Chromatin modifications in regulation of eukaryotic transcription
- Concept of writer, reader and eraser
- Concept of promoter and conventional enhancers
- Latent enhancers
- Super-enhancers in gene regulation
- Open chromatin regions (OCRs)
- DNA-methylation in regulation of gene expression
- Long non-coding RNAs
- DNA topology and transcription

C) Genome organization and gene regulation

- Role of genome organization in regulation of transcription
- Control of genome organization by transcription elongation

- Concept of chromatin domains and transcription factories
- 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
- Basics of RNA editing

E) Gene regulation and diseases

- Dysregulation of gene expression in diseases
- Drug treatment in diseases to revert dysfunctional transcription
- Epigenome as a target for drug development

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, ChIA-PET