

## **MBS-506: Metagenomics & Proteomics**

**40 h**

### **Unit I**

**13h**

Structure and organization of Genomes in Prokaryotes and Eukaryotes: gene structure, Open reading frames, Conceptual translation, Termination sequences and GC content. Genome Sequencing: High throughput sequencing, clone-by-clone approach, Whole genome shot gun approach, quality of genome sequence, human genome sequencing project.

### **Unit II**

**13h**

Comparative Genomics of prokaryotes and eukaryotes, Comparative genomics of organelles, Large scale mutagenesis and interference. Analysis of Transcriptomes: Introduction, DNA microarray technology, Functional genomics, Expressed Sequence Tags (ESTs) and Serial Analysis of Gene Expression (SAGE,) Allele mining and SNPs, Applications of genomics.

### **Unit III**

**14h**

Metagenomics: Introduction to sequence based and function based metagenomics. Analyses of community composition and change, Metabolic reconstruction analyses, metatranscriptome and metaproteome analyses  
Proteomics: Introduction to proteomics, Proteomics Technologies - Protein Arrays, Protein Chips and their applications, 2D Gel Electrophoresis and its application, Mass Spectrometry and Protein identification, Shotgun proteomics.

