Subject Code : P8BI11

CC – XI - GENOMICS AND PROTEOMICS

UNIT - I

Genome map & types – Polymorphic markers – Genome database (GDB) – NCBI Entrez Human genome map viewer – Online Mendelian Inheritance in Man (OMIM) – Mouse Genome database – Annotation of Genome – structural annotation – gene prediction approaches – Open Reading Frame (ORF) prediction – Hidden Markov Model – Pattern discrimination – Prediction of promoter sequences – Functional annotation – prediction of gene function – sequence similarity – gene family and metabolic pathway – conserved domain, Profile and motif comparison – EST comparison.

UNIT – II

Genome diversity – taxonomy and significance of genomes – Bacterial, Yeast, Coenorabditis, Homo sapiens, Arabidopsis thaliana. Comparative genomic databases – PEDANT, Cluster of Orthologous Groups (COG), Kyoto Encyclopedia of Genes and Genomes (KEGG) – Metabolic reconstruction – Network Databases –Statistical data on available genome sequenced species - Pathway Databases.

UNIT – III

Human genome (HGMP) and genomic analysis – sequence repeats, transposable elements, gene structure, pseudogenes – Gene analysis – gene order – chromosome rearrangement – compositional analysis – clustering of genes – composite genes.

UNIT – IV

Introduction to Proteome - proteome and technology - information and the proteome – Primary attributes for protein identification - protein species of origin - Protein N- and C-terminal sequence tags - cross species protein identification - Modifications that influence protein change on 2-D PAGE - Detection and analysis of co- and post-translational modification.

UNIT - V

Proteome databases – protein sequence database, SWISS-PROT, TrEMBL, specialized protein sequence databases, PROSITE, BLOCKS, 2-D PAGE databases, PDB, genomic databases, OMIM, Metabolic databases, Some specific metabolic databases – application of proteomics in medicine.

Reference Books

1. Wilkins M.R., Williams K.L., Appel D.F., Hochstrasser (eds) 1997. Proteome Research: New Frontiers in Functional Genomics Springer-Verlag Berlin Heidelberg, New York.
2. Bentley D.R., in Genomics (eds Dixon G.K., Coppin L.G. and Living Stone D.), Bios Scientifics, London, 1998.

3. Bauw, G. and Monatgu, M.V., in Differenmtially expressed genes in plant: A bench manual (eds Hansen, E and harper G.), Taylor and Francis, London, 1997.
4. T. A. Brown, Genomes, 2nd Edition, BIOS Scientific Publishers, Ltd., Oxford, UK, 2002.
5. David W. Mount, Bioinformatics – Sequence and Genome analysis, Cold Spring Harbor Laboratory Press, New York, 2001.
6. Eugene V. Koonin and Michael Y. Galperin, Sequence, Evolution Function, Computaional Approaches in Comparative Genomics, Kluwer Academic Press, Massachuttes, 2003.
7. Jenson, O.N., in Proteomics. A Trends Guide (eds Black Stock, Co- and Mann), Elsevier Science, London, 1998.
8. S.R.Pennington and M.J.Dunn, Proteomics, Viva Books Pvt. Ltd., New Delhi, 2002.