

Principles of biophysical chemistry pH, Buffer, Reaction kinetics, Thermodynamics, Colligative properties, Structure of atoms, Molecules and chemical bonds. Stabilizing interactions: Van der Waals, Electrostatic, Hydrogen bonding, Hydrophobic interaction, etc.

Composition, structure and function of Biomolecules: Carbohydrates, Lipids, Proteins, Nucleic acids and Vitamins. Bioenergetics and metabolism of Carbohydrates, Lipids, Amino Acids and Nucleotides.

Enzymology: Classification, Principles of catalysis, Mechanism of enzyme catalysis, Enzyme kinetics, Enzyme regulation, Isozymes Clinically important enzymes.

Protein Chemistry: Ramachandran plot, Secondary, Tertiary and Quaternary structure, Domains, Motif and Folds. Nucleic acids: A-, B-, Z-DNA, tRNA, micro-RNA, Stability of protein and Nucleic acid structures.

Biological databases: Nucleotide Sequence Databases, GenBank, DDBJ, EMBL, Sequence Flatfile and submission process, Protein sequence databases, UniProt in detail, Mapping databases, Genomic databases, Data mining.

Sequence analysis: Gene Prediction methods and programs, Promoter analysis, RNA secondary structure thermodynamics, Refining multiple sequence alignment based on RNA secondary structure predictions, SNP discovery methods and databases, Genotyping, International haplotype map project, 1000 genomes project.

Analysis for protein sequences: Predicting features of individual residues, Predicting function, Neural networks, Protein structure prediction, Protein structure databases, PDB in detail, 3D visualization softwares, Pathway and molecular interaction databases,

Inferring relationships: Global Vs. local sequence alignments, Dotplots, Scoring matrices, Pairwise sequence alignment, BLAST, Position-Specific scoring and PSI-BLAST, MegaBLAST, BL2SEQ, BLAT, FASTA Vs BLAST, Protein multiple sequence alignments, Multiple structural alignments, Shotgun sequencing, Sequence assembly and finishing.

Modelling and structure: From protein sequence to structure, theoretical and practical aspects of protein sequence alignments, secondary, tertiary structure prediction, comparative modeling, Docking, protein-protein and protein-ligand docking. Techniques for 3-D structure determination like X-ray, NMR, MS/MS analysis.

Computational drug designing: Structure-based drug design, virtual screening, quantitative structure activity relations, Cheminformatics and pharmacophore mapping in therapeutic development.