Contents

Prefac	re		บแ
1.	Nuc	leic Acid and Genome Organization	1.1
	1.1	Biochemistry of Nucleic Acid	1.1
	1.2	DNA Model	1.2
	1.3	Nucleic Acid Structure	1.3
	1.4	Dynamic Nature of DNA	1.4
	1.5	DNA's Other Structural Forms	1.4
	1.6	Chromosomal DNAs	1.7
	1.7	Organization of the Repeated DNA Sequences	1.8
	1.8	Special Function Repetitive Sequence	1.11
	1.9	Plant Genome Organization	1.13
	1.10	Human Genome Organization	1.14
	1.11	Other Types of DNA Sequences	1.14
	1.12	Causes of Variation in DNA Structure	1.15
	1.13	Methylated Bases Occurring in DNA	1.17
	1.14	Non coding DNA	1.20
	1.15	DNA Sequences with Unique Characteristics	1.20
	1.16	Triplet Repeat Sequences	1.20
	1.17	DNA of Organelles	1.20
	1.18	RNA (Ribonucleic Acid)	1.23
	1.19	Synthesis of RNA	1.24
	1.20	Ribosomal RNA (rRNA)	1.25
	1.21	Transfer RNA (tRNA)	1.27
	1.22	Messenger RNA (mRNA)	1.29
	1.23	Sense/Antisense Transcription	1.31
	1.24	Aberrant mRNA	1.32
	1.25	mRNA Degradation	1.32

	1.26	P-bodies	1.33
	1.27	Stress Granules (SGs)	1.33
	1.28	Hierarchical Structure of RNA	1.33
	1.29	RNA Localization	1.37
	1.30	Base Pairing Between Codon of an mRNA and Anti-codon of tRNA	1.37
	1.31	Small Nuclear RNA (snRNA)	1.37
	1.32	Variation in DNA/RNA Quantity in Plants	1.38
	1.33	Analysis of Nucleic Acid	1.39
	1.34	Determination of G+C Content	1.42
	1.35	Renaturation Kinetics	1.43
	1.36	Quantification of Cytosine Methylation	1.46
	1.37	Nearest Neighbor Sequence or Frequency Analysis	1.49
2.	RNA	A Editing	2.1
	2.1	Editing of tRNAs	2.1
	2.2	Editing of rRNA	2.3
	2.3	Editing of mRNA	2.3
	2.4	Editing in Non-coding RNAs, 5' UTRs and 3' UTRs	2.6
	2.5	miRNA Editing	2.7
	2.6	Translational Editing	2.7
	2.7	DNA Editing	2.8
3.	Gen	etic Code	3.1
	3.1	Definition and Properties of Genetic Code	3.1
	3.2	Codon Usage Bias	3.4
	3.3	Codon Usage Frequency	3.4
	3.4	Variation in Genetic Code	3.5
	3.5	Assignment of Amino Acid Codons	3.6
	3.6	Reading Frame	3.7
4.	Fun	ction of DNA	4.1
	4.1	Functions of DNA	4.1
	4.2	Replication	4.1
	4.3	Protein Synthesis	4.8
	4.4	Folding of Proteins and Degradation	4.10
	4.5	Differences in Mechanism of Protein Synthesis between Eukaryotes and Prokaryotes	4.11
	4.6	Place of Transcription/Translation	4.11
	4.7	Molecular Mechanics Underlying Key Steps in Eukaryotic Translation	
	40	Initiation	4.12
	4.8	Comparison between Eukaryote and Prokaryote	4.13

	4.9	Mechanisms of Transcription Termination in Prokaryote	4.15
	4.10	Regulation of Transcription in Prokaryote	4.16
	4.11	Antisense Transcription	4.16
	4.12	Translational Error	4.17
	4.13	Role of tRNA in Protein Synthesis	4.17
	4.14	Dissecting the Mechanism of Translation	4.18
5.	Gen	e, Gene Concept and Gene Organization	5.1
	5.1	Gene Definition	5.1
	5.2	Gene as a Unit of Transcription	5.3
	5.3	Effect of Exon/Intron	5.4
	5.4	Functions of Intron	5.4
	5.5	Types of Introns	5.6
	5.6	Splicing of Introns	5.8
	5.7	Different Products from the Same Transcript	5.12
	5.8	Changing Concept of Gene	5.13
	5.9	Change of Locus/Gene Restructuring	5.14
	5.10	Regulatory Elements	5.1ϵ
	5.11	Gene Structure- Gene Components and their Oligonucleotide Compositions	5.17
	5.12	Mechanisms of Translation Initiation	5.20
	5.13	Transcription Termination Sequence	5.22
	5.14	Types of Regulatory Elements	5.23
	5.15	Two Classes of Transcriptional Control Sequences	5.28
	5.16	Other cis-Regulatory Elements	5.32
	5.17	Transcription Factors	5.34
	5.18	Prokaryotic Promoter	5.36
	5.19	Eukaryotic Promoters	5.36
	5.20	Mammalian RNA Polymerase II Promoters	5.37
	5.21	Transcription in Eukaryotes	5.37
	5.22	Transcription Factor Binding Sites	5.38
	5.23	Different Types of Genes with Different Core Elements	5.38
	5.24	Gene Transcription Requiring Prior Protein Synthesis	5.40
	5.25	Regulation of Transcription Initiation Via Changes in DNA Topology	5.40
	5.26	Gene with two Promoters	5.41
	5.27	Trans-acting Factors	5.45
	5.28	Systems of Gene Organization	5.40
	5.29	Spacing/Spacers	5.50
	5.30	Gene Construct	5.5
	5 31	Regulation of Gene Expression	5.5

	5.32	Methods for Identification of Genes	5.53
	5.33	Additional Issues in Gene Identification	5.54
	5.34	Inefficient Translation	5.55
	5.35	Role of Intergenic RNA/Process of Transcription of DNA in	
		Regulation of Gene Expression	5.59
	5.36	Regulation at Translation Level can Occur Through Two Mechanisms	5.60
	5.37	Gene Families	5.61
	5.38	Pseudogenes	5.63
	5.39	Gene Amplification/Gene Duplication	5.66
	5.40	Order of Genes on Chromosomes	5.66
6.	Imp	rinting	6.1
	6.1	Defintion	6.1
	6.2	Imprinting as Mechanism for Homologue Recognition	6.3
	6.3	Theory of Imprinting	6.3
	6.4	Terms Related to Epigenetics	6.4
	6.5	Genetic/Genome Imprinting	6.6
	6.6	Chromatin Chemistry (Histone modification) and Chromatin Remodelling	6.8
	6.7	Histone Code Hypothesis	6.9
	6.8	Gene Expression	6.10
	6.9	DNA Methylation- The Molecular Basis of Imprinting	6.12
		DNA Methylation- The Molecular Basis of Imprinting Prion Hypothesis	6.12 6.16
7.	6.10		
7.	6.10	Prion Hypothesis	6.16
7.	6.10 The	Prion Hypothesis Other Types of Code	6.16 7.1
7.	6.10 The 7.1	Prion Hypothesis Other Types of Code Properties of Nucleotides and Nucleotide Sequences	6.16 7.1 7.1
7.	6.10 The 7.1 7.2	Prion Hypothesis Other Types of Code Properties of Nucleotides and Nucleotide Sequences The Other Types of Codes	6.16 7.1 7.1 7.1
7.	6.10 The 7.1 7.2 7.3	Prion Hypothesis Other Types of Code Properties of Nucleotides and Nucleotide Sequences The Other Types of Codes Regulatory Code	6.16 7.1 7.1 7.1 7.2
7.	6.10 The 7.1 7.2 7.3 7.4	Prion Hypothesis Other Types of Code Properties of Nucleotides and Nucleotide Sequences The Other Types of Codes Regulatory Code Structural Code	6.16 7.1 7.1 7.1 7.2 7.3
	6.10 The 7.1 7.2 7.3 7.4 7.5 7.6	Prion Hypothesis Other Types of Code Properties of Nucleotides and Nucleotide Sequences The Other Types of Codes Regulatory Code Structural Code Histone Code	6.16 7.1 7.1 7.1 7.2 7.3 7.8
	6.10 The 7.1 7.2 7.3 7.4 7.5 7.6	Prion Hypothesis Other Types of Code Properties of Nucleotides and Nucleotide Sequences The Other Types of Codes Regulatory Code Structural Code Histone Code Sequence-dependent DNA Structure ombinant DNA Technology and its Applications Biotechnology	6.16 7.1 7.1 7.1 7.2 7.3 7.8 7.10
	6.10 The 7.1 7.2 7.3 7.4 7.5 7.6 Rec	Prion Hypothesis Other Types of Code Properties of Nucleotides and Nucleotide Sequences The Other Types of Codes Regulatory Code Structural Code Histone Code Sequence-dependent DNA Structure ombinant DNA Technology and its Applications	6.16 7.1 7.1 7.1 7.2 7.3 7.8 7.10 8.1
	6.10 The 7.1 7.2 7.3 7.4 7.5 7.6 Rec 8.1 8.2 8.3	Prion Hypothesis Other Types of Code Properties of Nucleotides and Nucleotide Sequences The Other Types of Codes Regulatory Code Structural Code Histone Code Sequence-dependent DNA Structure ombinant DNA Technology and its Applications Biotechnology Genetic Engineering Methods of Cloning Genes Introduction of Specific Genes	6.16 7.1 7.1 7.1 7.2 7.3 7.8 7.10 8.1 8.1 8.3 8.4
	6.10 The 7.1 7.2 7.3 7.4 7.5 7.6 Rec 8.1 8.2 8.3 8.4	Prion Hypothesis Other Types of Code Properties of Nucleotides and Nucleotide Sequences The Other Types of Codes Regulatory Code Structural Code Histone Code Sequence-dependent DNA Structure ombinant DNA Technology and its Applications Biotechnology Genetic Engineering Methods of Cloning Genes Introduction of Specific Genes Potential Problems with Library-based Cloning	6.16 7.1 7.1 7.1 7.2 7.3 7.8 7.10 8.1 8.1 8.3 8.4 8.26
	6.10 The 7.1 7.2 7.3 7.4 7.5 7.6 Rec 8.1 8.2 8.3 8.4 8.5	Other Types of Code Properties of Nucleotides and Nucleotide Sequences The Other Types of Codes Regulatory Code Structural Code Histone Code Sequence-dependent DNA Structure ombinant DNA Technology and its Applications Biotechnology Genetic Engineering Methods of Cloning Genes Introduction of Specific Genes Potential Problems with Library-based Cloning Expression of Cloned Gene	6.16 7.1 7.1 7.1 7.2 7.3 7.8 7.10 8.1 8.1 8.3 8.4 8.26 8.28
	6.10 The 7.1 7.2 7.3 7.4 7.5 7.6 Rec 8.1 8.2 8.3 8.4 8.5 8.6	Other Types of Code Properties of Nucleotides and Nucleotide Sequences The Other Types of Codes Regulatory Code Structural Code Histone Code Sequence-dependent DNA Structure ombinant DNA Technology and its Applications Biotechnology Genetic Engineering Methods of Cloning Genes Introduction of Specific Genes Potential Problems with Library-based Cloning Expression of Cloned Gene Methods of Direct Gene Transfer	6.16 7.1 7.1 7.1 7.2 7.3 7.8 7.10 8.1 8.1 8.3 8.4 8.26 8.28 8.31
	6.10 The 7.1 7.2 7.3 7.4 7.5 7.6 Rec 8.1 8.2 8.3 8.4 8.5 8.6 8.7	Other Types of Code Properties of Nucleotides and Nucleotide Sequences The Other Types of Codes Regulatory Code Structural Code Histone Code Sequence-dependent DNA Structure ombinant DNA Technology and its Applications Biotechnology Genetic Engineering Methods of Cloning Genes Introduction of Specific Genes Potential Problems with Library-based Cloning Expression of Cloned Gene Methods of Direct Gene Transfer Transformation of Animal Cells	6.16 7.1 7.1 7.1 7.2 7.3 7.8 7.10 8.1 8.1 8.3 8.4 8.26 8.28 8.31 8.35
	6.10 The 7.1 7.2 7.3 7.4 7.5 7.6 Rec 8.1 8.2 8.3 8.4 8.5 8.6	Other Types of Code Properties of Nucleotides and Nucleotide Sequences The Other Types of Codes Regulatory Code Structural Code Histone Code Sequence-dependent DNA Structure ombinant DNA Technology and its Applications Biotechnology Genetic Engineering Methods of Cloning Genes Introduction of Specific Genes Potential Problems with Library-based Cloning Expression of Cloned Gene Methods of Direct Gene Transfer	6.16 7.1 7.1 7.1 7.2 7.3 7.8 7.10 8.1 8.1 8.3 8.4 8.26 8.28 8.31

	8.9	Recombineering	8.40
	8.10	Gene Therapy	8.42
9.	Rest	riction Endonuclease	9.1
	9.1	Types of Enzymes used in Recombinant DNA Technology	9.1
	9.2	Generation of Fragment of Suitable Size	9.5
	9.3	Digestion with Restriction Endonucleases	9.5
	9.4	Purpose of Generation of Fragments	9.6
	9.5	Construction of a Restriction Map	9.6
	9.6	Mapping with Restriction Enzymes with Many Recognition Sites	9.7
	9.7	Mapping of Circular DNA Molecule	9.8
	9.8	Methylation Assay	9.10
	9.9	Mechanical Shearing	9.10
10.	Vect	ors and Expression Vectors	10.1
	10.1	Definition and Types of Vector	10.1
	10.2	Shuttle Vector	10.5
	10.3	Artificial Chromosome (Minichromosome)	10.5
	10.4	Ti-plasmid	10.5
	10.5	Selectable Marker Gene	10.7
	10.6	Promoters	10.9
	10.7	Other Components of Transgenes	10.9
	10.8	Reporter Gene	10.9
		Ri-plasmid	10.10
		Problems with Ti Plasmids	10.10
	10.11	Plant Viruses	10.12
		Bacteriophage λ and M13	10.13
		Cosmids	10.18
		Fosmid	10.19
		Bacterial Artificial Chromosome	10.19
		Yeast Artificial Chromosome	10.19
		Plant Artificial Chromosome (PLAC)	10.21
		Human Artificial Chromosomes (HACs)	10.21
		Mammalian Artificial Chromosome (MAC)	10.22
		Retroviruses	10.22
		Retroviral Vector	10.23
		P1 Cloning Vector	10.23
		Baculovirus	10.24
		Simian Virus 40	10.25
		Transformation Competent Artificial Chromosome Vector (TAC Vector)	10.25
	10.26	Phagemids (Phage-plasmid)	10.26

	10.27	Expression Vectors	10.26
	10.28	Expression Shuttle Vector	10.29
	10.29	Problems Associated with Production of Recombinant Protein are Due to	10.31
	10.30	Over Expression	10.32
	10.31	Expression Vectors for Eukaryotes	10.32
	10.32	Study of Gene Regulation	10.33
	10.33	Study of Gene Family	10.34
	10.34	Enhancer trap/Gene Trap Vector	10.34
	10.35	Inducible Expression Vector	10.36
	10.36	Other Types of Vectors	10.37
11.	DNA	Library and its Construction	11.1
	11.1	DNA Library	11.1
	11.2	cDNA Library	11.4
	11.3	STS (Sequence Tagged Site) Library	11.9
	11.4	EST (Expressed Sequence Tag) Library	11.10
	11.5	Library Amplification	11.10
12.	DNA	Synthesis and DNA Sequencing Technology	12.1
	12.1	Chemical Synthesis of Nucleic Acid and Nucleotide Sequencing	12.1
	12.2	Methods of Nucleic Acid Synthesis	12.1
	12.3	DNA Sequencing	12.4
	12.4	Automatic Sequencing	12.11
	12.5	Massively Parallel System	12.13
	12.6	Maldi-tofms (Matrix-assisted Laser Desorption/Ionization Time-off-flight Mass Spectroscopy	12.15
	12.7	Sequencing by Hybridization (SBH)	12.16
	12.8	Probes and Primers and Labeling of Nucleic Acids	12.17
12		C	13.1
13.		ome Sequencing and Genome Assembly	
	13.1	Sequencing of Genome Human Genome Sequencing	13.1
		Whole Chromosome Sequencing	13.6 13.21
	13.4	Genome Sequencing of Nematode C. Elegans	13.26
	13.4	Shot Gun Strategy for whole Genome Sequencing of Bacteria,	13.40
	13.3	Haemophilius Influenzae	13.30
	13.6	Genome Sequencing of <i>S. Pombe</i>	13.33
	13.7	Sequencing Strategy for Arabidopsis Genome	13.34
	13.8	Rice Genome Analysis	13.35
	13.9	Maize Genome Analysis	13.36
		Genomic Analysis of Heterochromatin	13.36
		Genomic Sequence Annotation	13.37
	10.11	Continue dequerice Triniounion	10.01

14.	Prot	ein Synthesis and Sequencing	14.1
	14.1	Definition	14.1
	14.2	Venn Diagram	14.3
	14.3	Primary Structure	14.3
	14.4	Secondary Structure	14.4
	14.5	Tertiary Structure	14.6
	14.6	Quarternary Structure	14.6
	14.7	Function of Proteins	14.7
	14.8	Homoeobox Protein	14.8
	14.9	Protein Folding	14.8
	14.10	Prediction of Structure of a Protein	14.9
	14.11	Prediction of Three-dimensional Protein Structure	14.10
	14.12	Machine Learning Approaches	14.11
	14.13	Sequencing of Polypeptide	14.12
	14.14	Designing Gene Specific Probes	14.14
	14.15	Double Frameshift Analysis	14.15
	14.16	Proteome/Proteomics	14.15
	14.17	Gene Design	14.17
	14.18	Identification of Proteins	14.17
	14.19	Protein Signature	14.18
	14.20	Protein Posttranslational Modification	14.20
	14.21	Structural Classification of Proteins	14.20
	14.22	Hierarchical Domain Classification of Protein Structures	14.25
	14.23	Evolution of Proteins	14.26
	14.24	Rearrangement of Segments of Genome	14.27
15.	Mole	ecular Marker Technology and its Applications	15.1
	15.1	Definition- Markers	15.1
	15.2	Types of Genetic Markers	15.1
		Molecular Marker Technology	15.14
	15.4	Selection of Molecular Marker	15.14
	15.5	Applications of Molecular Marker Technology	15.15
16.	Stru	ictural Genomics and Structural Genomics Technology	16.1
	16.1	Definition	16.1
	16.2	Structural Analysis of Cloned DNA	16.2
	16.3	Gene Space	16.5
	16.4	Generating Genome-wide Chromatin State map	16.7
	16.5	Mapping Histone Marks	16.7

16.6	Mapping	16.8
16.7	Physical Mapping	16.10
16.8	Low Resolution Maps	16.12
16.9	Mapping Strategies	16.13
16.10	Contig Mapping	16.14
16.11	Use of 'Sequence-tagged Sites' for Mapping	16.15
16.12	Finer Detail Mapping	16.17
16.13	Comparison between Vectors for Suitability for Mapping and	
	Functional Analysis	16.18
16.14	Visual Mapping (Optical Mapping)	16.19
16.15	Happy Mapping	16.19
16.16	Gene Density	16.21
16.17	Gene Number	16.21
16.18	Gene Content	16.22
16.19	Coding Density	16.22
16.20	Architecture of Genomes of Some Model Species	16.23
16.21	Positional Cloning	16.25
16.22	Gene Screening	16.28
16.23	Methylation Interference Assay	16.31
16.24	Identification of RNA-protein Interaction Site	16.33
16.25	Determination of Spacing between Two Regulatory Sequences	16.34
16.26	Allocation of Cloned Gene (s) to Specific Chromosomes	16.34
16.27	Gene Identification	16.40
16.28	Detection in Situ of Genomic Regulatory Elements	16.42
16.29	Analysis of Enhancer	16.47
16.30	Transvection	16.48
16.31	Identification of Receptor-binding Sequence in the DNA	16.51
16.32	Identification and Characterization of Transcripts	16.52
16.33	Detection of Introns and Determination of Position of Intron	16.55
16.34	Exon Trapping	16.56
16.35	Determination of the Length of Poly(A) Tail of mRNA	16.58
16.36	Gene Identification by Complementation	16.59
16.37	Gene Identification by Gene Expression	16.59
16.38	Gene Identification using Gene from other Species or Group Boundaries	16.59
16.39	Gene Identification Through Disruption	16.60
16.40	Isolation of Chromosome Ends	16.61
16.41	Centromere Mapping	16.61
16.42	Analysis of Individual Genes	16.61

	5.43 Chromatin Structure	16.63
	6.44 DNA Fingerprinting/Profiling	16.65
	6.45 Ways of Finding Genes	16.67
17.	ystems Biology	17.1
	7.1 Systems Approach	17.1
	7.2 Qualitative Modeling of Biological Systems	17.4
	7.3 Applications of Systems Biology	17.4
	7.4 Protein Interaction Network	17.6
	7.5 Approaches to Study Systems Biology	17.6
	7.6 Genetic Network	17.7
	7.7 Approaches to Mapping of Networks	17.8
	7.8 Network of Over Expressing Genes	17.9
	7.9 Low Expressed Genes	17.9
	7.10 Combining Networks	17.10
	7.11 Developmental Networks	17.10
	7.12 Construction of Genetic Regulatory Network	17.11
	7.13 Trancriptional Regulatory Network Architecture or Network Motifs	17.12
	7.14 Gene Expression Regulation	17.13
	7.15 Identifying the Components of Regulatory Gene Network	17.13
	7.16 Data Mining Approach for Inferring Structures of Gene Regulatory Networks	17.14
	7.17 Redundancy in Signaling Networks	17.14
	7.18 Integration of Protein-protein-interaction Dataset	17.16
	7.19 Intergration of Multiple Datasets of Physical Protein-protein Interaction	on 17.16
	7.20 Integration of Genome-wide Protein-protein Interaction Data	17.17
	7.21 De novo Prediction of Protein Complexes	17.17
	7.22 Reconstructing Biological Pathways and Regulatory Networks	
	from Quantitative Measurements	17.17
	7.23 Prediction on Gene Expression Patterns	17.22
	7.24 Fuzzy Logic-based Approach	17.22
	7.25 Large Network Analysis	17.22
	7.26 Substructures within Networks	17.23
	7.27 Cross-referencing Different Networks	17.23
	7.28 Neural Networks	17.24
	7.29 Pathways and Networks	17.24
	7.30 Networks	17.28
	7.31 Hierarchical Organization of Networks	17.30
	7.32 Identification of Network	17.30

	17.33	Feature of Network	17.31
	17.34	Pathway Construction	17.33
	17.35	Biochemical Networks	17.33
	17.36	Approaches to Estimation of Parameters of Models of Biochemical	
		Network	17.34
	17.37	System Level Methods for Estimation of Parameter Estimation	17.34
18.	Anal	ysis of Single Nucleotide Polymorphism	18.1
	18.1	Study of Sequence Variation	18.1
	18.2	Identification of SNPs	18.1
	18.3	Single Nucleotide Polymorphism	18.2
	18.4	Methods for Identifying Sequence Variation	18.3
	18.5	Non Sequencing Methods for SNP Discovery	18.3
	18.6	Tiling Strategy	18.3
	18.7	SNP Assay	18.5
	18.8	Designing SNP Primer	18.7
	18.9	Large-scale Strategies for Mapping SNP	18.7
		Scanning mtDNA for Sequence Variation in Human	18.8
19.	Ana	lysis of Haplotypes	19.1
	19.1	Association or Linkage Disequilibrium (LD)	19.1
	19.2	Haplotype	19.2
		Number of Haplotypes	19.3
		Size of LD Blocks	19.3
	19.5	Construction of Haplotype	19.3
		Consensus Pattern	19.3
	19.7	Methodology for Molecular Haplotyping	19.4
		Measurement of Linkage Disequilibrium (LD)	19.6
	19.9	Measurement of Genome-wide LD	19.6
	19.10	Transmission/Disequilibrium Tests	19.7
		Genome-wide Association Study for Identification of Loci	19.8
	19.12	Detection of Structural Variation of the Genome	19.8
	19.13	Comparative Genomic Hybridization (CGH)	19.9
		Detection of Sequence Variants	19.10
20.	QTL	Analysis	20.1
	20.1	Types of Gene Involved in Quantitative Variation	20.1
	20.2	Identification of Mutation of Gene with Strong Effect	20.1
	20.3	Screening known Genes having Phenotypic Effects for Sequence Variation	20.4
		Variation within the Gene	20.9

	20.5	QTL Mapping	20.10
	20.6	Association Mapping/Linkage Disequilibrium Mapping	20.13
	20.7	Methods for Refining the Identification of QTL	20.15
	20.8	QTL Mapping Methods	20.17
	20.9	Use of Chromosome Substitution Strain for QTL Analysis	20.20
	20.10	Candidate Gene Approach	20.21
21.	In Vi	tro Mutagenesis and Directed Evolution	21.1
	21.1	Mutation-Definition and Types	21.1
		Classes of Single Base Change Mutations Resulting from Chemical Mutagenesis	21.3
	21.3	Suppressor and Enhancer Screens	21.3
	21.4	Deletion Mapping	21.4
	21.5	Saturating a Particular Locus with Mutations	21.4
	21.6	Tiling Mutagenesis	21.5
	21.7	Isolation of Mutations from Precisely Defined Chromosome Segments	21.6
	21.8	Genomic Subtraction	21.6
	21.9	Insertion Mutagenesis	21.7
	21.10	Site Directed Mutagenesis (SDM)	21.12
	21.11	Introduction of Point Mutation	21.16
	21.12	Insertion of Nucleotide Analogue	21.16
	21.13	Mutational Analysis	21.21
	21.14	Methods for Detection of Single Base Substitutions	21.23
	21.15	Protein Engineering	21.24
	21.16	Gene Targeting	21.25
	21.17	Detection of DNA Sequence Differences (Detection of Mutation)	21.27
22.	Tran	sposable Elements in Genome Organization	22.1
	22.1	Definition	22.1
	22.2	Prokaryotic Transposons-Bacterial Transposons	22.2
	22.3	Eukaryotic Transposons	22.3
	22.4	Retrotransposons	22.5
	22.5	Yeast Transposons	22.6
	22.6	Position Specific Preferences	22.7
	22.7	Long Interspersed Elements (LINES)	22.9
	22.8	Short Interspersed Elements (SINES)	22.10
	22.9	Classification of Transposable Elements	22.11
	22.10	Mechanism of Jumping	22.12
	22.11	Chromosome Rearrangements	22.15

23.	Gen	e Silencing	23.1
	23.1	Definition	23.1
	23.2	Transcriptional Gene Silencing (TGS)	23.2
	23.3	Approaches to Gene Silencing	23.4
	23.4	Category of Ribozymes	23.7
	23.5	Detection of Ribozymes	23.9
	23.6	Genome-wide Search for Ribozymes	23.9
	23.7	RNA Intereference	23.9
	23.8	Preparation of siRNA	23.14
	23.9	Designing siRNA	23.14
	23.10	RNAs as Activator of Gene Expression?	23.15
	23.11	Role of Polymerase	23.15
	23.12	RNA World	23.15
	23.13	Small Regulatory RNA	23.16
	23.14	Identification of Candidate Small Regulatory RNA	23.17
	23.15	miRNA Acting as Activator of Translation?	23.20
	23.16	Role of Small RNA	23.22
	23.17	Co-suppression	23.23
	23.18	Cloning of Antisense Genes	23.24
	23.19	VIGS (Viral Induced Gene Silencing)	23.25
	23.20	Targetted Gene Silencing via RNA	23.26
	23.21	Riboswitches	23.26
	23.22	Restriction-modification Systems	23.27
	23.23	Role of RNA in DNA Rearrangement	23.28
24.	Fun	ctional Genomics and Function Genomics Technology	24.1
	24.1	Definitions	24.1
	24.2	Approaches to Study of Functional Genomics	24.3
	24.3	Bioinformatics Approaches	24.5
	24.4	High Throughput Approaches for Determining Gene Function	24.6
	24.5	Array Technology	24.6
	24.6	Quantitative Monitoring of Gene Expression Pattern with cDNA Microarray	24.10
	24.7	Transcriptional Network Modeling	24.14
	24.8	Use of Gene Sets for Reconstruction of Pathways	24.16
	24.9	Statistical Data Mining Tools for Discovering Gene Networks	24.16
		Problem with Expression Data	24.17
		Techniques for Ascertaining the Function of Genes from Expression Data	24.18
		Methods of Clustering Genes	24.18

24.13	Hierarchical Clustering	24.19
24.14	Other Techniques of Clustering	24.20
24.15	SOMs (Self Organizing Maps)	24.20
24.16	Steps Involved in Gene Clustering	24.21
24.17	Clustering Results from S. Cerevisiae	24.22
24.18	Feature Selection	24.23
24.19	Methods for Automated Feature Selection	24.23
24.20	Inferring Signaling Pathways from Microarray Data	24.23
24.21	Matrix Decomposition Methods (MDMs) for Detecting	
	Transcriptional Modules	24.25
24.22	Singular Value Decomposition (SVD)	24.25
24.23	Functional Analyses of Cloned Genes	24.26
24.24	Kinds of Genes	24.27
24.25	ORFeome	24.27
24.26	Functional Clustering of Genes	24.28
24.27	Finding Genes	24.28
24.28	Standard Gene Model and its Shortcomings	24.30
24.29	Ensemble Gene Prediction	24.33
24.30	Analyzing a Novel Gene	24.34
24.31	Validation of Structures of Genes	24.35
24.32	Exon Arrays	24.35
24.33	Generation of cDNA Set	24.36
24.34	Tilling Array Technology	24.36
24.35	Formaldehyde Assisted Isolation of Regulatory Elements (FAIR)	24.38
24.36	Genome-wide Study of Splicing by Splicing Microarray	24.38
24.37	Digital Polony Exon Profiling (DPEP)	24.39
24.38	Functional Genomics Techniques	24.40
24.39	Comparative Genomics	24.42
24.40	Gene Expression Process	24.43
24.41	TF-binding Sites	24.45
24.42	Eukaryotic Polymerase II Promoters	24.45
24.43	Methods of Identification of TF Binding Sites	24.47
24.44	Quantitative Modeling of Regulatory Network	24.50
24.45	Integrated Analysis	24.51
24.46	Gene Expression Profiles as Fingerprints	24.51
24.47	Other Gene Expression Methods	24.52
24.48	RNA (Nothern) Blot Analysis	24.53
24.49	Expression Measurements from Small Amounts of RNA-Identification	
	of Genes Associated with Development and Differentiation	24.53

	24.50	Alternative Approach for cDNA Display on Gels	24.55
	24.51	Molecular Indexing	24.56
	24.52	Transcription based Amplification System (TAS)	24.56
	24.53	Cataloguing of Transcriptome	24.57
	24.54	Functional Analysis of Pseudogenes	24.58
	24.55	Cataloguing the Regulatory Elements	24.59
	24.56	Identification of Expressed Genes	24.60
	24.57	Genome Sequencing	24.64
	24.58	Isolation of mRNA, its Quantification and Amplification	24.65
	24.59	RNA Profiling	24.67
	24.60	Alternatives to Standards Subtractive Hybridization Techniques	24.69
	24.61	Applications of High Throughput RNAi Screens in Functional Genomics	24.74
	24.62	Conditional Knock Out/Gene Targetting	24.79
	24.63	Transcription/Expression Profiling	24.82
	24.64	Methods for Obtaining Genome-wide mRNA Expression Pattern	24.83
	24.65	Not all mRNAs Encode Proteins	24.98
	24.66	Tiled Oliginucleotide	24.100
	24.67	Imaging of Gene Expression	24.100
		Gene Redundancy	24.101
	24.69	Functional Analysis	24.101
	24.70	Identification of Ploidy Regulated Genes	24.113
	24.71	Sensitivity of Gene Expression to Mutations	24.113
		Measures of Biological Complexity	24.114
		Synthetic Biology	24.114
25		e Function and Interaction	25.1
25.	25.1		25.1
		Gene Interaction	25.1
	_	Molecular Mechanism of Gene Interaction	25.4
	25.4		23.3
	25.4	Methods for Determining the Binding Sites of TFs on a Genome-wide Scale	25.11
	25.5	Genome Wide Location Analysis for Yeast Transcription Regulators	25.12
	25.6	Identification of Genes and Regulatory Elements	25.13
	25.7	Dam ID Chromatin Profiling	25.14
	25.8	Predicting Protein-protein Interactions from Correlation between	
		Genomic Features	25.14
	25.9	Protein-protein Interaction	25.15
	25.10	Conditional Lethal Mutations	25.17
	25.11	Synthetic Lethal Mutations	25.18

	25.12	Mechanisms Contributing to Binding Specificity	25.19
	25.13	RNA-binding Protein	25.19
	25.14	Epistasis	25.22
	25.15	Method of Identifying Genetic Interactions	25.24
	25.16	Biomolecular Network	25.25
	25.17	Comparison of Networks (Expression and Regulatory Networks)	25.27
	25.18	Structure-based Prediction of Protein Function	25.29
26.	Prote	eomics	26.1
	26.1	Proteome	26.1
	26.2	Methods for Monitoring Proteins	26.2
	26.3	Cellular Expression Patterns/Protein Profiling	26.2
	26.4	Yeast-Two-Hybrid (Y2H) System	26.14
	26.5	Different 2H Systems	26.17
	26.6	Other Protein Interaction Methods	26.17
	26.7	Other Transcription-based Interaction Detection Methods	26.18
	26.8	Approaches for Large Scale Throughput Studies	26.19
	26.9	Interactome Analysis	26.22
	26.10	Large-scale Approaches to Assign Function to Gene Products	26.27
	26.11	Tandem Affinity Purification (TAP) System	26.27
	26.12	Affinity Tagging and Mass Spectroscopy	26.28
	26.13	Analysis of Biochemical Activities	26.28
	26.14	Genomic Method for Identifying Yeast Genes Encoding Biochemical	
		Activities	26.28
		Protein Microarrays	26.30
		Evanescent Wave Methods-Surface Plasmon Resonance	26.31
		Peptide Microarray/Peptide Chip	26.32
		Genetic Suppression vs 2H Methods	26.32
		Quantification of the Affinities of Molecular Interactions	26.33
		Protein Engineering	26.34
		Drug Discovery	26.34
		Readout Systems	26.37
		Nucleic Acids	26.38
		Small Molecules	26.42
		Analysis of Multiple Sets of Data	26.42
		Protein Localization	26.44
		Global Analysis of Protein Expression	26.46
		Computational Detection of Functional Linkages	26.47
	26.29	Prediction of Protein-protein Interactions based on Sequence and	27.49
		Structural Analysis	26.48

	26.30	Construction of Regulatory Networks	26.49
	26.31	Chemical Phenotyping/Profiling	26.50
	26.32	Modular Organization of the Cell Machinery	26.50
	26.33	Nanotechnology	26.50
27 .	Olig	os-Chemical Genomics	27.1
	27.1	Oligos	27.1
	27.2	Mechanism of Interference	27.1
		Classes of Oligos	27.2
	27.4	Sites of Antisense Activity	27.2
		Chemical Genomics/Proteomics	27.3
	27.6	Small Molecules	27.4
28.	Gen	ome Comparison	28.1
	28.1	Application of Comparative Genomics	28.1
	28.2	De novo Identification of Protein Coding Sequences/ORFs	28.2
	28.3	Genome-wide Identification of Regulatory Elements	28.3
	28.4	Methodology for Genome-wide Discovery of Motifs	28.4
		Distinction between Different Types of Functional Elements	28.5
		CHIP-bound Motifs and Conserved Motifs	28.5
		Relationship between Chromosomal Gene order and Function	28.5
	28.8	Comparative Gene Mapping	28.7
		Comparative Genome Mapping	28.7
	28.10	Comparison between Species	28.9
		Comparison of Distantly Related Genomes	28.9
		Comparison of Closely Related Genomes	28.10
	28.13	Computational Genomics	28.10
		Comparative Genomic Comparison	28.11
		Genome Evolution	28.11
		Consequences of Genomic Duplication	28.12
	28.17	Selection of Suitable Set of Related Species	28.14
29.	In V	ivo and in Vitro Systems for Transcription and	
	Tran	slation	29.1
	29.1	Need for Cell Free Systems	29.1
	29.2	Cell-free Extract	29.2
	29.3	In Vitro Transcription	29.3
	29.4	Coupled Transcription-translation System	29.4
	29.5	In Vivo Transcription-translation System	29.4

30.	Chro	omatography and Electrophoresis	30.1
	30.1	Chromatography	30.1
	30.2	Mass spectrometry and Nuclear Magnetic Resonance	30.6
	30.3	X-ray Diffraction/Crystallography	30.8
	30.4	Electrophoresis	30.8
	30.5	Western Blotting	30.14
	30.6	Agarose Gel Electrophoresis	30.15
	30.7	Polyacrylamide Gel Electrophoresis	30.16
	30.8	Pulsed field Gel Electrophoresis (PFGE)/Orthogonal Field Alteration Gel Electrophoresis	30.18
	30 Q	Contour Clamped Homogeneous Electric Field Electrophoresis (CHEF)	30.20
		Denaturing Gradient Gel Electrophoresis (DGGE)	30.20
		Southern Blot	30.22
		Nothern Blot	30.23
		Autoradiography	30.24
		Electron Microscopy	30.24
31	31. Molecular Cytogenetic and Genetic Engineering Technique		
0 1.	31.1	Flow Cytometry	31.1 31.1
		Flow Sorting	31.3
		Chromsome Stretching	31.4
		Chromosome Fiber Stretching	31.4
		Molecular Combing	31.5
		Chromosome Microdissection	31.5
		DNA Cytophotometry	31.5
		Image Analysis	31.5
	31.9	Microdensitometer (Scanner)	31.5
	31.10	Matrix Assisted Laser Description Ionization Mass Spectrometer	
		(MALADI)	31.6
	31.11	Molecular Cytogenetics Techniques	31.6
	31.12	Interphase Cytogenetics	31.10
	31.13	RNase Protection Assay	31.20
	31.14	Imaging and Visualization Research Tools	31.20
	31.15	Polymerase Chain Reaction (PCR)	31.21
	31.16	Variants of PCR	31.28
	31.17	Fluorescence Probes for Imaging in Cell Biology	31.38
Refer	ences		R.1
Index	:		I.1