CONTENTS IN BRIEF

CHAPTER 1	GENOMES, TRANSCRIPTOMES, AND PROTEOMES	1
CHAPTER 2	STUDYING DNA	27
CHAPTER 3	MAPPING GENOMES	55
CHAPTER 4	SEQUENCING GENOMES	87
CHAPTER 5	GENOME ANNOTATION	119
CHAPTER 6	IDENTIFYING GENE FUNCTIONS	135
CHAPTER 7	EUKARYOTIC NUCLEAR GENOMES	155
CHAPTER 8	GENOMES OF PROKARYOTES AND EUKARYOTIC ORGANELLES	181
CHAPTER 9	VIRAL GENOMES AND MOBILE GENETIC ELEMENTS	203
CHAPTER 10	ACCESSING THE GENOME	219
CHAPTER 11	THE ROLE OF DNA-BINDING PROTEINS IN GENOME EXPRESSION	241
CHAPTER 12	TRANSCRIPTOMES	257
CHAPTER 13	PROTEOMES	293
CHAPTER 14	GENOME EXPRESSION IN THE CONTEXT OF CELL AND ORGANISM	329
CHAPTER 15	GENOME REPLICATION	357
CHAPTER 16	MUTATIONS AND DNA REPAIR	389
CHAPTER 17	RECOMBINATION AND TRANSPOSITION	411
CHAPTER 18	HOW GENOMES EVOLVE	429
GLOSSARY		463
INDEX		491

CONTENTS

CHAPTER 1		Ligases join DNA fragments together	37
GENOMES, TRANSCRIPTOMES,		End-modification enzymes	38
AND PROTEOMES	1	2.2 THE POLYMERASE CHAIN REACTION	38
ANDTHOTEOMES		Carrying out a PCR	39
1.1 DNA	2	The rate of product formation can be followed	1110
Genes are made of DNA	3	during a PCR	40
DNA is a polymer of nucleotides	4	PCR has many and diverse applications	41
The double helix is stabilized by base pairing		CHMONAP PANIANARA A HATA	
and base stacking	8	2.3 DNA CLONING	41
The double helix has structural flexibility	9	Why is gene cloning important?	41
1.2 RNA AND THE TRANSCRIPTOME	11	The simplest cloning vectors are based on <i>E. coli</i>	42
RNA is a second type of polynucleotide	12	plasmids	43
The RNA content of the cell	12	Bacteriophages can also be used as cloning vectors	44
Many RNAs are synthesized as precursor molecules	13	Vectors for longer pieces of DNA	47
There are different definitions of the transcriptome	15	DNA can be cloned in organisms other	
	1Aia	than E. coli	48
1.3 PROTEINS AND THE PROTEOME	16		
There are four hierarchical levels of protein structure	16	SUMMARY	50
Amino acid diversity underlies protein diversity	17	SHORT ANSWER QUESTIONS	51
The link between the transcriptome and the		里克林色切迹的 等目形态的 229000人 1015万里埃	
proteome	19	IN-DEPTH PROBLEMS	51
The genetic code is not universal	20	FURTHER READING	52
The link between the proteome and the	22		
biochemistry of the cell	22	TOTAL THE TOTAL TO	
SUMMARY	23	CHAPTER 3	
SHORT ANSWER QUESTIONS	24	MAPPING GENOMES	55
202		PEER 12 PROTEOMES	
IN-DEPTH PROBLEMS	24	3.1 WHY A GENOME MAP IS	
FURTHER READING	25	IMPORTANT Genome maps are needed in order to sequence	55
		the more complex genomes	55
CHAPTER		Genome maps are not just sequencing aids	57
CHAPTER 2		MODINALIGARANAMAA AFRATTO	ALLO
STUDYING DNA	27	3.2 MARKERS FOR GENETIC MAPPING	58
2 4 FNZVMES FOR DNA MANIEUM ATION	20	Genes were the first markers to be used	58
2.1 ENZYMES FOR DNA MANIPULATION The mode of action of a template-dependent DNA	28	RFLPs and SSLPs are examples of DNA markers	59
polymerase	28	Single-nucleotide polymorphisms are the most	
The types of DNA polymerase used in research	30	useful type of DNA marker	61
Restriction endonucleases enable DNA molecules	50	3.3 THE BASIS TO GENETIC MAPPING	63
to be cut at defined positions	32	The principles of inheritance and the discovery	03
Gel electrophoresis is used to examine the results		of linkage	63
of a restriction digest	34	Partial linkage is explained by the behavior of	
Interesting DNA fragments can be identified by		chromosomes during meiosis	65
Southern hybridization	35	From partial linkage to genetic mapping	68

3.4 LINKAGE ANALYSIS WITH DIFFERENT TYPES OF ORGANISMS Linkage analysis when planned breeding	69	Shotgun sequencing of eukaryotic genomes requires sophisticated assembly programs More complex genomes can be sequenced by a	102
experiments are possible	69	hierarchical shotgun approach	104
Gene mapping by human pedigree analysis	71	What is a genome sequence and do we always	
Genetic mapping in bacteria	73	need one?	107
The limitations of linkage analysis	74	4.4 A SURVEY OF EUKARYOTIC GENOME	
DUNGICAL MADDING BY DIDECT		SEQUENCING PROJECTS	109
3.5 PHYSICAL MAPPING BY DIRECT EXAMINATION OF DNA MOLECULES	75	The Human Genome Project: genome sequencing	109
Conventional restriction mapping is applicable	13	in the heroic age	109
only to small DNA molecules	75	The Neanderthal genome: assembly of an extinct	
Optical mapping can locate restriction sites in		genome by use of the human sequence as a	FUNC
longer DNA molecules	77	reference	110
Optical mapping can be used to map other	140	The giant panda genome: shotgun sequencing based entirely on next-generation data	111
features in a DNA molecule	79	The barley genome: the concept of gene space	113
3.6 PHYSICAL MAPPING BY ASSIGNING		The bulley genome: the concept of gene space	ubisse
MARKERS TO DNA FRAGMENTS	81	SUMMARY	115
Any unique sequence can be used as an STS	81	SHORT ANSWER QUESTIONS	115
DNA fragments for STS mapping can be obtained as			
radiation hybrids	82	IN-DEPTH PROBLEMS	116
A clone library can be used as the mapping reagent	83	FURTHER READING	117
SUMMARY	84		
SHORT ANSWER QUESTIONS	85	CHAPTER 5	
IN-DEPTH PROBLEMS	85	GENOME ANNOTATION	119
FURTHER READING	86	5.1 GENOME ANNOTATION BY COMPUTER	
		ANALYSIS OF THE DNA SEQUENCE	119
CHAPTER 4		The coding regions of genes are open reading	110
	07	frames	119
SEQUENCING GENOMES	87	Simple ORF scans are less effective with genomes of higher eukaryotes	120
4.1 CHAIN-TERMINATION SEQUENCING	87	Locating genes for noncoding RNA	122
Chain-termination sequencing in outline	87	Homology searches and comparative genomics	GIA
Not all DNA polymerases can be used for		give an extra dimension to gene prediction	123
sequencing	89	FURT A Extend of Mark Mark State of the Stat	
Chain-termination sequencing with <i>Taq</i> polymerase	90	5.2 GENOME ANNOTATION BY ANALYSIS OF GENE TRANSCRIPTS	124
Strengths and limitations of chain-termination sequencing	91	Hybridization tests can determine if a fragment	124
sequencing	21	contains transcribed sequences	125
4.2 NEXT-GENERATION SEQUENCING	92	Methods are available for precise mapping of the	
Preparation of a sequencing library is the common	SE	ends of transcripts	126
feature of next-generation methods	93	Exon-intron boundaries can also be located with	
Various next-generation sequencing methods have been devised	95	precision	126
Third- and fourth-generation methods enable		5.3 ANNOTATION BY GENOMEWIDE RNA	
sequencing in real time	97	MAPPING	127
4 3 HOW TO SEQUENCE A GENOME	00	Tiling arrays enable transcripts to be mapped onto	ntuza
4.3 HOW TO SEQUENCE A GENOME The potential of the shotgun method was proven	98	chromosomes or entire genomes	128
by the Haemophilus influenzae sequence	99	Transcript sequences can be directly mapped onto a genome	129
Many prokaryotic genomes have been sequenced		EPTH PROBLEMS AND SOURCE OF THE LOCAL PROPERTY AND ADDRESS OF THE PROPERTY AND ADDRESS	125
by the shotgun method	100	5.4 GENOME BROWSERS	131

SUMMARY	132	СНАРТЕЯ 7 ПО НТИМ ВІЗУПАМА ВОДИМ	
SHORT ANSWER QUESTIONS	132	EUKARYOTIC NUCLEAR	
IN-DEPTH PROBLEMS	133	GENOMES	155
FURTHER READING	133	7.1 NUCLEAR GENOMES ARE CONTAINED IN CHROMOSOMES	155
CHAPTER 6		Chromosomes are much shorter than the DNA molecules they contain	155
IDENTIFYING GENE FUNCTIONS	135	Special features of metaphase chromosomes	157
6.1 COMPUTER ANALYSIS OF GENE FUNCTION	135	DNA-protein interactions in centromeres and telomeres	159
Homology reflects evolutionary relationships	135	7.2 HOW ARE THE GENES ARRANGED IN A	
Homology analysis can provide information on the function of a gene	136	NUCLEAR GENOME? Genes are not evenly distributed within a genome	161 161
Identification of protein domains can help to		A segment of the human genome	162
assign function to an unknown gene	137	The yeast genome is very compact	164
Annotation of gene function requires a common terminology	138	Gene organization in other eukaryotes	165
6.2 ASSIGNING FUNCTION BY	30-11	7.3 HOW MANY GENES ARE THERE AND WHAT ARE THEIR FUNCTIONS?	167
GENE INACTIVATION AND	TRUE	Gene numbers can be misleading	168
OVEREXPRESSION Functional analysis by gene inactivation	139 140	Gene catalogs reveal the distinctive features of different organisms	169
Individual genes can be inactivated by	ALLES	Families of genes	172
homologous recombination	140	Pseudogenes and other evolutionary relics	174
Gene inactivation without homologous recombination	142	7.4 THE REPETITIVE DNA CONTENT OF	
Gene overexpression can also be used to assess function		EUKARYOTIC NUCLEAR GENOMES	176
The phenotypic effect of gene inactivation or	144	Tandemly repeated DNA is found at centromeres and elsewhere in eukaryotic chromosomes	176
overexpression may be difficult to discern	145	Minisatellites and microsatellites	176
6.3 UNDERSTANDING GENE FUNCTION		Interspersed repeats	177
BY STUDIES OF EXPRESSION PATTERN		SUMMARY	178
AND PROTEIN PRODUCT	146	SHORT ANSWER QUESTIONS	178
Reporter genes and immunocytochemistry can be used to locate where and when genes		IN-DEPTH PROBLEMS	179
are expressed	146	FURTHER READING	
Directed mutagenesis can be used to probe gene function in detail	147	FORTHER READING	179
6.4 USING CONVENTIONAL GENETIC		CHAPTER 8	
ANALYSIS TO IDENTIFY GENE		GENOMES OF PROKARYOTES	
FUNCTION Identification of human genes responsible for	149	AND EUKARYOTIC ORGANELLES	181
inherited diseases Genomewide association studies can also	150	8.1 PHYSICAL FEATURES OF PROKARYOTIC	need
identify genes for diseases and other traits	151	GENOMES The traditional view of the prokaryotic	181
SUMMARY	152	chromosome	181
SHORT ANSWER QUESTIONS	153	Some bacteria have linear or multipartite genomes	183
IN-DEPTH PROBLEMS		8.2 GENETIC FEATURES OF PROKARYOTIC	
	153	GENOMES	186
FURTHER READING	154	Gene organization in the E. coli K12 genome	186

Operons are characteristic features of prokaryotic		CHAPTER 10	
genomes	188	ACCESSING THE GENOME	219
Prokaryotic genome sizes and numbers of genes vary according to biological complexity	189	Abbass and the second recognition of the	
Genome sizes and numbers of genes vary within		10.1 INSIDE THE NUCLEUS The nucleus has an ordered internal	219
individual species	190	structure	220
Distinctions between prokaryotic species are further blurred by lateral gene transfer	192	The DNA content of a nondividing nucleus	14 8 500
Metagenomes describe the members of a	98 911	displays different degrees of packaging The nuclear matrix is thought to provide	221
community	194	attachment points for chromosomal DNA	222
8.3 EUKARYOTIC ORGANELLAR		Each chromosome has its own territory	
GENOMES	195	within the nucleus	223
The endosymbiont theory explains the origin of		Each chromosome comprises a series of topologically associated domains	224
organellar genomes	195	Insulators mark the boundaries of topologically	Idille
Most organellar genomes are circular	196	associated domains	226
The gene catalogs of organellar genomes	197	10.2 NUCLEOSOME MODIFICATIONS AND	eltects
SUMMARY	198	GENOME EXPRESSION	228
SHORT ANSWER QUESTIONS	200	Acetylation of histones influences many nuclear	
IN-DEPTH PROBLEMS	201	activities including genome expression	228
Manual Inches of Internation THAN		Histone deacetylation represses active regions of the genome	229
FURTHER READING	201	Acetylation is not the only type of histone	ag-M
		modification	230
CHAPTER 9		Nucleosome repositioning also influences gene expression	231
VIRAL GENOMES AND		expression	231
MOBILE GENETIC ELEMENTS	203	10.3 DNA MODIFICATION AND GENOME	
	11920	EXPRESSION Genome silencing by DNA methylation	234 234
9.1 THE GENOMES OF BACTERIOPHAGES AND EUKARYOTIC VIRUSES	202	Methylation is involved in genomic imprinting	234
Bacteriophage genomes have diverse structures	203	and X inactivation	235
and organizations	203	SUMMARY	236
Replication strategies for bacteriophage	205		
genomes Structures and replication strategies for	205	SHORT ANSWER QUESTIONS	237
eukaryotic viral genomes	206	IN-DEPTH PROBLEMS	238
Some retroviruses cause cancer	207	FURTHER READING	238
Genomes at the edge of life	209		
9.2 MOBILE GENETIC ELEMENTS	210	CHAPTER 11	
RNA transposons with long terminal repeats are	210	THE ROLE OF DNA-BINDING	
related to viral retroelements	210	PROTEINS IN GENOME	
Some RNA transposons lack long terminal repeats	212	EXPRESSION	241
DNA transposons are common in prokaryotic genomes	213	EXPRESSION AND ADDRESS OF THE PROPERTY OF THE	241
DNA transposons are less common in eukaryotic	identil	11.1 METHODS FOR STUDYING	
genomes	214	DNA-BINDING PROTEINS AND THEIR	241
SUMMARY	216	ATTACHMENT SITES X-ray crystallography provides structural data for	241
	216	any protein that can be crystallized	241
SHORT ANSWER QUESTIONS	216	NMR spectroscopy is used to study the structures	242
IN-DEPTH PROBLEMS	217	of small proteins Gel retardation identifies DNA fragments that	243
FURTHER READING	217	bind to proteins	244

Protection assays pinpoint binding sites with	244	RNA silencing was first identified as a means of destroying invading viral RNA	276
greater accuracy	244	MicroRNAs regulate genome expression by	Proka
Modification interference identifies nucleotides	246	causing specific target mRNAs to be degraded	278
central to protein binding	247	causing specific target minutes to be adjusted	Book
Genomewide scans for protein attachment sites	24/	12.4 INFLUENCE OF RNA PROCESSING	
11.2 THE SPECIAL FEATURES OF		ON THE COMPOSITION OF A	
DNA-BINDING PROTEINS	249	TRANSCRIPTOME	278
The helix-turn-helix motif is present in	213	The splicing pathway for eukaryotic pre-mRNA	
prokaryotic and eukaryotic proteins	249	introns	279
Zinc fingers are common in eukaryotic proteins	250	The splicing process must have a high degree of	
Other nucleic acid-binding motifs	251	precision	280
Other nucleic acid binding motils	III THE	Enhancer and silencer elements specify alternative	MHE
11.3 INTERACTION BETWEEN DNA AND ITS	5	splicing pathways	282
BINDING PROTEINS	252	THE PARTY OF THE PROPERTY OF THE PARTY OF TH	204
Direct readout of the nucleotide sequence	252	12.5 TRANSCRIPTOMES IN RESEARCH	284
The nucleotide sequence has a number of indirect		Transcriptome analysis as an aid to genome	284
effects on helix structure	253	annotation	286
Contacts between DNA and proteins	253	Cancer transcriptomes	200
ation of histories influencement a viscosity of the policy		Transcriptomes and the responses of plants	287
SUMMARY	254	to stress	207
SHORT ANSWER QUESTIONS	255	SUMMARY	289
IN-DEPTH PROBLEMS	256	SHORT ANSWER QUESTIONS	289
FURTHER READING	256	IN-DEPTH PROBLEMS	290
		FURTHER READING	290
CHAPTER 12			
	257	CUARTER 13	
TRANSCRIPTOMES	231	CHAPTER 13	176
12.1 COMPONENTS OF THE		PROTEOMES	293
TRANSCRIPTOME	257	A CONTROL OF THE COMPOSITION OF	
The mRNA fraction of a transcriptome is small		13.1 STUDYING THE COMPOSITION OF	202
but complex	257	A PROTEOME	293
Short noncoding RNAs have diverse functions	259	The separation stage of a protein profiling	294
Long noncoding RNAs are enigmatic transcripts	260	project	271
Microarray analysis and RNA sequencing are		The identification stage of a protein profiling	297
used to study the contents of transcriptomes	262	project Comparing the compositions of two proteomes	299
are empressed			2,,
12.2 SYNTHESIS OF THE COMPONENTS		Analytical protein arrays offer an alternative approach to protein profiling	300
OF THE TRANSCRIPTOME	263	approach to protein proming	ME C D
RNA polymerases are molecular machines	264	13.2 IDENTIFYING PROTEINS THAT	
for making RNA	264	INTERACT WITH ONE ANOTHER	301
Transcription start points are indicated by	266	Identifying pairs of interacting proteins	301
promoter sequences	200	Identifying the components of multiprotein	
Synthesis of bacterial RNA is regulated by	268	complexes	304
repressor and activator proteins	200	Identifying proteins with functional interactions	305
Synthesis of bacterial RNA is also regulated by control over transcription termination	271	Protein interaction maps display the interactions	
	ATTA	within a proteome	306
Synthesis of eukaryotic RNA is regulated primarily by activator proteins	272	c)ygmosoma YRAN	
primarily by activator proteins	any pro	13.3 SYNTHESIS AND DEGRADATION	
12.3 DEGRADATION OF THE		OF THE COMPONENTS OF THE	
COMPONENTS OF THE TRANSCRIPTOME	275	PROTEOME	308
Several processes are known for nonspecific		Ribosomes are molecular machines for making	200
PNA turnover	275	proteins	308

During stress, bacteria inactivate their ribosomes in order to downsize the proteome	311	Yeast mating types are determined by gene conversion events	338
Initiation factors mediate large-scale remodeling of eukaryotic proteomes	312	Genome rearrangements are responsible for immunoglobulin and T-cell receptor	
The translation of individual mRNAs can also be regulated	313	diversity MOTAL	339
Degradation of the components of the		14.3 CHANGES IN GENOME ACTIVITY	s reletativ
proteome	314	UNDERLYING DEVELOPMENT Bacteriophage λ: a genetic switch enables a choice to be made between alternative	34
13.4 INFLUENCE OF PROTEIN PROCESSING ON THE COMPOSITION		developmental pathways	342
OF THE PROTEOME The amino acid sequence contains instructions	315	Bacillus sporulation: coordination of activities in two distinct cell types	343
for protein folding	315	Caenorhabditis elegans: the genetic basis of	
Some proteins are activated by proteolytic cleavage	318	positional information and the determination of cell fate	346
Important changes in protein activity can be brought about by chemical modification	320	Fruit flies: conversion of positional information into a segmented body plan	348
as audionation for pour mean presta and un		Homeotic selector genes are universal features	monsi
13.5 BEYOND THE PROTEOME The metabolome is the complete set of	322	of higher eukaryotic development Homeotic genes also underlie plant	350
metabolites present in a cell	322	development	352
Systems biology provides an integrated description of cellular activity	323	SUMMARY	352
SUMMARY	326	SHORT ANSWER QUESTIONS	353
SHORT ANSWER QUESTIONS	326	IN-DEPTH PROBLEMS	354
IN-DEPTH PROBLEMS	327	FURTHER READING MOTTE BUD HEWEMAN	354
FURTHER READING	327		
		CHAPTER 15 DINIGABR REL	
CHAPTER 14		GENOME REPLICATION	357
GENOME EXPRESSION		15.1 THE TOPOLOGY OF GENOME	
IN THE CONTEXT OF CELL		REPLICATION The double-helical structure complicates the	357
AND ORGANISM	329	replication process	358
14.1 THE RESPONSE OF THE GENOME		The Meselson–Stahl experiment proved that replication is semiconservative	359
TO EXTERNAL SIGNALS Signal transmission by import of the	330	DNA topoisomerases provide a solution to the topological problem	261
extracellular signaling compound	330	Variations on the semiconservative theme	361 363
Receptor proteins transmit signals across cell membranes	332	15.2 THE INITIATION PHASE OF GENOME	
Some signal transduction pathways have few steps between receptor and genome		REPLICATION	364
Some signal transduction pathways have many	333	Initiation at the <i>E. coli</i> origin of replication Origins of replication have been clearly defined	364
steps between receptor and genome	334	in yeast	365
Some signal transduction pathways operate via second messengers	336	Origins in higher eukaryotes have been less easy to identify	366
14.2 CHANGES IN GENOME ACTIVITY		15.3 EVENTS AT THE REPLICATION FORK	367
RESULTING IN CELLULAR DIFFERENTIATION	336	DNA polymerases are molecular machines for making (and degrading) DNA	367
Some differentiation processes involve changes to chromatin structure		DNA polymerases have limitations that	
- Indin Structure	336	complicate genome replication	369

Okazaki fragments must be joined together to complete lagging-strand replication	370	Defects in DNA repair underlie human diseases, including cancers	406
15.4 TERMINATION OF GENOME		SUMMARY	406
REPLICATION	372	SHORT ANSWER QUESTIONS	407
Replication of the <i>E. coli</i> genome terminates within a defined region	373	IN-DEPTH PROBLEMS	407
Little is known about termination of replication in eukaryotes	374	FURTHER READING	408
Telomerase completes replication of chromosomal DNA molecules, at least in some cells	375	NELUENCE OF PROTEIN	
Telomere length is implicated in cell senescence	3/3	CHAPTER 17	
and cancer	378	RECOMBINATION AND	444
Drosophila has a unique solution to the	379	TRANSPOSITION	411
end-shortening problem 15.5 REGULATION OF EUKARYOTIC	3/9	17.1 HOMOLOGOUS RECOMBINATION The Holliday and Meselson–Radding models for	412
GENOME REPLICATION	380	homologous recombination	412
Genome replication must be synchronized with the cell cycle	380	The double-strand break model for homologous recombination	414
Origin licensing is the prerequisite for passing		RecBCD is the most important pathway for	445
the G1–S checkpoint	380	homologous recombination in bacteria <i>E. coli</i> can also carry out homologous	415
Replication origins do not all fire at the same time The cell has various options if the genome is	382	recombination by the RecFOR pathway	417
damaged	383	Homologous recombination pathways in eukaryotes	417
SUMMARY	384	The primary role of homologous recombination	418
SHORT ANSWER QUESTIONS	385	is thought to be DNA repair	
IN-DEPTH PROBLEMS	385	17.2 SITE-SPECIFIC RECOMBINATION Bacteriophage λ uses site-specific recombination	419
FURTHER READING	386	during the lysogenic infection cycle Site-specific recombination is an aid in	419
		construction of genetically modified plants	421
CHAPTER 16		17.3 TRANSPOSITION	421
MUTATIONS AND DNA REPAIR	389	Replicative and conservative transposition of DNA transposons	422
16.1 THE CAUSES OF MUTATIONS Errors in replication are a source of point	389	Retroelements transpose replicatively via an	O MA
mutations	390	RNA intermediate	423
Replication errors can also lead to insertion and deletion mutations	391	SUMMARY	425
Mutations are also caused by chemical and	JE DE V	SHORT ANSWER QUESTIONS	426
physical mutagens	394	IN-DEPTH PROBLEMS	427
16.2 REPAIR OF MUTATIONS AND OTHER		FURTHER READING	427
TYPES OF DNA DAMAGE	398		
Direct repair systems fill in nicks and correct some types of nucleotide modification	398	CHAPTER 18	
Base excision repairs many types of damaged nucleotide	399	HOW GENOMES EVOLVE	429
Nucleotide excision repair is used to correct more	401	18.1 GENOMES: THE FIRST 10 BILLION	100
extensive types of damage Mismatch repair corrects replication errors	401 402	YEARS The first biochemical systems were centered	429
Single- and double-strand breaks can be repaired	403	on RNA	429
If necessary, DNA damage can be bypassed during	74/10	The first DNA genomes	432
genome replication	405	How unique is life?	433

491