16.3 DNA Density

strands bands

First generation (grown on light W 14N medium)

Second generatiOn (grown on light 14N medium) W @

16.4 The phosphate end of each strand is the 5' end, and the hydroxyl group extending from the 3' carbon of the sugar marks the 3' end. See Figure 16.7 in the text.

16.5
helicase
single-strand binding protein
DNA pol Ill
leading strand
lagging strand
DNA ligase
DNA pol 1 (replacing primer)
Okazaki fragment
RNA primer
replication fork
primase
3' end of parental strand

m. 5' end

SUGGESTED ANSWERS T0 STRUCTURE YOUR KNOWLEDGE

1. Watson and Crick used the X-ray diffraction photo of Franklin to deduce that DNA was a helix 2 nm wide, with nitrogenous bases stacked 0.34 nm apart, and making a full turn every 3.4 nm. Franklin had concluded that the sugar—phosphate backbones were on the outside of the helix with the bases extending inside. Using molecular models of wire, Watson and Crick experimented with various arrangements and finally paired of a purine base with a pyrimidine base, which produced the proper diameter. Specificity of base pairing (A with T and C with G) is assured by hydrogen bonds.

Replication bubbles form where proteins recognize spedfic base sequences and open up the two strands. Helicase, an enzyme that works at the replication fork, untwists the helix and separates the strands. Topoisomemse eases the twisting ahead of the replication fork. Single—strand binding proteins support the separated strands while replication takes place. Primase lays down about 10 RNA bases to start the new strand. After a proper base pairs up on the exposed template, DNA polymerase III joins the nucleotide to the 3' end of the new strand. On the lagging strand, short Okazaki fragments are formed by primase and polymerase (again moving 5' —> 3'). DNA polymerase I replaces the primer. Ligase joins the 3' end of one fragment to the 5' end of its neighbor. Proofreading enzymes check for mispaired bases, and nucleases, DNA polymerase, and other enzymes repair damage or mismatches.

ANSWERS TO TEST YOUR KNOWLEDGE

Multiple Choice:

1. c 6. a 10. a 14. a 18. d
2. a 7. b 11. e 15. d 19. e
3. b 8. e 12. cl 16. b 20. c
4. cl **9** c 13. e 17. c 21. a
5. b

CHAPTER 17: FROM GENE TO PROTEIN

[INTERACTIVE QU ESTIONS

17.1 DNA transcription; RNA translation protein

17.2 Met Pro Asp Phe Lys stop

17.3 a. Initiation: Transcription factors bind to promoter and facilitate the binding of RNA polymerase II, forming a transcription initiation complex; RNA polymerase II separates DNA strands at initiation site.

b. Elongation: RNA polymerase II moves along DNA strand, connecting RNA nucleotides that have paired to the DNA template to the 3' end of the growing RNA strand.

c. Termination: After polymerase transcribes past a termination and a polyadenylation signal sequence, the pre-mRNA is cut and released.

17.4 A 5' cap consisting of a modified guanosine triphosphate is added to the 5' UTR. A poly-A tail consisting of up to 250 adenine nucleotides is

attached to the 3' UTR. Spliceosomes have cut out the introns and spliced the exons together.

17.5 17.7 A ribosome that is translating an mRNA that codes for a secretory or membrane protein will become QNA mRNA . . . bound to the ER when an SRP binds to the initial THPIEt Codon AntICOdon Ammo Amd signal peptide and then to an ER receptor protein **3'—>5'** 5'—>3' 3'fi5' '

TAG AUG UAC **memmmne** that specifies the amino acid sequence of a protein carries the code from DNA

GGA CCU GGA profine teins to ribosomes.

TTC AAG UUC lysme its position in a polypeptide base Transfer RNA carries a specific amino acid to

ATC UAG AUC stop its anticodon to an mRN A codon.

c. Ribosomal RNA makes up 60% of ribosomes

17.6 1. Codon recognition: An elongation factor (not and has structural and catalytic functions.
shown) helps an aminoacyl tRNA into the A site d. Small nuclear RNA is part of spliceosomes
where its anticodon base—pairs to the 'mRN A and plays a catalytic role in splicing pre—mRNA.
codon; two GTP increase accuraty and efficiency, e. SRP RNA is part of Signal-recognition particle
2. Peptide bond formation: Ribosome catalyzes that binds to signal peptides of polypeptides tar-
peptide bond formation between new amino geted to the ER.
acid and polypeptide held in P site. f. Small nucleolar RNA aids in processing pre-
3. Translocation: The tRNA in the P site is moved rRNA transcripts in the nucleolus.
to the E site and released; the tRNA now holding g. Small interfering RNA and microRNA are
the polypeptide is moved from the A to the P site, small single— and double—stranded RNA mole-
taking the mRN A with it; one GTP is required. cules that play role in regulating gene expression.
4' Term1nat10n: Release factor b1nds to stop 17.9 a. Silent: a base—pair substitution producing a
codon in the A site. Free polypeptide is released codon that still codes for the same amino acid.
from the P site. Ribosomal subunits and other as- b. Missense: a base—pair substitution or frameshift
sembly components separate. mutation that results in a codon for a different
a. amino end of grow- g. peptide bond amino acid.
ing polypeptide formation c. Nonsense: a base—pair substitution or
b.' aminoacyl tRNA h. **E** site frameshift mutation that creates a stop codon
c. large subunit i. release factor and prematurely terminates translation.
of ribosome j. termination d. Frameshift: an insertion or deletion of one,
d. A site (stop) codon two, or more than three nucleotides that disrupts
e. small subunit k. P site the reading frame and creates extensive mis-
of ribosome 1. free polypeptide sense and nonsense mutations.
f. 5' end of mRNA

SUGGESTED ANSWERS TO STRUCTURE YOUR KNOWLEDGE

1.

	Transcription	Translation
Template	DNA	RNA
Location	nucleus (cytoplasm in prokaryotes)	cytoplasm; ribosomes can be free or attached to ER
Molecules involved	RNA nucleotides, DNA template strand, RNA polymerase, transcription factors	amino acids, tRNA, mRN A, ribosomes, ATP, GTP, enzymes, initiation, elongation, and release factors
Enzymes involved	RNA polymerases, RNA processing enzymes	aminoacyl—tRNA synthetase, ribosomal ribozymes enzymes
Control	transcription factors locate promoter region with initiation factors, initiation sequence (AUG), start and stop	TATA box, polyadenylation signal sequence	stop codons, release factor
Product	primary transcript (pre-mRNA)	protein

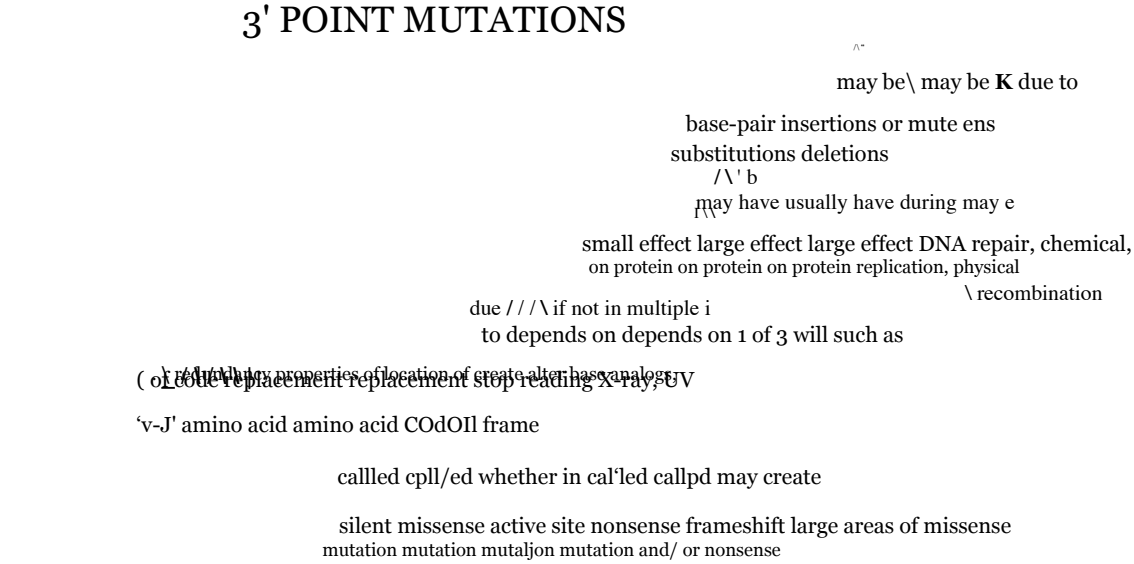
Product RNA processing: 5' cap and poly-A tail, spontaneous folding, disulfide bridges, signal processing Splicing of pre-mRNA—"introns removed by peptide removed, cleaving, quaternary structure,	snRNPs in spliceosomes	modification with sugars, etc.
Energy source	ribonucleoside triphosphate	ATP and GTP

2. The genetic code is the RNA triplets that code for amino acids. The order of these codons is specified by the sequence of nucleotides on DNA, which is transcribed into the codons found on mRNA and translated into their corresponding amino acids. There are 64 possible mRNA codons created from the four nucleotides used in the triplet code (43).

Redundancy of the code refers to the fact that several triplets may code for the same amino acid. Often these triplets differ only in the third nucleotide. The wobble phenomenon explains the fact that there are only about 45 different tRNA molecules that pair with the 61 possible codons (three codons are stop codons). The third nucleotide of many tRNAs can pair with more than one base. Because of the redundancy of the genetic code, these wobble tRNAs still place the correct amino acid in position.

The genetic code is nearly universal; each codon codes for exactly the same amino acid in almost all organisms. (Some exceptions have been found.) This universality points to an early evolution of the code in the history of life and the evolutionary relationship of all life on Earth.

3' POINT MUTATIONS



ANSWERS TO TEST YOUR KNOWLEDGE

Multiple Choice:

1. d 4. e 7. c 10. e 13. d 16. e 19. b 22. d
2. a 5. c 8. c 11. d 14. c 17. e 20. a 23. e
3. b 6 b 9. b 12. d 15. b 18. b 21. a 24. b

CHAPTER 18: THE GENETICS OF VIRUSES AND BACTERIA

I INTERACTIVE QUESTIONS

18.1 1. Phage attaches to host cell and injects DNA.
2. Phage DNA forms circle. Certain factors determine which cycle is entered.
3. New phage DNA and proteins are synthesized.
4. Bacterium lyses, releasing phages.
5. Phage DNA integrates into bacterial chromosome.
6. Bacterium reproduces, passing prophage to daughter cells.

sized and self-assemble into phages.

7. Colony of infected bacteria forms.

Page 4

8. Occasionally, prophage exits bacterial chromosome and begins lytic cycle.

phage DNA

. bacterial chromosome

new phages

. prophage

replicated bacterial chromosome with

p ophage

18.2 RNA —> DNA —> RNA; viral reverse transcriptase, host RNA polymerase

18.3 DNA
RNA
protein capsid
host
bacterium
lytic or lysogenic cycles
animal
viral envelope
reverse transcriptase
plant
viroids
plasmids
m. transposons

18.4 A temperate phage that leaves the lysogenic cycle and enters the lytic cycle may carry bacterial genes that were adjacent to the insertion site of the prophage.

18.5 circular chromosome

. F plasmid, **R** plasmid
mutation
transformation
naked DNA
transduction
phage
conjugation
FL or Hfr, and F‘ cells
transposons
antibiotic-resistant genes

18.6 regulatory gene

. promoter
operator

. genes
operon
RNA polymerase
active repressor

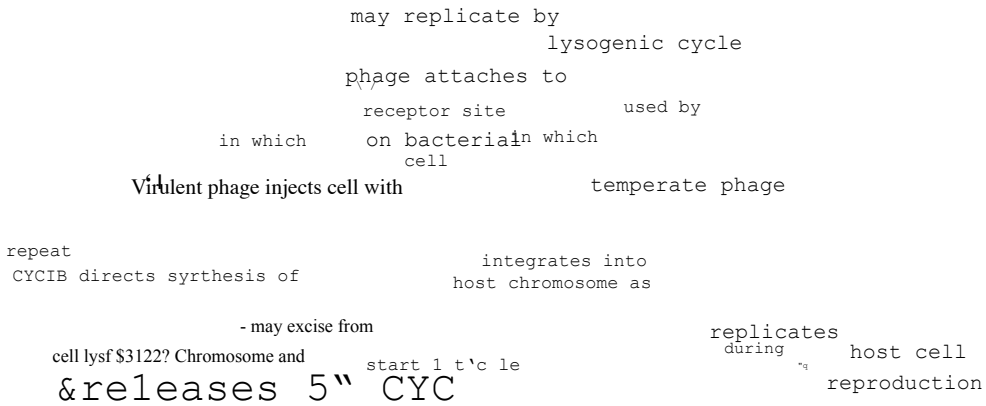
. inducer (allolactose)
mRNA for enzymes of pathway

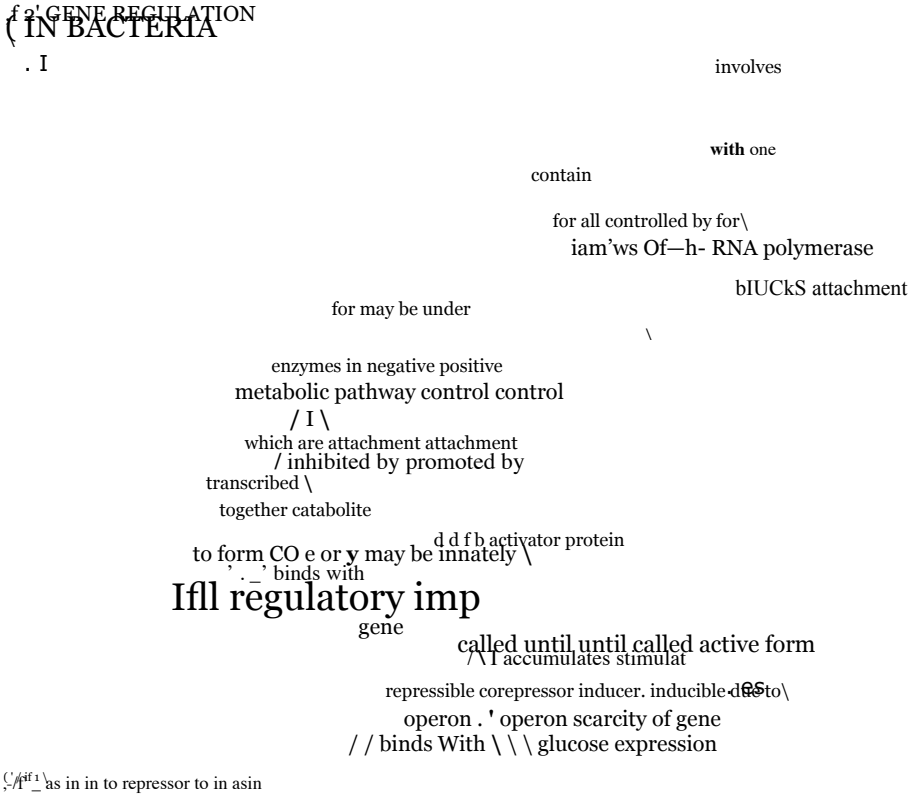
18.7 anabolic; corepressor; on; inactive

. catabolic; inducers; off; active

SUGGESTED ANSWERS To STRUCTURE YOUR KNOWLEDGE

1.





ANSWERS TO **TEST** YOUR KNOWLEDGE

Multiple Choice:

1. b 4. e 7. b 10. d 13. a 16. d 19. b 22. e 25. a
2. d 5. a 8. b 11. a 14. e 17. c 20. aord 23. b 26. a
3. C 6. d 9. **C** 12. b 15. c 18. e 21. d 24. c

Matching:

1. C 3. G 5. F 7. A
2. D **4** E 6. B 8 H

CHAPTER 19 EUKARYOTIC GENOMES: ORGANIZATION. REGULATION, AND EVOLUTION

I INT E RACTIV E Q U E ST] 0 N S b. Histone tail deacetylation would decrease transcription because it would make genes in the

19.1 nucleosomes (lO-nm fiber); SO-nm fiber; looped .

domains (BOO—run fiber); coiling and folding of looped domains into highly condensed meta— phase chromosome

nucleosome less accesmble.

(. a. distal control elements in enhancer b. activators

‘ 19.2 a. Barr body—compacted X chromosome in cells of female

3 DNA-bending protein

. pr0moter

e. mediator proteins
f. transcription factors
g. TATA box
h. RNA polymerase

19.4 a. Regulatory proteins may bind to sequences in the 5’ UTR and block attachment of ribosomes, thus decreasing gene expression. Sequences in the 3' UTR may affect the length of time an mRNA remains intact, thus either increasing or decreasing gene expression.
b. These small, single—stranded RNA molecules (miRNAs) join with a complex of proteins and act to decrease gene expressiOn by base-pairing with target mRNA and either blocking translation or degrading the mRNA.

19.5 Cell-cycle simulating pathway involving Ras: (1) and (2) growth factor binds with receptor. (3) G protein Ras is activated, and (4) sets off protein kinase cascade. (5) Transcription factor is activated that turns on gene. (6) Protein produced that stimulates cell cycle. Mutation to the Ras gene may create a hyperactive Ras protein that signals without binding of growth factor.
Cell-cycle inhibiting pathway involving p53: (1) Damage to DNA signals (2) protein kinase cascade that (3) activates p53. This transcription factor turns on gene for (4) protein that inhibits cell cycle so that damaged DNA does not replicate. **A** mutation may result in a missing or defective p53 transcription factor. The protein that inhibits the cell cycle would not be produced.

19.6 1. D 1.5%
2. **F** 24
3. B 44
4. A 3
5. E 5
6. C 15

19.7 The lysozyme gene, which codes for a bacterial infection—fighting enzyme, was present in the last common ancestor of birds and mammals. After their lineages split, the gene underwent a duplication event in the mammalian lineage, and a copy of the lysozyme gene evolved into a gene coding for a protein involved in milk production.

SUGGESTED ANSWERS T0 STRUCTURE YOUR KNOWLEDGE

b. Transcription factors (activators) bind with enhancers, then interact with mediator proteins and promoter regiOns to form transcription initiation complex; repressors can inhibit transcription; steroid hormones or other chemical messages may bind with receptor proteins, producing transcription factors
c. RNA processing (alternative splicing, 5’ cap and poly—A tail added); mRNA degradation by shortening of poly-A tail, removal of 5’cap, and miRNA targeting
d. Repressor proteins may prevent ribosome binding so mRNA can be stockpiled (awaiting fertilization in ovum); activation of initiation factors
e. Protein processing by cleavage or modification; transport to target location; selective degradation by proteosomes of proteins marked with ubiquitin

a. Proto—oncogenes are key genes that control cellular growth and division. When such genes mutate to form a more active product, become amplified (multiple copies), or have changes in their normal control mechanisms, they may become oncogenes and produce the uncontrolled cell division that leads to formation of a tumor.
b. Tumor-suppressor genes code for proteins that regulate cell division. Loss or mutation of both alleles of a tumor-suppressor gene may allow tumors to develop. Usually mutations or other changes must occur both in oncogenes and in several suppressor genes for cancer to develop.

a. Retrotransposons are transposable elements that move about a genome as an RNA intermediate, which is converted back into DNA by reverse transcriptase, coded for by the retrotransposon.
19. By moving copies of themselves around the genome, retrotransposons provide locations for recombination between different chromosomes. They may also transport genes or exons to new locations and interrupt coding or regulatory sequences.

ANSWERS TO TEST YOUR KNOWLEDGE

Multiple Choice:

1. b 6. e 11. d 16. d

1. a. DNA packing into nucleosomes; histone tail acetylation increases, whereas deacetylation and methylation of tails decreases transcription; methylation of DNA may be involved in long-term inactivation of genes

2. a 7. c 12. e 17. c
3. e 8. d 13. a 18. e
4. b 9. c 14. b 19. c
5. d 10. e 15. b 20. e