Chapter 17: From Gene to Protein

1. What is gene expression?

Gene expression is the process by which DNA directs the synthesis of proteins (or, in some cases, just RNAs). The expression of genes that code for proteins includes two stages: transcription and translation.

2. What situation did Archibald Garrod suggest caused inborn errors of metabolism?

In 1902, Garrod suggested that genes dictate phenotypes through enzymes that catalyze specific chemical reactions in the cell. He postulated that the symptoms of an inherited disease reflect a person's inability to synthesize a particular enzyme.

3. Describe one example Garrod used to illustrate his hypothesis.

Garrod gave as one example the hereditary condition called alkaptonuria. In this disorder, the urine is black because it contains the chemical alkapton, which darkens upon exposure to air. Garrod reasoned that most people have an enzyme that metabolizes alkapton, whereas people with alkaptonuria have inherited an inability to synthesize that enzyme.

4. State the hypothesis formulated by George Beadle while studying eye color mutations in fruit flies.

In the 1930s, Beadle speculated that in *Drosophila*, each of the various mutations affecting eye color blocks pigment synthesis at a specific step by preventing production of the enzyme that catalyzes that step. However, neither the chemical reactions nor the enzymes that catalyze them were known at the time.

5. What strategy did Beadle and Tatum adopt to test this hypothesis?

Beadle and Tatum bombarded *Neurospora* with X-rays, shown in the 1920s to cause genetic changes, and then looked among the survivors for mutants that differed in their nutritional needs from the wild-type bread mold. Beadle and Tatum identified mutants that could not survive on minimal medium, apparently because they were unable to synthesize certain essential molecules from the minimal ingredients. To characterize the metabolic defect in each nutritional mutant, Beadle and Tatum took samples from the mutant growing on complete medium and distributed them to a number of different vials. Each vial contained minimal medium plus a single additional nutrient. The particular supplement that allowed growth indicated the metabolic defect.

6. Which organism did Beadle and Tatum use in their research? How did its nutritional requirements facilitate this research?

Wild-type *Neurospora* has modest food requirements. It can grow in the laboratory on a simple solution of inorganic salts, glucose, and the vitamin biotin, incorporated into agar, a support medium. From this minimal medium, the mold cells use their metabolic pathways to produce all the other molecules they need. Mutating the wild type allowed Beadle and Tatum to identify metabolic defects.

7. How were Neurospora *spores treated to increase the mutation rate?*

The spores were treated with radioactivity.

8. Outline the technique used to identify and isolate mutant fungi.

Srb and Horowitz grew three classes of mutants, each defective in a different gene, under four different conditions: minimal medium (MM) as control, MM with ornithine, MM with citrulline, and MM with arginine as another control. They knew that wild-type cells could grow on MM but mutant cells could not. The results showed that the wild-type strain was capable of growth under all experimental conditions, requiring only MM. The three classes of mutants each had specific growth requirements from which Srb and Horowitz deduced that each class of mutant was unable to carry out one step in the pathway for synthesizing arginine, presumably because it lacked the necessary enzyme. Because each of their mutants was mutated in a single gene, they concluded that each mutated gene must normally dictate the production of one enzyme.

9. Cite two significant findings that resulted from the research of Beadle and Tatum.

Beadle and Tatum's research suggested that each class of mutants was blocked at a different step in the metabolic pathway because mutants in that class lacked the enzyme that catalyzes the blocked step. Because each mutant was defective in a single gene, Beadle and Tatum saw that, taken together, the collected results provided strong support for a working hypothesis they had proposed earlier. The "one gene, one enzyme" hypothesis states that the function of a gene is to dictate the production of a specific enzyme.

10. What revision of detail (but not of basic principle) did this hypothesis undergo as more information was gained?

Not all proteins are enzymes! Many proteins are constructed from two or more different polypeptide chains, and each polypeptide is specified by its own gene. Beadle and Tatum's hypothesis was therefore restated as the "one gene, one polypeptide" hypothesis.

11. What are three ways in which RNA differs from DNA?

RNA is chemically similar to DNA, except that it contains ribose instead of deoxyribose as its sugar and has the nitrogenous base uracil rather than thymine. Thus, each nucleotide along a DNA strand has A, G, C, or T as its base, and each nucleotide along an RNA strand has A, G, C, or U as its base. An RNA molecule usually consists of a single strand. Unlike DNA, RNA does not have repair enzymes.

12. What are the monomers of DNA and RNA? Of proteins?

The monomers of DNA and RNA are nucleotides. The monomers of proteins are amino acids.

13. Discuss transcription and translation, which are essential to the function of a protein.

Transcription is the synthesis of RNA using information in the DNA. The two nucleic acids are written in different forms of the same language, and the information is simply transcribed, or "rewritten," from DNA to RNA. Just as a DNA strand provides a template for making a new complementary strand during DNA replication, it can also serve as a template for assembling a complementary sequence of RNA nucleotides. For a protein-coding gene, the resulting RNA molecule is a faithful transcript of the gene's protein-building instructions. This type of RNA molecule is called messenger RNA because it carries a genetic message from the DNA to the protein-synthesizing machinery of the cell.

Translation is the synthesis of a polypeptide using the information in the mRNA. During this stage, there is a change in language: the cell must translate the nucleotide sequence of an mRNA molecule into the amino acid sequence of a polypeptide. The sites of translation are ribosomes, complex particles that facilitate the orderly linking of amino acids into polypeptide chains.

14. Complete the table to summarize each process.

	Template	*Product Synthesized*	*Location in Eukaryotic Cell*
Transcription	DNA	RNA	nucleus
Translation	mRNA	polypeptide	cytoplasm

15. What is the pre-mRNA called in eukaryotes?

The initial RNA transcript from any gene, including those specifying RNA that is not translated into protein, is more generally called a primary transcript.

16. What is the central dogma of molecular genetics, as proclaimed by Francis Crick?

Genes program protein synthesis via genetic messages in the form of messenger RNA. Cells are governed by a molecular chain of command with a directional flow of genetic information: DNA → RNA → protein

17–19. How many nucleotide bases are there?

There are four nucleotide bases and 20 amino acids. Three nucleotides are required to code for these 20 amino acids. So, the language of DNA is a triplet code, and 64 unique triplets exist.

20. DNA is double-stranded, but for each protein, only one of these two strands is used to produce an mRNA transcript.

The template strand provides the pattern, or template, for the sequence of nucleotides in an RNA transcript. For any given gene, the same strand is used as the template every time the gene is transcribed. For other genes on the same DNA molecule, however, the opposite strand may be the one that always functions as a template.

21. Assemble the complementary mRNA strand of the DNA template: 3' A C G A C C A G T A A A 5'

5' U G C U G G U C A U U U 3'

22. How many codons are there? Label one codon.

There are four codons: UGC, UGG, UCA, and UUU.

23. Describe Nirenberg's experiment in which he identified the first codon.

Nirenberg synthesized an artificial mRNA by linking identical RNA nucleotides containing uracil as their base. No matter where this message started or stopped, it could contain only one codon in repetition: UUU. Nirenberg added this "poly-U" to a test-tube mixture containing amino acids, ribosomes, and the other components required for protein synthesis. His artificial system translated the poly-U into a polypeptide containing many units of the amino acid phenylalanine (Phe), strung together as a long polyphenylalanine chain. Thus, Nirenberg determined that the mRNA codon UUU specifies the amino acid phenylalanine.

24. What was the first codon–amino acid pair to be identified?

UUU codes for the amino acid phenylalanine.

25. Of the 64 possible codons, how many code for amino acids?

61 code for amino acids, while 3 others function as "stop" signals, marking where ribosomes end translation.

26. What event is coded for by UAA, UAG and UGA?

UAA, UAG and UGA are the three stop codons.

27. What is the start codon?

AUG stands for both the amino acid methionine and the "start" signal for ribosomes to begin translating the mRNA at that point.

28. Why is the genetic code redundant but not ambiguous?

Although different codons may code for the same amino acid (redundancy), no codon ever specifies for more than one amino acid (ambiguity). Thus, there is redundancy in the genetic code, but no ambiguity.

29. Explain the concept of reading frame.

Our ability to extract the intended message from a written language depends on reading the symbols in the correct groupings; that is, in the proper reading frame. On a strand of mRNA, the reading frame is the left to right (5' to 3') triplet grouping of nucleotides used by the cell's protein-synthesizing machinery.

31. Name the enzyme that uses the DNA template strand to transcribe a new mRNA strand.

RNA polymerase priest the two strands of DNA apart and joins together RNA nucleotides complementary to the DNA template strand, thus elongating the RNA polynucleotide.

32. DNA polymerase III adds new nucleotides to the template DNA strand to assemble each new strand of DNA.

Both enzymes can assemble a new polynucleotide only in the 5' (left to right) direction. However, RNA polymerase does not require a primer to begin synthesis.

33. What is a transcription unit?

In bacteria, the RNA polymerase itself specifically recognizes and binds to the promoter. In eukaryotes, a collection of proteins called transcription factors mediate the binding of RNA polymerase and the initiation of transcription. Only after transcription factors are attached to the promoter does RNA polymerase II bind to it.

34. Name the three stages of transcription and briefly describe each stage.

Initiation: After RNA polymerase binds to the promoter, the DNA strands unwind, and the polymerase initiates RNA synthesis at the start point on the template strand. Elongation: The polymerase moves downstream, unwinding the DNA

and elongating the RNA transcript 5' to 3'. In the wake of transcription, the DNA strands re-form a double helix. Termination: Eventually, the RNA transcript is released, and the polymerase detaches from the DNA.

35. List three important facts about RNA polymerase binding and initiation of transcription.

The promoter of a gene includes the transcription start point and typically extends for several dozen more nucleotide pairs upstream from the start point. RNA polymerase binds in a precise location and orientation on the promoter.

36. Explain the three stages of initiation.

A eukaryotic promoter commonly includes a TATA box, a nucleotide sequence containing TATA, about 25 nucleotides upstream from the transcriptional start point. Several transcription factors, one recognizing the TATA box, must bind to the DNA before RNA polymerase II can bind in the correct position and orientation.

37. What is the TATA box?

The TATA box is a crucial promoter DNA sequence consisting of thymine and adenine.

38. What comprises a transcription initiation complex?

The whole complex of transcription factors and RNA polymerase II bound to the promoter is called a transcription initiation complex.

39. Describe the process by which mRNA is formed.

A promoter, often including a TATA box in eukaryotes, establishes where RNA synthesis is initiated. Beginning at the start point on the template strand, RNA synthesis is catalyzed by RNA polymerase, which links together RNA nucleotides complementary to a DNA template strand. The RNA transcript runs 5' to 3', the reverse of the template. Transcription factors help eukaryotic RNA polymerase recognize promoter sequences, forming a transcription initiation complex. Transcription follows the same base-pairing rules as DNA replication, except that in RNA, uracil substitutes for thymine. The three stages of transcription are initiation, elongation, and termination. The mechanisms of termination are different in bacteria and eukaryotes. In bacteria, transcription proceeds through a terminator sequence in DNA. In eukaryotes, RNA pol II transcribes a specific signal sequence, which codes for a termination signal.

40. RNA processing occurs only in eukaryotic cells. The primary transcript is altered at both ends, and sections in the middle are removed. What happens at each end?

The 5' end is synthesized first; it receives a 5' cap, a modified form of a guanine nucleotide added onto the 5' end after the transcription of the first 20 to 40 nucleotides. The 3' end of the pre-mRNA molecule is also modified before the mRNA exits the nucleus. Recall that the pre-mRNA is released soon after the polyadenylation signal, AAUAAA, is transcribed. At the 3' end, an enzyme adds 50 to 250 more adenine nucleotides, forming a poly-A tail.

41. What are three important functions of the 5' cap and poly-A tail?

First, they seem to facilitate the export of the mature mRNA from the nucleus. Second, they help protect the mRNA from degradation by hydrolytic enzymes. Third, they help ribosomes attach to the 5' end of the mRNA once the mRNA reaches the cytoplasm.

42. Distinguish between introns and exons.

The noncoding segments of nucleic acid that lie between coding regions are called intervening sequences, or introns. The other regions are called exons, because they are eventually expressed, usually by being translated into the amino acid sequences. (Exceptions include the UTRs of the exons at the ends of the RNA, which make up part of the mRNA but are not translated into protein. Exons are sequences of RNA that exit the nucleus.

44. What are snRNPs? What two types of molecules make up a snurp?

The signal for RNA splicing is a short nucleotide sequence at each end of an intron. Particles called small nuclear ribonucleoproteins (snRNPs), recognize these splice sites. SnRNPs are located in the cell nucleus and are composed of RNA and protein molecules.

45. You will be introduced to a number of small RNAs in this course. What type is the RNA in a snRNP?

The RNA in a snRNP particle is called a small nuclear RNA (snRNA). Each snRNA molecule is about 150 nucleotides long.

46. Snurps band together in little snurp groups to form spliceosomes. How do spliceosomes work?

A spliceosome, almost as big as a ribosome, interacts with certain sites along an intron, releasing the intron, which is rapidly degraded, and joining together the two exons that flanked the intron. SnRNAs catalyze these processes, as well as participating in spliceosome assembly and splice site recognition.

48. Explain how the splice sites are recognized.

SnRNPs and other proteins from a molecular complex called a spliceosome on a pre-mRNA molecule containing exons and introns. Within the spliceosome, snRNA base-pairs with nucleotides at specific sites along the intron. The spliceosome cuts the pre-mRNA, releasing the intron for rapid degradation, and at the same time splices the exons together. The spliceosome then comes apart, releasing mRNA, which now contains only exons.

49. What is a ribozyme?

Ribozymes are RNA molecules that function as enzymes. In some organisms, RNA splicing can occur without proteins or even additional RNA molecules: the intron RNA functions as a ribozyme and catalyzes its own excision!

50. What commonly held idea was rendered obsolete by the discovery of ribozymes?

The discovery of ribozymes rendered obsolete the idea that all biological catalysts are proteins.

51. What are three properties of RNA that allow it to function as an enzyme?

First, because RNA is single-stranded, a region of an RNA molecule may base-pair with a complementary region elsewhere in the same molecule, which gives the molecule a particular three-dimensional structure. A specific structure is essential to the catalytic function of ribozymes, just as it is for enzymatic proteins. Second, like certain amino acids in an enzymatic protein, some of the bases in RNA contain functional groups that may participate in catalysis. Third, the ability of RNA to hydrogen-bond with other nucleic acid molecules (either RNA or DNA) adds specificity to its catalytic activity. For example, complementary base pairing between the RNA of the spliceosome and the RNA of a primary RNA transcript precisely locates the region where the ribozyme catalyzes splicing.

52. What is the consequence of alternative splicing of identical mRNA transcripts?

Many genes are known to give rise to two or more different polypeptides, depending on which segments are treated as exons during RNA processing; this is called alternative RNA splicing. Because of alternative splicing, the number of different protein products an organism produces can be much greater than its number of genes.

53. Three types of RNA are needed for protein synthesis.

Type of RNA	*Description*	*Function*
mRNA	messenger; single-stranded	carries genetic material from DNA to protein-synthesizing machinery of the cell
tRNA	transfer; about 75 nucleotides long; folds into clover-leaf shape	transfers amino acids from cytoplasmic pool of amino acids to growing polypeptide in ribosome
rRNA	ribosomal; most abundant type of RNA	makes up ribosomes together with proteins

54-55. What is an anticodon? What binds at each site of tRNA?

A tRNA molecule arrives at a ribosome bearing a specific amino acid at one end. At the other end of the tRNA is a nucleotide triplet called an anticodon, which base-pairs with a complementary codon on mRNA.

56. How many different aminoacyl-tRNA synthetases are there?

There are 20 different synthetases, one for each amino acid.

57. Scientists expected to find one aminoacyl-tRNA synthetase per codon, but far fewer have been discovered. What is wobble?

If one tRNA variety existed for each mRNA codon specifying an amino acid, there would be 61 tRNAs. In fact, there are only about 45, signifying that some tRNAs must be able to bind to more than one codon. Such versatility is possible

because the rules for base pairing between the third nucleotide base of a codon and the corresponding base of a tRNA anticodon are relaxed compared to those at other codon positions. The flexible base pairing at this codon position is called wobble.

58. Explain the process of a specific amino acid being joined to a tRNA.

Linkage of the tRNA and amino acid is an endergonic process that occurs at the expense of ATP. The ATP loses two phosphate groups, becoming AMP.

59. Describe the structure of a eukaryotic ribosome.

A ribosome consists of a large subunit and a small subunit, each made up of proteins and one or more ribosomal RNAs.

60. How does a prokaryotic ribosome differ from a eukaryotic ribosome? What is the medical significance of this difference?

In both bacteria and eukaryotes, large and small subunits join to form a functional ribosome only when they attach to an mRNA molecule. Although the ribosomes of bacteria and eukaryotes are very similar in structure and function, those of eukaryotes are slightly larger and differ somewhat from bacterial ribosomes in their molecular composition. Certain antibiotic drugs can inactivate bacterial ribosomes without inhibiting the ability of eukaryotic ribosomes to make proteins. These drugs are used to combat bacterial infections.

61. Explain the functions of the A, P, and E sites on a ribosome.

The peptidyl-tRNA binding site holds the tRNA carrying the growing polypeptide chain, while the aminoacyl-tRNA binding site holds the tRNA carrying the next amino acid to be added to the chain. Discharged tRNAs leave the ribosome from the exit site.

62. List the three stages of translation.

Translation, the synthesis of a polypeptide chain, can be divided into three stages analogous to those of transcription: initiation, elongation, and termination.

63. Summarize the events of initiation.

The initiation stage of translation brings together mRNA, a tRNA bearing the first amino acid of the polypeptide, and the two subunits of a ribosome. First, a small ribosomal subunit binds to a molecule of mRNA. In a bacterial cell, the mRNA binding site on this subunit recognizes a specific nucleotide sequence on the mRNA just upstream of the start codon. An initiator tRNA with the anticodon UAC base-pairs with the start codon, AUG. This tRNA carries the amino acid methionine. The arrival of a large ribosomal subunit completes the initiation complex. Proteins called initiation factors are required to bring all the translation components together. Hydrolysis of GTP provides the energy for the assembly. The initiator tRNA is in the P site; the A site is available to the tRNA bearing the next amino acid.

64. What is always the first amino acid in the new polypeptide?

Methionine (Met) is always the first amino acid in the new polypeptide.

65. Summarize the events of elongation.

First, the anticodon of an incoming aminoacyl tRNA base-pairs with the complementary mRNA codon in the A site. Hydrolysis of GTP increases the accuracy and efficiency of this step. Although not shown, many different aminoacyl tRNAs are present, but only the one with the appropriate anticodon will bind and allow the cycle to progress. Second, an rRNA molecule of the large ribosomal subunit catalyzes the formation of a peptide bond between the amino group of the new amino acid in the A site and the carboxyl end of the growing polypeptide in the P site. This step removes the polypeptide from the tRNA in the P site and attaches it to the amino acid on the tRNA in the A site. Finally, the ribosome translocates the tRNA in the A site to the P site. At the same time, the empty tRNA in the P site is moved to the E site, where it is released. The mRNA moves along with its bound tRNAs, bringing the next codon to be translated into the A site.

66. What is a release factor? By what mechanism is termination accomplished?

A release factor, a protein shaped like an aminoacyl tRNA, binds directly to the stop codon in the A site. The release factor causes the addition of a water molecule instead of an amino acid to the polypeptide chain. (There are plenty of water molecules available in the aqueous cellular movement.) This reaction breaks (hydrolyzes) the bond between the completed polypeptide and the tRNA in the P site, releasing the polypeptide through the exit tunnel of the ribosome's

large subunit. The remainder of the translation assembly then comes apart in a multistep process, aided by other protein factors. Breakdown of the translation assembly requires the hydrolysis of two more GTP molecules.

67. What is a polyribosome?

A single ribosome can make an average-sized polypeptide in less than a minute. Typically, however, multiple ribosomes translate an mRNA at the same time; that is, a single mRNA is used to make many copies of a polypeptide simultaneously. Once a ribosome is far enough past the start codon, a second ribosome can attach to the mRNA, eventually resulting in a number of ribosomes trailing along the mRNA. Such strings of ribosomes, called polyribosomes, can be seen with an electron microscope. Polyribosomes, found in both bacterial and eukaryotic cells, enable a cell to make many copies of a polypeptide very quickly.

68. What are some of the things that will result in a final-form functional protein?

During its synthesis, a polypeptide chain begins to coil and fold spontaneously as a consequence of its amino acid sequence (primary structure), forming a protein with a specific shape: a three-dimensional molecule with secondary and tertiary structure. Thus, a gene determines primary structure, and primary structure in turn determines shape. In many cases, a chaperone protein (chaperonin) helps the polypeptide form correctly.

69. Describe at least three types of post-translational modifications.

Certain amino acids may be chemically modified by the attachment of sugars, lipids, phosphate groups, or other additions. Enzymes may remove one or more amino acids from the leading (amino) end of the polypeptide chain. In some cases, a polypeptide chain may be enzymatically cleaved into two or more pieces. For example, the protein insulin is first synthesized as a single polypeptide chain but becomes active only after an enzyme cuts out a central part of the chain, leaving a protein made up two polypeptide chains connected by disulfide bridges. In other cases, two or more polypeptides that are synthesized separately may come together, becoming the subunits of a protein that has quaternary structure (such as hemoglobin).

70. Explain how proteins are targeted for the ER.

Polypeptide synthesis begins on a free ribosome in the cytosol. An SRP binds to the signal peptide, halting synthesis momentarily. The SRP binds to a receptor protein in the ER membrane. This receptor is part of a protein complex (a translocation complex) that has a membrane pore and a signal-cleaving enzyme. The SRP leaves, and polypeptide synthesis resumes, with simultaneous translocation across the membrane. (The signal peptide stays attached to the translocation complex.) The signal-cleaving enzyme cuts off the signal peptide. Finally, the rest of the completed polypeptide leaves the ribosome and folds into its final conformation.

71. Define a mutation in terms of molecular genetics.

A mutation is a change in the nucleotide sequence of an organism's DNA or in the DNA or RNA of a virus.

72. Define point mutations.

Small-scale mutations of one or a few nucleotide pairs include point mutations, changes in a single nucleotide pair of a gene.

73–74. What are frameshift mutations?

Insertions and deletions are additions or losses of nucleotide pairs in a gene. These mutations have a disastrous effect on the resulting protein more often than substitutions do. Insertion or deletion of nucleotides may alter the reading frame of the genetic message, the triplet grouping of nucleotides on the mRNA that is read during translation. Such a frameshift mutation will occur whenever the number of nucleotides inserted or deleted is not a multiple of three. All the nucleotides that are downstream of the deletion or insertion will be improperly grouped into codons, and the result will be extensive missense, usually ending sooner or later in nonsense and premature termination. Unless the frameshift is very near the end of the gene, the protein is almost certain to be nonfunctional.

75. What is the difference between a nonsense and missense mutation?

Substitutions that change one amino acid to another one are called missense mutations. Such a mutation may have little effect on the protein: the new amino acid may have properties similar to those of the amino acid it replaces, or it may be in a region of the protein where the exact sequence of amino acids is not essential to the protein's function. However, the alteration of a single amino acid in a crucial area of a protein will significantly alter protein activity. Occasionally, such a mutation leads to an improved protein or one with novel capabilities, but much more often such mutations are detrimental, leading to a useless or less active protein that impairs cellular function.

Substitution mutations are usually missense mutations; that is, the altered codon still codes for an amino acid and thus makes sense, although not necessarily the *right* sense. But a point mutation can also change a codon for an amino acid into a stop codon. This is called a nonsense mutation, and it causes translation to be terminated prematurely; the resulting polypeptide will be shorter than the polypeptide encoded by the normal gene. Nearly all nonsesne mutations lead to nonfunctional proteins.

76. How can a base-pair substitution result in a silent mutation?

A change in a nucleotide pair may transform one codon into another that is translated into the same amino acid. Such a change is an example of a silent mutation, which has no observable effect on the phenotype.

77. What are the two categories of mutagens?

Mutagens are physical and chemical agents that interact with DNA in ways that cause mutations.

78. Describe the action of different types of chemical mutagens.

Nucleotide analogs are chemicals that are similar to normal DNA nucleotides but that pair incorrectly during DNA replication. Some other chemical mutagens interfere with correct DNA replication by inserting themselves into the DNA and distorting the double helix. Still other mutagens cause chemical changes in bases that change their pairing properties.

79. Describe two important ways in which bacterial and eukaryotic gene expression differ.

In the absence of a nucleus, a bacterial cell can simultaneously transcribe and translate the same gene, and the newly made protein can quickly diffuse to its site of function. In contrast, the eukaryotic cell's nuclear envelope segregates transcription from translation and provides a compartment for extensive RNA processing. Moreover, bacterial and eukaryotic RNA polymerases differ significantly from each other, while the single archaeal RNA polymerase resembles the three eukaryotic ones. Archaea and eukaryotes use a complex set of transcription factors, unlike the smaller set of accessory proteins in bacteria. Also, transcription is terminated differently in bacteria and eukaryotes.

80. What is a gene? It used to be simply stated that one gene codes for one polypeptide. That definition has now been modified.

A gene is a region of DNA that can be expressed to produce a final functional product that is either a polypeptide or an RNA molecule.