C1. The start codon begins at the fifth nucleotide. The amino acid sequence would be Met Gly Asn Lys Pro Gly Gln STOP.

C2. When we say the genetic code is degenerate, it means that more than one codon can specify the same amino acid. For example, GGG, GGC, GGA, and GGU all specify glycine.

In general, the genetic code is nearly universal, because it is used in the same way by viruses, prokaryotes, fungi, plants, and animals. As discussed in Table 13.3, there are a few exceptions, which occur primarily in protozoa and organellar genetic codes.

C3. A. true

B. false

C. false

C4. A. This mutant tRNA would recognize glycine codons in the mRNA but would put in tryptophan amino acids where glycine amino acids are supposed to be in the polypeptide chain.

B. This mutation tells us that the aminoacyl-tRNA synthetase is primarily recognizing other regions of the tRNA molecule besides the anticodon region. In other words, tryptophanyl-tRNA synthetase (i.e., the aminoacyl-tRNA synthetase that attaches tryptophan) primarily recognizes other regions of the $tRNA^{trp}$ sequence (i.e., other than the anticodon region), such as the T- and D-loops. If aminoacyl-tRNA synthetases recognized only the anticodon region, we would expect glycyl-tRNA synthetase to recognize this mutant tRNA and attach glycine. That is not what happens.

C5. As shown in Figure 13.11, the energy comes from ATP. It is this energy conversion that explains the term *charged* tRNA.

C6. A. The answer is three. There are six leucine codons: UUA, UUG, CUU, CUC, CUA, and CUG. The anticodon AAU would recognize UUA and UUG. You would need two other tRNAs to *efficiently* recognize the other four leucine codons. These could be GAG and GAU or GAA and GAU.

B. The answer is one. There is only one codon, AUG, so you need only one tRNA with the anticodon UAC.

C. The answer is three. There are six serine codons: AGU, AGC, UCU, UCC, UCA, and UCG. You would need only one tRNA to recognize AGU and AGC. This tRNA could have the anticodon UCG or UCA. You would need two tRNAs to efficiently recognize the other four tRNAs. These could be AGG and AGU or AGA and AGU.

C7. There are four proline codons, four glycine codons, one methionine codon, and six serine codons. We apply the product rule to solve this problem.

$$4 \times 4 \times 1 \times 6 = 96$$

C8. 3′–CUU–5′ or 3′–CUC–5′

C9. The codon is 5′–CCA–3′, which specifies proline.

C10. It can recognize 5′–GGU–3′, 5′–GGC–3′, and 5′–GGA–3′. All of these specify glycine.

C11. An anticodon that was 3′–UUG–5′ would recognize the two codons. To recognize 5′–AAA–3′, it would have to be modified to 3′–UUI–5′.

C12. All tRNA molecules have some basic features in common. They all have a cloverleaf structure with three stem-loop structures. The second stem-loop contains the anticodon sequence that recognizes the codon sequence in mRNA. At the 3′ end, there is an acceptor site, with the sequence CCA, that serves as an attachment site for an amino acid. Most tRNAs also have base modifications that occur within their nucleotide sequences.

C13. They are very far apart, at opposite ends of the molecule.

C14. The role of aminoacyl-tRNA synthetase enzymes is to specifically recognize tRNA molecules and attach the correct amino acid to them. They are sometimes described as the second genetic code because the specificity of their attachment is a critical step in deciphering the genetic code. For example, if a tRNA has a 3′–GGG–5′ anticodon, it will recognize a 5′–CCC–3′ codon, which should specify proline. It is essential that the prolyl-tRNA-synthetase recognizes this tRNA and attaches proline to the 3′ end. The other aminoacyl-tRNA synthetases should not recognize this tRNA.

C15. In the context of translation, an activated amino acid has had AMP attached to it. This provides necessary energy so that the amino acid can be attached to the correct tRNA.

C16. Bases that have been chemically modified can occur at various locations throughout the tRNA molecule. The significance of all of these modifications is not entirely known. However, within the anticodon region, base modification alters base pairing to allow the anticodon to recognize two or more different bases within the codon.

C17. A formyl group is covalently attached to methionine after the methionine has been attached to the tRNA containing a UAC anticodon.

C18. No, it is not. Due to the wobble rules, the 5′ base in the anticodon of a tRNA can sometimes recognize two or more bases in the third (3′) position of the mRNA. Therefore, any given cell type synthesizes far fewer than 61 types of tRNAs.

C19. Translation requires mRNA, tRNAs, ribosomes, many proteins such as initiation, elongation, and termination factors, and many small molecules. ATP and GTP are small molecules that contain high-energy bonds. The mRNA, tRNAs, and proteins are macromolecules. The ribosomes are a large complex of macromolecules.

C20. The assembly process is very complex at the molecular level. In eukaryotes, 33 proteins and one rRNA assemble to form a 40S subunit, and 49 proteins and three rRNAs assemble to form a 60S subunit. This assembly occurs within the nucleolus.

C21. A protein subunit is a polypeptide. A ribosomal subunit is a much larger complex that is composed of RNA and many proteins. A ribosomal subunit is a much larger structure compared to a protein subunit.

C22. A. On the surface of the 30S subunit and at the interface

B. Within the 50S subunit

C. From the 50S subunit

D. To the 30S subunit

C23. *Initiation:* The mRNA, initiator tRNA, and initiation factors associate with the small ribosomal subunit; then the large subunit associates.

Elongation: The ribosome moves one codon at a time down the mRNA, adding one amino acid at a time to the growing polypeptide chain. There are three sites on the ribosome, the A, P, and E sites, that are important in this process. The A site is where the tRNA (except for the initiator tRNA) binds to the ribosome and recognizes the codon in the mRNA. The growing polypeptide chain is then transferred to the amino acid attached to this tRNA. The ribosome then translocates so that this tRNA is now moved to the P site. The empty tRNA that was in the P site is moved into the E site. This empty tRNA in the E site is then expelled, and now the next charged tRNA can bind to the A site.

Termination: A stop codon is reached and a termination factor binds to the A site. The hydrolysis of GTP initiates a series of events that leads to the disassembly of the ribosomal subunits and the release of the completed polypeptide chain.

C24. Most bacterial mRNAs contain a Shine-Dalgarno sequence, which is necessary for the binding of the mRNA to the small ribosomal subunit. This sequence, UAGGAGGU, is complementary to a sequence in the 16S rRNA. Due to this complementarity, these sequences will hydrogen bond to each other during the initiation stage of translation.

C25. A. The initiator tRNA would not bind to the small ribosomal subunit.

B. It may prevent the mRNA from binding to the small ribosomal subunit, and/or it may prevent the start codon from being recognized due to secondary structure in the mRNA.

C. The large ribosomal subunit would not assemble after the start codon had been identified by the small ribosomal subunit.

C26. The ribosome binds at the 5′ end of the mRNA and then scans in the 3′ direction in search of an AUG start codon. If it finds one that reasonably obeys the Kozak's rules, it will begin translation at that site. Aside from an AUG start codon, the two other features are a purine at the –3 position and a guanosine at the +4 position.

C27. 1. GCCACCAUGG

2. GACGCCAUGG

3. GCCUCCAUGC

4. GCCAUCAAGG

The last one does not have a start codon, so it would not work. The third one may be translated, but very poorly.

C28. The A site is the acceptor site. It is the location where a tRNA initially “floats in” and recognizes a codon in the mRNA. The only exception is the initiator tRNA that binds to the P site. The P site is the next location where the tRNA moves. When it first moves to the P site, it carries with it the polypeptide chain. In each round of elongation, the polypeptide chain is transferred from the tRNA in the P site to the amino acid attached to the tRNA in the A site. The third site is the E site. During translocation, the uncharged tRNA in the P site is transferred to the E site. It exits or is released from this site.

C29. The amino acid sequence is methionine tyrosine tyrosine glycine alanine. Methionine is at the amino terminus, alanine at the carboxyl terminus. The peptide bonds should be drawn as shown in Figure 13.20.

C30. Sorting signals provide an address that sends the protein to the correct location (i.e., compartment) within the cell. Proteins destined for the ER, Golgi, lysosomes, plasma membrane, or secretion have an SRP sorting signal at their amino terminal end. Nuclear proteins have an NLS sequence, etc. These sorting signals are recognized by cellular proteins/complexes that then act in a way to traffic the proteins to their correct destination.

C31. Cotranslational sorting occurs via the SRP signal. This form of sorting is necessary for proteins that are destined for the ER, Golgi, lysosomes, plasma membrane, or secretion. The SRP recognizes the signal in the amino terminus of the protein as it is being translated. It then directs the ribosome to proteins within the ER membrane so that the protein is synthesized into the ER. By comparison, posttranslational sorting occurs after the protein has been completely made. In this case, the protein usually contains a different amino acid sequence that acts as a traffic signal for its direction to a particular cellular organelle. Examples of these types of sorting signals include mitochondrial, chloroplast, and nuclear sorting signals.

C32. The initiation phase involves the binding of the Shine-Dalgarno sequence to the rRNA in the small ribosomal subunit. The elongation phase involves the binding of anticodons in tRNA to codons in mRNA.

C33. The nucleolus is a region inside the eukaryotic nucleus where the assembly of ribosomal subunits occurs.

C34. A. E site and P site (Note: A tRNA without an amino acid attached is only briefly found in the P site, just before translocation occurs.)

B. P site and A site (Note: A tRNA with a polypeptide chain attached is only briefly found in the A site, just before translocation occurs.)

C. Usually the A site, except the initiator tRNA can be found in the P site.

C35. A polysome is an mRNA molecule with many ribosomes attached to it.

C36. The tRNAs bind to the mRNA because their anticodon and codon sequences are complementary. When the ribosome translocates in the 5′ to 3′ direction, the tRNAs remain bound to their complementary codons, and the two tRNAs shift from the A site and P site to the P site and E site. If the ribosome tried to move in the 3′ direction, it would have to dislodge the tRNAs and drag them to a new position where they would not (necessarily) be complementary to the mRNA.

C37. A. False.

B. True.

C38. 52

C39. This means that translation can begin before transcription of the mRNA is completed. This cannot occur in eukaryotic cells because transcription and translation occur in different cellular compartments. Transcription occurs in the nucleus, while translation occurs in the cytosol.