Genetics and Genomics in Medicine Chapter 2 Questions

Multiple Choice Questions

Question 2.1

Regarding exons, which, if any, of the following statements is correct?

a) Some exons in protein-coding genes consist of noncoding DNA.
b) The first exon of a protein-coding gene always contains the translational start site.
c) The last exon of a protein-coding gene always contains the normal termination codon.
d) A coding exon is always translated in just one of the three possible forward reading frames.

Question 2.2

Regarding the structures of amino acids, which, if any, of the following statements is incorrect?

a) The general formula for a nonionised amino acid is H_2N-CH(R)-COOH, that is, a central carbon atom is linked to an amino group, a carboxyl group, a hydrogen atom, and a side chain, R.
b) The identity of the amino acid is determined by the side chain that is connected to the central carbon atom.
c) The side chain of an amino acid is based on a branch that contains one or more carbon atoms
d) Proline is unique in having a side chain that is connected to both the central carbon and also to the nitrogen atom of the amino group.

Question 2.3

Regarding polypeptide structure, which, if any of the following statements is incorrect.

a) A polypeptide is a polymer composed of a linear sequence of amino acids.
b) A polypeptide normally adopts a rod-like conformation, with the side chains orientated in the same direction relative to the polypeptide backbone.
c) The amino acids within a polypeptide are joined by a covalent bond known as a peptide bond.
d) Peptide bonds form by a condensation reaction between the amino group of an amino acid and the carboxyl group of its neighbor.

Question 2.4

Regarding protein structure, which, if any, of the following statements is incorrect?

a) The primary structure is the linear sequence of amino acids.
b) The secondary structure is the path followed by the polypeptide backbone over its length.
c) The secondary structure of every protein contains an alpha-helix.
d) The structure of an alpha-helix is primarily determined by hydrogen bonding between chemical groups on the side chains.

Question 2.5

Which, if any, of the following statements is false?

a) Unlike DNA, RNAs are unmethylated, and only the four standard bases – A, C, G and U – are found in RNAs.
b) The primary structure of an RNA is the linear sequence of nucleotides.
c) The secondary structure of an RNA is dominated by hydrogen bonding between bases on the same strand.
d) Stem-loop structures are common in RNA and consist of complementary sequences that form stable base pairs, separated by a short sequence of unpaired bases.

Question 2.6

Which, if any, of the following statements is false?

a) A ribosome is a large ribonucleoprotein that contains multiple different types of RNA but just one type of protein.
b) During translation, a ribosome binds to the 5' end of a mRNA, slides along it until the initiator AUG codon is identified, and continues until reaching an in-frame termination codon.
c) The single type of ribosomal protein is a crucially important peptidyltransferase.
d) The peptidyltransferase catalyzes the condensation reaction that allows joining of amino acids using peptide bonds.

Question 2.7

Which, if any, of the following statements are false?

a) During translation, the individual codons of an mRNA are "read" by transient hydrogen bonding to a complementary anticodon sequence on a transfer RNA.
b) According to their anticodon, transfer RNAs usually have a specific amino acid attached to their 3' end.
c) When the anticodon of a tRNA binds to a codon with a suitably complementary sequence, the amino acid is released and becomes part of a polypeptide.

d) Translation terminates at an in-frame termination codon (UAA, UAG, or UGA in the universal genetic code) because for these codons, there are no transfer RNAs with a complementary anticodon sequence.

Question 2.8

Which, if any, of the following statements are false?

a) Stem-loop structures are formed by base pairing of complementary sequences that are separated by a short sequence of nucleotides with unpaired bases.
b) Stem-loop structures are common occurrences in both DNA and RNA.
c) Stem-loop structures are important for structural reasons only.
d) Stem-loop structures can be important functional elements.

Question 2.9

Which, if any, of the following statements are false?

a) A naked DNA double helix has a stiff rod-like structure.
b) An RNA usually has a stiff rod-like structure, but occasionally has elements of secondary structure caused by intrachain hydrogen bonding
c) Some proteins have stiff rod-like structures.
d) Some proteins have globular structures.

Question 2.10

With respect to expression of an RNA gene, which, if any, of the following statements are false?

a) RNA processing sometimes includes RNA splicing
b) Regulatory antisense RNAs sometimes undergo splicing
c) Ribosomal RNAs and transfer RNAs are formed by cleavage of RNA precursors.
d) Ribosomal RNAs and transfer RNAs undergo base modification.

Question 2.11

Roughly what percentage of our genome is made up of coding sequence?

a) 1%
b) 5%
c) 10%
d) 25%

Question 2.12

In addition to coding sequence, which is generally very highly conserved, what additional percentage of our genome is highly to moderately conserved?

a) 0.4%
b) 4%
c) 14%
d) 24%

Question 2.13

Roughly what percentage of our genome is made up of constitutive heterochromatin?

a) 0.7%
b) 7%
c) 27%
d) 57%

Question 2.14

Roughly what percentage of our genome is made up of transposon repeats?

a) 0.45%
b) 4.5%
c) 25%
d) 45%

Question 2.15

Which, if any, of the following statements are false?

a) The broadest definition of a pseudogene is any gene that has received inactivating mutations and can no longer make a functional product
b) A retropseudogene is a non-functional cDNA copy of a processed RNA that has integrated elsewhere into the genome.
c) A non-processed pseudogene is an inactive copy of a gene that has arisen by some type of gene duplication.
d) An estimated 14,000 pseudogenes are found in the human genome.

Question 2.16

Which, if any, of the following statements are false?

a) Constitutive heterochromatin remains highly condensed throughout the cell cycle.

b) Unlike constitutive heterochromatin, facultative heterochromatin describes chromatin that can de-condense and behave as euchromatin under certain circumstances.
c) Most of the long arm of the Y chromatin is made up of constitutive heterochromatin.
d) In women one of the two X chromosomes in each diploid cell is heterochromatinised.

Question 2.17

What is the total DNA content of (a) our genome; (b) an average human chromosome; (c) the human mitochondrial genome?

Question 2.18

What is the approximate ratio between the DNA content of our nuclear genome and our mitochondrial genome?

a) 2,000:1
b) 20,000:1
c) 200,000:1
d) 2,000,000:1

Question 2.19

Of the various electronic resources listed below, which is (a) a genome browser; (b) a resource that identifies closely similar genes and proteins in different organisms; (c) a program that allows very fast searching of genome sequences for identity or similarity to a nucleotide or amino acid sequence query?

HOMOLOGENE
BLAT
ENSEMBL

Question 2.20

Nearly half of our genome is composed of transposon repeats, some of which can actively transpose, occasionally causing disease by inserting into or close to genes, (causing gene inactivation or inappropriate expression of oncogenes). Many of them work by making copies that transpose and so can increase in copy number, and so there is a need to limit the number of actively transposing sequences in case they overwhelm the genome. Two types of small RNAs act to limit the spread of transposons. What are these RNAs and where do they work?

Question 2.21

In what ways are the transcription and processing of our mitochondrial genes rather different from that of most of our nuclear genes?

Fill in the Blanks Questions

Question 2.22

Fill in the blanks below with single words.

When a gene is expressed, the two DNA strands are locally unwound to allow access by the ____1_____ machinery. One of the DNA strands serves as a ____2____ for an RNA polymerase to synthesize a complementary RNA. The initial transcript, often called the ____3____ transcript, is identical in base sequence (except that U replaces T) to the sequence of the other DNA strand, which is known as the ____4____ strand (and so the opposing strand that serves as the ___2____ is also known as the ____5____ strand). The segment of genomic DNA that corresponds to the ____3____ transcript is known as the ___6___ ___7____.

Question 2.23

Fill in the blanks below.

During gene expression, the initial RNA transcript needs to undergo processing to make a mature RNA, either a ____1____ RNA or a ____2___ RNA. For many of our genes, the initial RNA transcript needs to be cleaved into pieces. Some of the pieces, called ____3____, are discarded, but other alternating pieces called ___4____ are retained and fused in the same linear order as their order when transcribed. The junctions between ___4____ and ____3____ contain some highly conserved nucleotides, notably a ____5____ dinucleotide at the beginning of ___3____ and an ___6____ dinucleotide at the ends of ____3____. For ____4_____ and _____3_____ the original definitions have been broadened to include the corresponding segments of _____7_____ ____8_____

Question 2.24

Fill in the blanks below.

Two important RNA processing events lead to specialized end sequences in most human mRNAs: ____1____ at the 5' end, and ____2____ at the 3' end. The altered sequences protect the RNA from attack by cellular ____3_____ and confer a measure of stability. In ____1____ the most distinctive change is a specialized end nucleotide, ____4_____ _____5_____, that is joined to its neighbor using a distinctive ____6_____ bond. In this case, the ____7____ carbon atom of the end nucleotide is joined to the ____7_____ carbon atom of its neighbor. In

____2_____ a sequence of about 200 ____8____ is enzymatically added to the 3' end by a dedicated enzyme called _____9_____ ____10_____.

Question 2.25

Fill in the blanks below.

During evolution duplication of a gene produces two copies. The sequence of one copy may continue to be conserved (because it remains subject to ____1_____ ____2____; the other copy is free to mutate. The latter will most likely acquire deleterious mutations and degenerate to become a ____3_____. If duplication occurs at the genome level, the _____3_____ will often be located close to the parent gene. It may contain copies of the full length sequence of the parent gene (including the promoter, exons, and introns), and is known as a ____4_____ _____3_____ . Sometimes, however, the duplication involves making a cDNA copy of an mRNA after which the cDNA copy integrates into a new locus that is often very distant from the parent gene. Because the cDNA copy lacks promoter sequences, it is usually not expressed and will acquire inactivating mutations and degenerates. This type of _____3____ is known as a _____5____ ___3_____ or a ____6_____. Sometimes, the cDNA copy integrates close to a promoter sequence and is expressed, and if so, on rare occasions, the expression of this gene copy becomes an asset to the cell so that it becomes subject to ____1____ ____2____ and is a conserved functional gene. Such a cDNA copy is known as a ____7____.

Question 2.26

Fill in the blanks below.

Our genome has numerous identical or similar copies of certain DNA sequences. Some of these are ____1____ ____2_____, neighboring duplicated segments that are more than 1 kb in length (and often much larger), and that show more than 90% sequence identity, having duplicated very recently during evolution. Many of our genes are present in multiple copies that are collectively known as ____3_____ ____4_____ (and often contain both functional gene copies and ____5_____). They arose by a slow process of intermittent gene duplication over sometimes long periods of evolutionary time. Extremely similar gene copies, such as the two human ___6____ - globin genes that make identical proteins, arose by evolutionarily recent gene duplications. More distantly related gene copies generally arose from comparatively ___7___ gene duplications.

Question 2.27

In some gene families the genes are clustered in defined chromosomal regions as a result of ___1____ gene duplication. That often occurs as a result of misalignment of chromatids: over a limited chromosomal region, the DNA sequences are paired but out of register. Subsequent ___2_____ in the mispaired region can generate chromatids with two copies of a gene. Successive gene duplications results in a cluster of highly related genes. Not all the gene copies are functional: some acquire inactivating mutations to become a type of ____3_____ known as a _____4_____ ____3____. In other gene families there may be up to many hundreds of more members scattered across the genome. They often have large numbers of ____5____ ____3______ , also known as ____6_____ that arose by copying the RNA transcripts of a functional gene using a ____7____ _____8_____ to make cDNA copies that integrated into the genome at other locations but subsequently acquired deleterious mutations.

Question 2.28

Fill in the blanks below.

More than half of our genome is composed of families of highly repetitive DNA sequences. Close to 15% of these are composed of tandem repeats of short sequences that are found predominantly at or close to ____1____ and in other regions of ____2____ heterochromatin (which includes much of the long arm of the ___3____ chromosome, and much of the short arms of the five acrocentric chromosomes). The remaining 85% or so of the highly repetitive DNA is made up of interspersed repetitive DNA sequences that are scattered across the genome and belong to families of ____4____ repeats. Only a small fraction of the ____4____ repeats are based on DNA ____4___ (which transpose by a ___5___-and-paste mechanism). The great majority are ____6____ repeats, some of which can actively transpose by a ___7___-and-paste mechanism (which involves using a _____8____ ____9_____ to make cDNA copies of RNA transcripts, with the copies integrating elsewhere in the genome).

Question 2.29

Fill in the blanks below.

Retrotransposon repeats account for just over ___1___ % of our genome and are classified into three broad families. One family resembles a class of RNA virus, known as a ___2____. Like a ___2____, they contain direct repeats at their ends, known as ___3____ ____4____ repeats, and full-length family members have the same gene structure as a simple ____2____. A second family of retrotransposon repeats, known as ____5____ , has some full-length copies with sizes of 6-8 kb, and like the retrovirus-like family some of them are able to make a specialized DNA polymerase known as _____6____ ____7_____. A third family of retrotransposon repeats,

known as ___8____, have short full-length sequences of between 100 and 300 bp, and are exemplified by ___9____ repeats, the most prolific DNA sequence in the human genome, with a copy number of more than ____10____ ____11_____ repeats. Only a small fraction of the retrotransposon repeats can actively transpose (most are truncated copies or have ____11_____ mutations). ___8____ repeats and other _____8_____ are unable to make a ____6____ ____7_____ but very occasionally do transpose using a ____6____ ____7_____ produced by another retrotransposon.

Essay Questions

Question 2.30
Illustrate, with examples, how noncoding RNAs are more than ubiquitous general regulators of transcription or protein synthesis.

Question 2.31
Four different levels of protein structure are recognized. What are they? Illustrate your answer with examples, wherever possible.

Question 2.32
What is the purpose of RNA splicing? Why do some of our genes not undergo RNA splicing?

Question 2.33
What are the different natural ways in which proteins are chemically modified in cells and why do they need to be modified?

Question 2.34
What roles do snRNA, snoRNA and scaRNA have in RNA maturation? Do any of them participate in other functions?

Question 2.35
What is the type of natural selection that is responsible for strong evolutionary conservation of functionally important DNA sequences, and how does it work?

Question 2.36

Sequence conservation analyses often use computer-based alignment of the nucleotide sequences of equivalent genes in different organisms, or of the amino acid sequences of the corresponding proteins. The alignment below shows a BLAST alignment of the first 100 amino acids of the human CFTR (cystic fibrosis transmembrane receptor) protein (shown as the Query) and the equivalent sequence in the corresponding mouse protein (shown as Sbjct, an abbreviation of

subject). The intervening middle line shows whether at the same position in the two sequences the amino acids are identical or chemically similar.

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Query   1    MQRSPLEKASVVSKLFFSWTRPILRKGYRQRLELSDIYQIPSVDSADNLSEKLEREWDRE  60
             MQ+SPLEKAS +SKLFFSWT PILRKGYR  LELSDIYQ PS DSAD+LSEKLEREWDRE
Sbjct   1    MQKSPLEKASFISKLFFSWTTPILRKGYRHHLELSDIYQAPSADSADHLSEKLEREWDRE  60


Query  61    LASKKNPKLINALRRCFFWRFMFYGIFLYLGEVTKAVQPL  100
              ASKKNP+LI+ALRRCFFWRF+FYGI LYLGEVTKAVQP+
Sbjct  61    QASKKNPQLIHALRRCFFWRFLFYGILLYLGEVTKAVQPV  100
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Calculate (a) the degree of sequence identity for the aligned sequences (b) the degree of sequence similarity.

Question 2.37

Following the completion of the Human Genome Project the ENCODE Project was developed as a major follow-up project. What were the aims, and what the outcome?

Question 2.38

The endosymbiont hypothesis can explain why we have two very different genomes in our cells. What does it propose?

Question 2.39

During evolution, as multicellular organisms became ever more complex, there has been a relentless drive to duplicate DNA sequences. As a result, our genome contains many examples of duplicated exons, duplicated genes, plus duplications of large chromosomal regions. What kinds of advantages might DNA duplication events confer that could enable ever greater functional complexity?

Question 2.40

Explain what is meant by a functional pseudogene and illustrate your answer with an example.

Question 2.41

Exon shuffling has been thought to have occurred periodically during the evolution of me. What advantages might it have, and how might it have arisen?

Question 2.42

Describe the DNA composition of the centromeres of our chromosomes. To what extent are these DNA sequences conserved between different chromosomes, and to what extent do they resemble the sequences of centromeres in other organisms?