

NAME: \_\_\_\_\_  
KK marking scheme

STUDENT #: \_\_\_\_\_

**BIO 1140 Introduction to Cell Biology**  
**MIDTERM #2, March 22, 2014**  
**Dr. D.A Johnson**  
**Total points on this exam is 32 pts**

**YOU HAVE ONE HOUR TO COMPLETE THIS EXAM**

**MULTIPLE CHOICE QUESTIONNAIRE KK**

**Instructions:**

1. Make sure that you have a complete test package. You should have a set of multiple choice questions with a written-answer questionnaire, and a Scantron. Both components must be returned at the end of the midterm.
2. Fill in the Scantron with your name, student number and course code **BIO 1140 KK**.

Answer the following 10 multiple choice questions **on the Scantron sheet** provided. Choose only one answer from among the choices. (10 marks)

1. DNA binding proteins often can read the sequence of nucleotides along the DNA without having to separate the chains. How do they do this?
  - a. The conformations of the phosphate groups reflect the DNA sequence.
  - b. The DNA binding proteins often contain domains that fit into the DNA grooves.**
  - c. The conformations of the deoxyribose sugars reflect the DNA sequence.
  - d. The conformations of the ribose sugars reflect the DNA sequence.
2. Chargaff's Rule is derived from the observation that in the DNAs he studied  $A=T$  and  $G=C$ . This true for
  - a. all DNA.
  - b. all eucaryotic, genomic DNA.**
  - c. all viral DNA.
  - d. all viral RNA.
3. Why is the DNA of interphase chromosomes very dispersed?
  - a. to protect the DNA
  - b. to allow replication to occur
  - c. to allow transcription to occur
  - d. to allow ribosome translocation to the cytoplasm
  - e. b and c**
4. When histone H1 has been removed from chromatin prior to being prepared for electron microscopy, what phrase below describes what investigators see in the resultant electron micrographs?
  - a. a coiled coil
  - b. beads on a string**
  - c. a hollow tube
  - d. a windmill
  - e. a sunburst

5. DNA repair enzymes typically find mismatched base pairs by scanning for
- Okazaki fragments.
  - missing hydrogen bonds.
  - distortions in the newly synthesized chain.
  - unsealed nicks in the DNA strands.
6. Since a DNA polymerase cannot synthesize DNA without a primer, some molecule other than DNA must be laid down as a primer to start replication. What molecule is laid down as a primer and which end of that molecule must be free and thus available to attach to new nucleotides?
- carbohydrates, free 5' end
  - RNA, free 5' end
  - carbohydrate, free 3' end
  - RNA, free 3' end
  - protein, free 3' end
7. What is the explanation for the wide discrepancies in genome sizes from species to species?
- More advanced organisms have more DNA.
  - Genomes have an extremely variable number of repeated DNA sequences that do not code for proteins.
  - Some organisms have multiple repeats of each gene.
  - More advanced organisms have more genes.
  - More advanced organisms have more centromeric DNA.
8. The greatest variability among codons specifying the same amino acid occurs \_\_\_\_\_.
- in the first two nucleotides of the triplet
  - in the last two nucleotides of the triplet
  - in the first and third nucleotides of the triplet
  - in the third nucleotide of the triplet
  - in the middle nucleotide of the triplet.
9. Why is a mistake made during mRNA synthesis not as serious as a mistake during DNA synthesis when both can result in the synthesis of a defective protein?
- An mRNA is one short-lived template among a large population of such molecules.
  - A DNA replication error causes a permanent mutation and possible elimination of that cell's progeny.
  - There is little lasting damaged caused by a mistake made during mRNA synthesis.
  - There is little lasting damaged caused by a mistake made during DNA synthesis.
  - a, b and c
10. A symmetrical sequence of DNA in which the two strands of DNA have the same 5' to 3' sequence is called a(n) \_\_\_\_\_.
- response element
  - palindrome
  - aerodrome
  - velodrome
  - melodrama

**BIO 1140 Introduction to Cell Biology****MIDTERM #2 KK****March 22, 2014****Dr. D.A Johnson****FILL IN THE BLANKS (10 Marks)****Everyone must answer this question! Each answer is worth 0.5 marks.**

Chromatin is organized into different structural levels – we call it hierarchical organization.

The genome contains many types of sequences in addition to the genes. Four types of sequences found in your genome are \_\_\_\_\_\*, \_\_\_\_\_\*, \_\_\_\_\_\*, and \_\_\_\_\_\*. Some sequences have interesting properties. For example \_\_\_\_\_ **introns** \_\_\_\_\_ need to be removed before translation; ~~and some can move by processes called~~ \_\_\_\_\_ **transposition** \_\_\_\_\_ and \_\_\_\_\_ **retrotransposition** \_\_\_\_\_.

Transcription is the process by which the DNA sequences in your cell are copied into RNA. This process requires \_\_\_\_\_ **multiple/several/3/different** \_\_\_\_\_ RNA polymerases **because each one transcribes (recognizes) different sets of gene (different genes) OR is involved of transcription of different messages rRNA, tRNA, and mRNA OR there are 3 different RNA polymerases RNA pol I, RNA pol II, RNA pol III** \_\_\_\_\_ and \_\_\_\_\_ **there are organelles (or mitochondria or chloroplasts) that have their own genes (or transcribe etc)** \_\_\_\_\_.

Chromatin is organized into different levels – hierarchical organization.

Chromatin consists of DNA, \_\_\_\_\_ **histone (OR H1, H2A, H2B, H3, H4)** \_\_\_\_\_ protein and \_\_\_\_\_ **non-histone** \_\_\_\_\_ protein. 146bp of DNA wrapped around the 8 histones is called the \_\_\_\_\_ **core nucleosome** \_\_\_\_\_ (two words). When viewed by electron microscopy we see this as the \_\_\_\_\_ **10 nanometre** \_\_\_\_\_ fibre.

When H1 is added to this structure, we now have the \_\_\_\_\_ **nucleosome** \_\_\_\_\_.

The next level of organization is the \_\_\_\_\_ **solenoid** \_\_\_\_\_. When viewed by electron microscopy we see this as the \_\_\_\_\_ **30 nanometre** \_\_\_\_\_ fibre. This structure can further fold into a \_\_\_\_\_ **looped domain or looped structure or loop** \_\_\_\_\_ and finally into a chromosome.

A key element in hierarchical organization is that when a structure forms, DNA that was \_\_\_\_\_ **far apart or distant** \_\_\_\_\_ is now \_\_\_\_\_ **close together** \_\_\_\_\_.

\* = any four from this list:

Retroposons (retrotransposons) ; Transposons; Introns; Protein coding genes (exons); Simple sequence repeats VNTRs Segmental duplication: low copy number repeats. LINES, SINES, LTR or retroposons, Tandem repeats (long or short).

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**WRITTEN-ANSWER QUESTIONNAIRE KK**  
**ONLY RESPONSES WRITTEN WITHIN THE BOXES WILL BE MARKED.**

**Answer 3 questions. Each is worth 4 marks.**

1. How was transformation used to determine that DNA was the genetic information?
2. Replication of your DNA requires multiple replication origins. What are two reasons for this observation?
3. Transcription terminates when the transcription complex recognizes signals at the end of the gene and falls off the DNA. Explain
4. Is the genetic code universal?

**Response to Question: 1**

**How was transformation used to determine that DNA was the genetic information?**

- **Griffith's experiment:** The original transformation experiments established that a heat-killed bacterial extract (or lysate) could change a non-lethal bacterium (rough) into a lethal bacterium (smooth) (1 mark)
  - **If students confuse bacteria with virus, deduct 0.5 marks**
- 0.5 marks for enzyme/function + 0.5 marks for conclusion on transformation
  - A protease that breaks down protein did not affect transformation (1 mark)
  - An RNase that degrades RNA did not affect transformation (1 mark)
  - Only DNA degradation (or DNase treatment) led to the loss of the transforming principle (1 mark)

**Response to Question: 2**

**Replication of your DNA requires multiple replication origins. What are two reasons for this observation?**

**There are three. Mark ONLY the first two in the answer.**

- You have multiple chromosomes (1 mark) so each must have at least one (1 mark).
- Replication starting from a single chromosome is too slow to complete the cell cycle (1 mark). You will need to have more one (recruit more, have more, use more, etc.) (1 mark).
- Finally you have two genomes or more than one chromosome (1 mark). and mito DNA needs one too (1 mark).

**Response to Question: 3**

**Transcription terminates when the transcription complex recognizes signals at the end of the gene and falls off the DNA. Explain.**

**There are three. Mark ONLY the first two in the answer.**

Termination involves proteins recognizing conserved DNA or RNA sequences (or consensus sequences) (2 marks).

In bacteria (or E. coli) Rho-dependent ( “ $\rho$ ” = rho) stops RNA synthesis at specific sites. (1 mark).

In bacteria (or E. coli) intrinsic or  $\rho$ -independent stops synthesis at a terminator sequence ( or palindrome)(1 mark).

In eucaryotes, the polyA signal leads to RNA cleavage (break or digestion, etc.) (1 mark)

Simply mentioning terminator sequence (0.5 marks)

Codons are involved in translation NOT transcription

**Response to Question: 4**

**Is the genetic code universal?**

- While there is a standard genetic code (codon table), (0.5 marks) the code is not universal. (0.5 marks).
- Variants are found in nuclear and mitochondrial **or chloroplast (organelles)** genes in eukaryotes and in prokaryotes (1 mark).

Any two examples from this list. Each example is 1 mark. for a max of 2.0 marks

- i. in some E.coli (bacteria) genes GUG (or UUG ) can be used as a start codon
- ii. in the plant gene “agamous” ACG is used as a start codon;
- iii. in Eubacteria AUG (start codon) encodes fMet-tRNA; in Archaea and eukaryotes AUG encodes Met-tRNA.