

UNIVERSITY OF TORONTO
Faculty of Arts and Science

March Mid-Term
Wednesday, March 5th, 2014

BIO130H1S
From 6:10 – 7:45 pm
DURATION: 95 minutes

No Test Aids Allowed

Number of pages: 9 (not including this one) **Number of questions:** 40 multiple choice

This mid-term is worth **30%** of your final mark.

INSTRUCTIONS: Please read carefully!

1. All questions are based on lecture material of Section I. You are to choose the **BEST** answer; there is **ONE** and only one correct answer per question (multiple answers for a question will be marked wrong). There is no additional penalty for incorrect answers, so **do NOT leave any questions unanswered (blank)** on your answer sheet. **Write your name on your test question paper.**
2. **Green Computer Answer Sheet: SCANTRON** (See sample on the back of this page) Transfer your answers to the computer scantron answer sheet using a soft lead pencil and darken inside one box ONLY as multiple answers will be marked wrong. Erase all corrections completely. *ONLY your answer sheet will be marked.* On the left side of your computer answer sheet:
 - a) **Print your last name** in the boxes provided, and darken the appropriate letters in each column. Print your first name initial(s) in the far right columns and darken the appropriate letters.
 - b) **Print your student number** and carefully darken the appropriate numbers. Do not leave this section blank. **If you have a 9-digit student number, please add a '0' at the beginning of your student number and then fill in your 9 digit student number.**
 - c) **Print the exam version in "CODE"** and darken in the appropriate numbers. The test version is at the bottom of every page of this test.

Hand in BOTH your COMPUTER ANSWER SHEET and your Test PAPER

TEST VERSION 22

1. Which of the following is TRUE regarding the "Tree of Life"?
- It is comprised of two domains: the prokaryotes and eukaryotes.
 - The common ancestor cell does not currently exist.
 - In terms of evolutionary origin, eukaryotes diverged much earlier than the prokaryotes.
 - It is based on the type of habitat in which organisms live.
2. What is the minimum number of mutational steps between proline and lysine? (Use the genetic code at the end of this exam)
- 0
 - 1
 - 2
 - 3
3. Which of the following is NOT evidence that mitochondria and/or chloroplasts were originally free-living bacteria?
- Mitochondria and chloroplasts have their own ribosomes.
 - Mitochondrial DNA is a linear DNA molecule.
 - Mitochondria contain a double membrane.
 - Single celled, predatory eukaryotes can still be observed.
4. Which of the following is TRUE with respect to prokaryotes and eukaryotes?
- Prokaryotes and eukaryotes have complex cytoskeletons.
 - Eukaryotes and prokaryotes have an endomembrane system.
 - Eukaryotic cells are typically 1000x larger in volume compared with prokaryotic cells.
 - Prokaryotes and eukaryotes have a nucleolus where ribosomes and snRNAs are produced.
5. Imagine that you have an unlabeled culture of cells. You know they are human cells, but you don't know from which tissue they originated (e.g. kidney, brain, etc.). Which of the following is the least likely to give information that could help determine the originating tissue?
- Genome
 - Proteome
 - Transcriptome
 - Interactome
6. Which of the following is TRUE with respect to model organisms?
- They.....
- are difficult to grow and have very specialized growth requirements.
 - tend to be rare so that horizontal transfer of genetic information is less likely.
 - tend to be tetraploid so that the genetics is more complex and realistic.
 - can be genetically modified.

7. In comparing the complete genomes of five prokaryotes and one eukaryote (yeast), it was found that 239 families of protein-coding genes have representatives in both groups. Which of the following families of genes would you NOT expect to be included here?

Those related to....

- a. amino acid metabolism and transport.
 - b. the production and function of ribosomes.
 - c. the trafficking of molecules in and out of the nucleus.
 - d. energy metabolism.
8. Which of the following is TRUE?
- a. Pyrimidine bases include adenine and guanine.
 - b. A nucleotide consists of a nitrogenous base, pentose sugar, and at least one phosphate group.
 - c. Uracil has a methyl group attached to the nitrogen ring.
 - d. Nucleotides are used for synthesizing DNA or RNA only.
9. Which of the following is TRUE regarding the DNA double helix?
- a. The strands are parallel.
 - b. Base-pairing is the result of ionic interactions.
 - c. AT-rich DNA is more stable at high temperatures.
 - d. 5' ends of DNA have at least one phosphate group.
10. Which of the following CORRECTLY describes the DNA content of a typical human cell?
- a. The DNA is located entirely within the nucleus.
 - b. There are approximately 3 billion nucleotides spread across 46 chromosomes.
 - c. Approximately 3 billion nucleotides are classified as repeated sequences.
 - d. The DNA codes for more than 150,000 different genes.
11. Which of the following statements regarding amino acids and proteins is FALSE?
- a. The free carboxyl group on one amino acid is covalently bound to the amino group on a second amino acid to form a peptide bond plus one molecule of water.
 - b. The hydrogen bonds in beta-sheets are formed between the hydrogen atoms of the carbonyl groups and the oxygen atoms on the side chains of anti-parallel amino acids.
 - c. An alpha-helix is formed through hydrogen bonds between one amino acid and another amino acid four peptide bonds away on the same strand.
 - d. Amino acid side chains play a significant role in the function of the polypeptide.

12. Which of the following statements is CORRECT?

- a. Polypeptides only have one domain, but multiple polypeptides may make up a protein.
- b. Polypeptides may have multiple domains, and multiple polypeptides may make up one protein.
- c. A polypeptide with multiple domains is considered to have a quaternary structure.
- d. A polypeptide containing multiple domains is always a protein or a supramolecular assembly.

13. The advantages to the cell of being able to package DNA into a heterochromatic state include all of the following EXCEPT:

- a. Heterochromatic DNA is at the correct nuclear neighbourhood for high levels of transcription to take place.
- b. Heterochromatic DNA is less likely to become tangled when sister chromatids separate during mitosis and meiosis.
- c. DNA strands in a heterochromatic state are less likely to become broken during cellular processes.
- d. Heterochromatic DNA allows for the process of X-inactivation, which helps equalize the number of genes in human males and females.

14. Prokaryotic DNA packaging involves:

- a. histone-like proteins to form nucleosomes.
- b. supercoiling by topoisomerase.
- c. negatively-charged polyamines.
- d. compacting the DNA into a structure called the transcriptosome.

15. Which of the following statements is CORRECT?

- a. Single-stranded DNA-binding proteins stabilize the unwound, single-stranded conformation of DNA.
- b. DNA polymerase catalyzes the addition of nucleotides with no "proof-reading".
- c. Exonucleases cleave nucleotides one at a time from the ends of polynucleotide chains to cause DNA replication errors.
- d. DNA replication does not require a primer.

16. Fluorescence *in-situ* hybridization (FISH) can be used to:

- a. induce interphase chromosomes to condense.
- b. induce M phase chromosomes to decondense.
- c. gently break nuclei so that the 30 nm fibre can be examined using electron microscopy.
- d. investigate the nuclear position of particular genes throughout the cell cycle.

17. Which of the following statements regarding eukaryotic chromatin packaging is TRUE?

- a. The H1 histone protein is found in the octameric histone core.
- b. The negative charge of the core histone proteins aids the formation of the 30 nm fibre.
- c. A class of proteins requiring ATP is needed to compact the 30 nm fibre.
- d. The net result is a DNA molecule that is packaged into a mitotic chromosome 1000 times shorter than its extended length.

18. The cellular process that reversibly changes heterochromatin to euchromatin is called:

- a. cytosolic compartmentalization.
- b. chromatin remodelling.
- c. developmental positional control.
- d. chromatin immunoprecipitation.

19. What is the maximum number of leading strands that can be observed in the replication of a eukaryotic chromosome with 5 origins of replication?

- a. 1
- b. 2
- c. 5
- d. 10

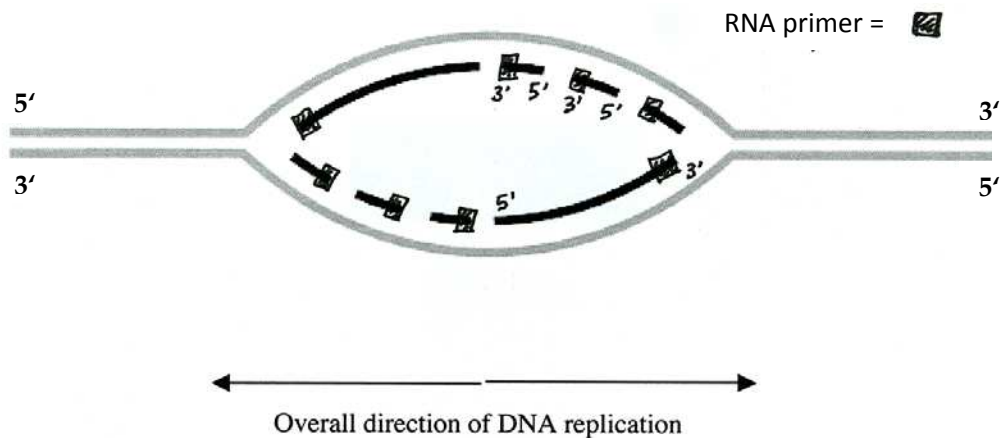
20. Which of the following statements CORRECTLY describes the end replication problem that is solved by telomerase?

- a. If a single, linear, double-stranded DNA exhibits bidirectional, semiconservative growth from one starting point, replication will be incomplete at two 3' ends.
- b. If a single, circular, double-stranded DNA exhibits bidirectional, semiconservative growth from one starting point, replication will be incomplete at one 3' end.
- c. If a single eukaryotic chromosome is replicated using multiple origins of replication, replication will be incomplete at the 5' end of every lagging strand.
- d. If a single eukaryotic chromosome is replicated using one origin of replication, replication will be incomplete at the 5' end of every leading and lagging strand.

21. What is the MOST LIKELY explanation for the fact that a DNA strand is not synthesized in both the 3' to 5' and 5' to 3' directions in the cell?

- a. Only 3' to 5' growth provides the activating triphosphate for elongation of the strand after error correction.
- b. Only 3' to 5' growth allows the new strand to be flipped into the editing pocket on the DNA polymerase when an error is detected.
- c. Only 5' to 3' growth provides the activating triphosphate for elongation of the strand after error correction.
- d. Only 5' to 3' growth allows the new strand to be flipped into the editing pocket on the DNA polymerase when an error is detected.

22. The following is a partially-labelled diagram of DNA replication in prokaryotes. What is WRONG with this diagram?



- a. The 5' and 3' ends of the parental strand are labeled incorrectly.
- b. The 5' and 3' ends of the Okazaki fragments are labeled incorrectly.
- c. The number of replication forks is incorrect.
- d. The positions of the RNA primers are incorrect.

23. Copying errors not caught by the replication machinery can be corrected by:

- a. RNA polymerase.
- b. Strand-directed mismatch repair.
- c. DNA telomerase.
- d. DNA maintenance methyltransferase.

24. Which of the following statements regarding telomeres is FALSE?

- a. Extensive shortening of telomeres is usually recognized by the cell as a type of DNA damage.
- b. Most cancer cells produce high levels of telomerase.
- c. Stem cells have very short telomeres.
- d. Telomeres are non-coding repetitive DNA sequences.

25. Which of the following projects should a summer research student select if he/she wishes to successfully publish a research article?

- a. Measuring the speed of the 3' to 5' movement by the predominant helicase on the lagging strand template.
- b. Describing the structural changes in topoisomerase I as it catalyzes double-stranded DNA breaks.
- c. Measuring the heat required to break the hydrogen bonds between the telomerase RNA template and the 5' end of the newly synthesized lagging strand.
- d. Measuring the number of pyrimidine dimers repaired by nucleotide excision repair after UV radiation.

26. Which of the following BEST describes the experiment used to identify an ARS?

- a. The amino acid histidine is added to culture media to test for growth in yeast that lack the *His* gene.
- b. Abundant yeast growth is detected in yeast cells containing the *His* plasmid with random DNA sequences.
- c. The ability of a *His* plasmid to replicate independently of the host chromosome and be passed onto daughter yeast cells is used to identify an ARS.
- d. Sequences that enable transcription will enable *His* gene transcription in the plasmid and are therefore positive in this test.

27. Which of the following CORRECTLY describes promoters?

- a. Prokaryotic promoters are the sites where RNA polymerase begins transcription.
- b. Both prokaryotic and eukaryotic promoters are the sites where RNA polymerase begins transcription.
- c. Consensus sequences present within eukaryotic promoters are recognized by general transcription factors.
- d. Eukaryotic promoters must contain 4 elements.

28. What kind of bond is formed when RNA polymerase joins nucleotides together to synthesize an RNA molecule?

- a. Peptide
- b. Hydrogen
- c. Phosphodiester
- d. Glycosidic

29. Which of the following statements is CORRECT?

- a. All fully spliced eukaryotic mRNAs contain noncoding regions.
- b. All prokaryotic mRNAs have only two noncoding regions.
- c. All fully processed eukaryotic RNAs contain a 5' CAP and poly-A tail.
- d. All tRNAs contain only A, G, C or U.

30. Which of the following statements regarding mRNA splicing is TRUE?

- a. Prokaryotic mRNA splicing is similar to that of eukaryotes except it is simpler and does not require as many processing proteins.
- b. mRNA splicing is catalyzed by snRNPs which recognize consensus sequences in introns and exons.
- c. The 3'OH group is required for lariat formation.
- d. The intron sequences at the intron/exon boundaries can be completely changed and correct splicing will still occur.

31. Which of the following is TRUE regarding RNA processing of the 3' end of mRNA?

- a. It is initiated by dephosphorylation of the RNA polymerase, which causes the enzyme to stall and fall off the template strand.
- b. Cleavage and poly-A signals are encoded in the DNA but are recognized in the RNA by RNA-binding proteins and RNA-processing proteins.
- c. Poly-A Polymerase (PAP) requires a template.
- d. Cleavage and polyadenylation specificity factor recognizes a GC-rich region followed by an AT-rich region in order to terminate transcription and initiate RNA processing.

32. Which of the following CORRECTLY describes an elongation factor?

- a. EF-G helps the large ribosomal subunit ratchet forward by 1 codon.
- b. EF-Tu is not required for proper ribosome function.
- c. EF-G helps to check binding between the codon and anti-codon.
- d. EF-Tu will bend the t-RNA to reduce steric hindrance within the ribosome.

33. Which of the following is TRUE regarding prokaryotic and/or eukaryotic translation?

- a. Many commonly-used antibiotics do not affect translation in either prokaryotes or eukaryotes and are more often targeted to transcription.
- b. In prokaryotes, translation cannot begin until the mRNA is released from the RNA polymerase.
- c. Wobble base-pairing is an important mechanism for translation in both prokaryotes and eukaryotes.
- d. tRNA synthetases in prokaryotes are not able to remove incorrect amino acids once the high energy bond between the amino acid and the tRNA has been formed.

34. Which of the following statements regarding eukaryotic transcription is FALSE?

- a. TFIIH has a kinase domain that phosphorylates the C-terminal domain of RNA polymerase II.
- b. Only dephosphorylated RNA polymerase II is competent to initiate a new transcription cycle of protein-coding RNAs.
- c. Phosphorylation of Serine 2 residues on the C-terminal domain of RNA polymerase II is required for the attraction of splicing proteins.
- d. Binding of the activator protein to the mediator protein is required so that the histone-modifying enzyme can be released.

35. Base-pairing can be observed between which of the following during eukaryotic cellular processes?

- a. snRNAs and pre-mRNAs.
- b. Nuclear DNA and tRNA.
- c. mRNA and tRNA.
- d. All of the above.

36. Below is a portion of the sequence for a fully-processed eukaryotic mRNA. The AUG represents the usual start codon. Imagine that there was a mutation in the DNA that codes for this mRNA so that the base indicated at either position 1 or 2 (arrows) was deleted. Which of the following would be a CORRECT prediction of what could happen during translation of mRNA made from DNA mutated in either of these positions?

1



2



5'- UACUUGGAACUCCAAACCAAUGGUCCAGUUACUCAAGGCU.....-3'

- a. A deletion of the G at '1' will not affect the amino acid sequence because EF-Tu will check the base-pairing between the mRNA and tRNA.
- b. A deletion of the C at '2' will not affect the amino acid sequence since the deletion occurs before the ribosome will start translation.
- c. A deletion of the G at '1' will affect the amino acid sequence because the deletion will change the reading frame.
- d. A deletion of the C at '2' will affect the amino acid sequence because the deletion will change the reading frame.
37. Which of the following will most affect translation in prokaryotes or eukaryotes?
- a. The deletion of eukaryotic Shine-Dalgarno sequences.
- b. The deletion of prokaryotic eIF2.
- c. The deletion of eukaryotic poly-A-binding proteins.
- d. The addition of Shine-Dalgarno sequences to the 3' end of eukaryotic mRNAs.
38. Imagine that you discover a drug that prevents EF-G from hydrolyzing GTP. What is the MOST likely outcome if you were to treat cells with this drug?
- a. t-RNAs will not be escorted to the ribosome.
- b. Incorrect amino acids will be added to the growing polypeptide chain.
- c. Hydrolytic editing by tRNA synthetase will be inhibited.
- d. Elongation will be slower.
39. All of the following events are involved in maintaining fidelity during translation EXCEPT:
- a. hydrolysis of aminoacyl-tRNA bonds if the amino acid fits into the tRNA synthetase editing site.
- b. correct base-pairing between the peptidyl t-RNA anti-codons and the codons in the P-site.
- c. correct base-pairing between 16S RNA, codons, and anti-codons.
- d. preferential dissociation of incorrectly base-paired tRNAs.
40. Which of the following correctly describes Hsp60?
- a. This protein helps improperly folded proteins to fold properly.
- b. This protein is a "Heat shock protein" that is only expressed at high temperatures.
- c. This protein causes improperly folded proteins to aggregate into insoluble particles.
- d. This protein is a protease that degrades unfolded proteins.

Second base

		U	C	A	G	
First base	U	UUU } Phenyl-alanine UUC } UUA } Leucine UUG }	UCU } UCC } Serine UCA } UCG }	UAU } Tyrosine UAC } UAA } Stop codon UAG } Stop codon	UGU } Cysteine UGC } UGA } Stop codon UGG } Tryptophan	U C A G
	C	CUU } Leucine CUC } CUA } CUG }	CCU } CCC } Proline CCA } CCG }	CAU } Histidine CAC } CAA } Glutamine CAG }	CGU } Arginine CGC } CGA } CGG }	U C A G
	A	AUU } Isoleucine AUC } AUA } AUG } Methionine start codon	ACU } ACC } Threonine ACA } ACG }	AAU } Asparagine AAC } AAA } Lysine AAG }	AGU } Serine AGC } AGA } Arginine AGG }	U C A G
	G	GUU } Valine GUC } GUA } GUG }	GCU } GCC } Alanine GCA } GCG }	GAU } Aspartic acid GAC } GAA } Glutamic acid GAG }	GGU } Glycine GGC } GGA } GGG }	U C A G

Third base

THE END