BIOL 367 Fall 2020 (MIDTERM EXAM 1)

OCT 14, 2020

MATERIALS ALLOWED - Class notes and textbooks

MATERIALS NOT ALLOWED - Laptops, tablets or phones

CALCULATORS ALLOWED - Yes

INTERNET USAGE - No, except on the device used only for taking the EXAM on TopHat.

Time allowed - 60 minutes

SPECIAL INSTRUCTIONS: DONOT take the screenshot of the exam. Total marks = 100.

Question 1A Hide Correct Answer Show Responses

Which of the following is NOT a cause or a consequence of the Chargaff's rules for a DNA double helix/genome?

A	The ratio sf pyrinridines : purines is 1 : 1
B	The ratio of A+C : G+T is 1 : 1
C	The molecular weight of two DNA strands of a double helix is identical
D	G+C : A+T ratio may vary among different species
E	A basepairs with T & G basepairs with C

Question 1B Grade Responses (0)

Briefly explain your choice for QUESTION 1A. (Maximum 3-4 sentences)

Students will write their responses here...

We now know that the reason for Chargaff's rules is unique base-pairing between two complementary bases in a DNA double helix. However, each base has a particular molecular weight and the sequence on one strand will not be identical to the sequence on another (unless in a palindrome). Therefore, their molecular weight's wouldn't be identical.

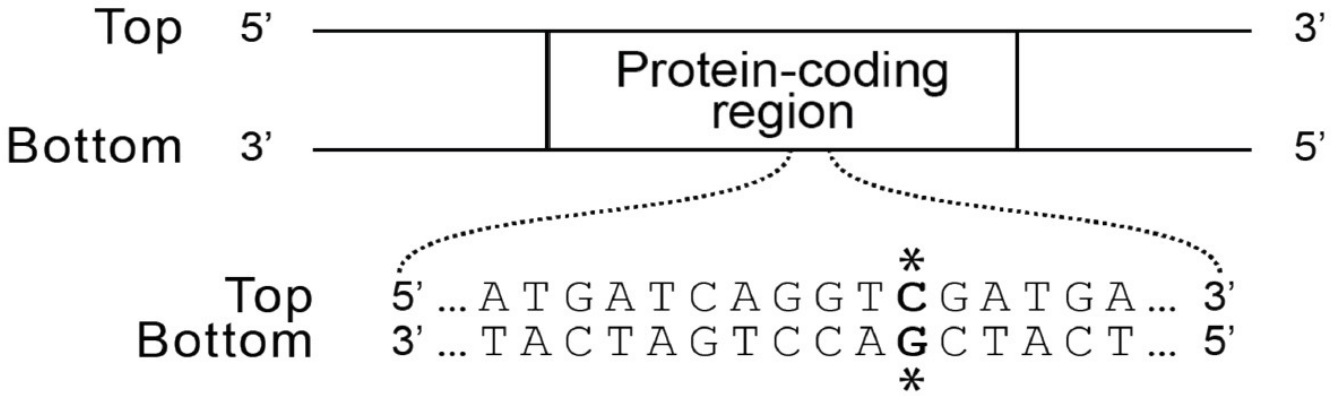
Question 1C Grade Responses (0)

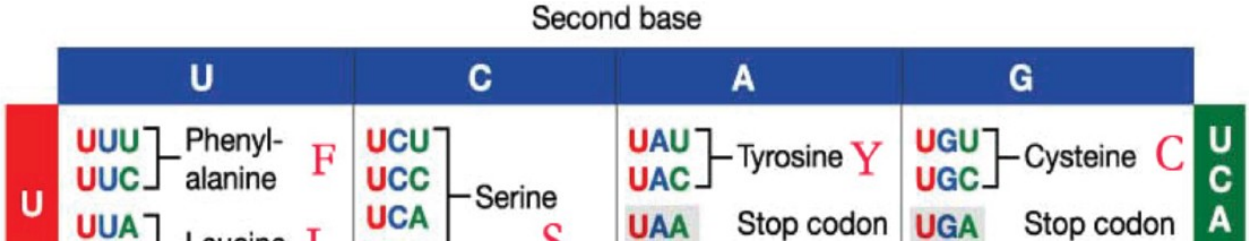
Briefly explain why Chargaff's rule will FAIL if single-stranded DNA is used to measure purines and pyrimidines? (Maximum 2-3 sentences).

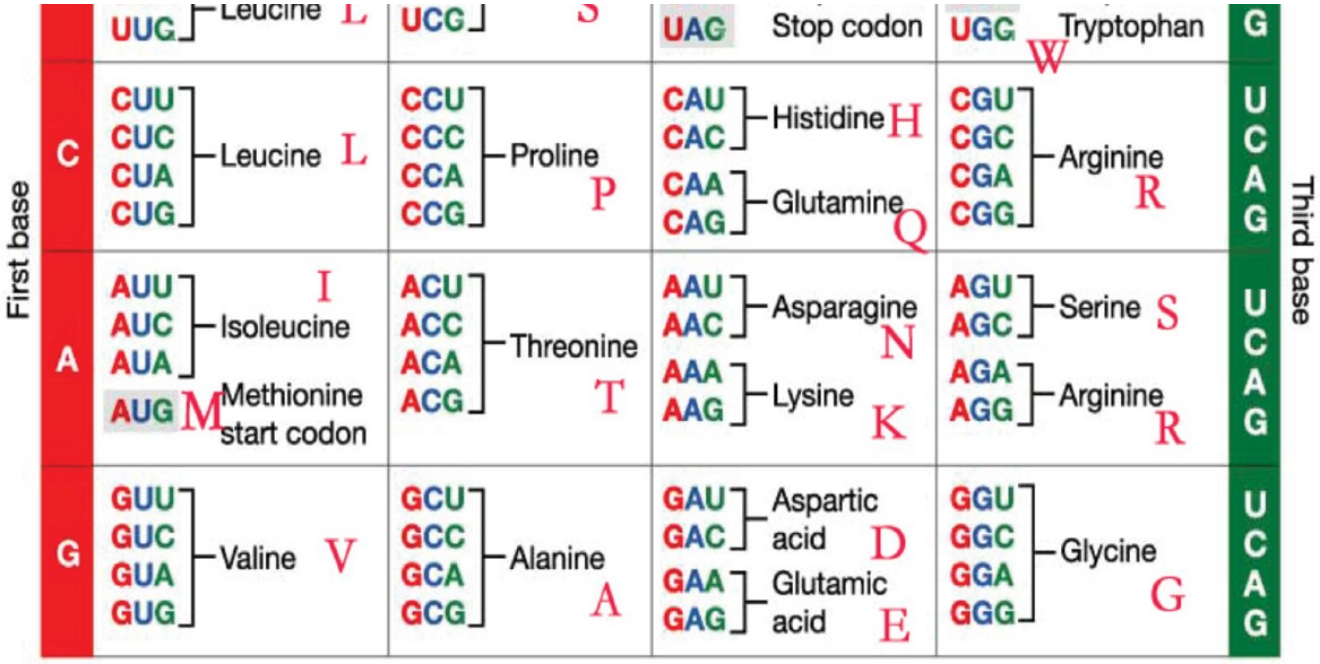
The underlying basis of Chargaff's rule is the unique purine-pyrimidine base pairing between the two bases of the double-stranded DNA helix. In a single-stranded DNA, since there is no base pairing, the percentage equality is highly unlikely.

Question 2A Hide Correct Answer Show Responses

Given below (see picture) is a partial DNA sequence of a hypothetical gene. The direction of transcription is from RIGHT to LEFT. The nucleotides in bold with asterisks are mutated to a T/A base-pair (T at the top, A at the bottom strand)]. This mutation leads to an amino acid change from Aspartic acid (D) to Asparagine (N) in the protein. The genetic code table is provided.
(A) The correct reading frame of the nucleotides in an mRNA is:







A	AUG, AUC, AGG, UCG, AUG, A
B	A, UGA, UCA, GGU, CGA, UGA
C	AU, GAU, CAG, GUC, GAU, GA
D	UCA, UCG, ACC, UGA, UCA, U
E	UC, AUC, GAC, CUG, AUC, AU
F	U, CAU, CGA, CCU, GAU, CAU
G	TC, ATC, GAC, CTG, ATC, AT

Question 2B

Grade Responses (0)

Refer to Question 2A for the image. A partial DNA sequence of a hypothetical gene is shown. The direction of transcription is from RIGHT to LEFT. The nucleotides in bold with asterisks are mutated to a T/A base-pair (T at the top, A at the bottom strand)]. This mutation leads to an amino acid change from Aspartic acid (D) to Asparagine (N) in the protein.

(B)

(i) Briefly describe why a particular reading frame you choose for Question 2A is correct?

(ii) Based on your interpretation above, which DNA strand (top or bottom) is the template strand and the coding strand?

i) All except for "G" could be the reading frames in the mRNA. However, since the direction of transcription is from Right to Left, we can conclude that the bottom strand should be the coding sequence. Which narrows down the frames to :
D. UCA, UCG, ACC, UGA, UCA, U
E. UC, AUC, GAC, CUG, AUC, AU
F. U, CAU, CGA, CCU, GAU, CAU

Now, according to the question, one of the codons encodes "D" which if we change the "G" to "A" changes the amino acid to "N". That leaves only one possibility "E" which has a GAC that if changes to AAC will encode "N" instead of "D" in the protein.
Also, this is the middle of the gene and we do not need to worry about the start codon in frame.

Question 3A Hide Correct Answer Show Responses

You are a young researcher having joined as an undergraduate trainee in a molecular biology lab. Your first task is to amplify two DNA sequences from a genome using Polymerase Chain Reaction (PCR). The sizes of the two DNA sequences to be amplified are different (DNA sequence 1 = 500bp & DNA sequence 2 = 5000bp). You choose a high fidelity DNA polymerase that adds 500 bases per minute for the PCR. Assuming that you use primers with similar melting temperatures, which of the following parameters will you change between the two PCRs?

A	Annealing temperature
B	Extension temperature
C	Denaturation temperature
D	The time of annealing
E	The time of extension
F	The time of denaturation

Question 3B Grade Responses (0)

Briefly explain your choice for Question 3A. (Maximum 2-3 sentences)

Annealing temperature is dependent on the primers and their Tm and that is same for the primers. Extension temperature is dependent on the DNA polymerase and that is similar for the two reactions. Denaturation temperature for all PCRs is usually "95-100C" and at that temperature nearly every DNA molecule denatures. The time of annealing is again dependent on the primers and is similar between the two reactions. The time of denaturation is also constant for the two reactions. The only difference is the size of PCR fragment to be amplified. That is driven by the DNA polymerase (500b/ min) used. The smaller DNA will require lesser extension time than the larger DNA.

Question 3C Hide Correct Answer Show Responses

Replicating DNA polymerase can amplify nearly an entire genome in a single binding event. However, the same DNA polymerase fails to show similar processivity in a test tube (PCR). The lack of which of the following activity/component contributes to this anomaly?

A	3' to 5' exonulcease activity	
B	5' to 3' polymerase activity	
C	Clamp loader & clamp protein	✓
D	DNA helicase	
E	All of the above	

Question 3D Hide Correct Answer Show Responses

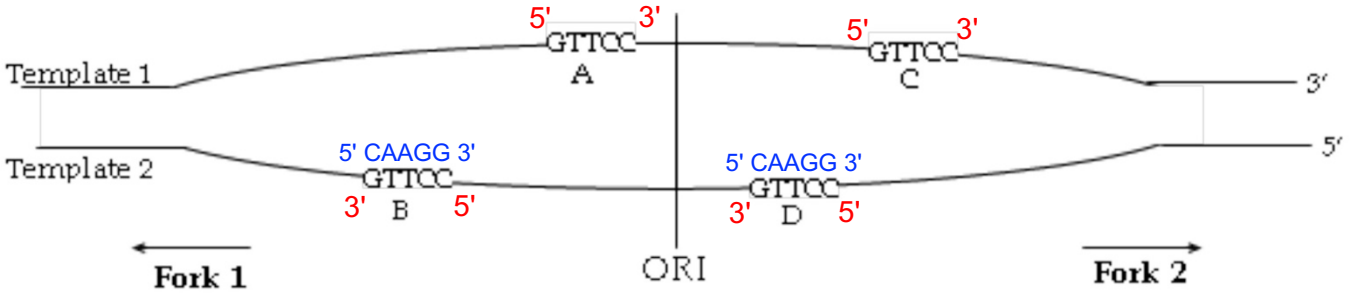
In Polymerase Chain Reaction, what determines the annealing temperature of the reaction?

A	The length of DNA to be amplified.	
B	The type of DNA polymerase used.	
C	The type of nucleotides used.	
D	The sequence of primers used.	✓
E	The sequence of DNA template used.	

Question4A Hide Correct Answer Show Responses

Below is a representation of an origin of replication and the two associated replication forks in bacteria. Synthesis of new DNA occurs on both strands.
(A) To which site or sites can the primer 5'-CAAGG-3' bind to initiate replication?

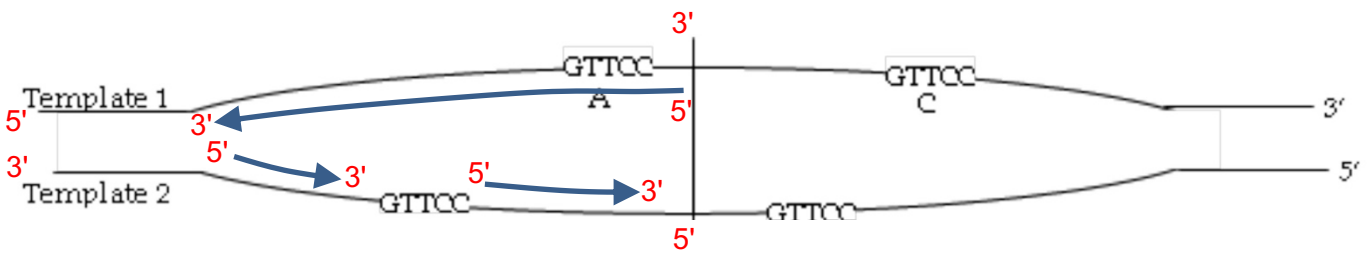
(B)



A	Only Site A
B	Only Site B
C	Only Site C
D	Only Site D
E	Sites A and B
F	Sites B and D
G	All Sites

Question4B Hide Correct Answer Show Responses

(C) In the case of replication fork 1, which is the leading strand?



A	Template 1	✓
B	Template 2	

Question 4C Hide Correct Answer Show Responses

(D) A bacterium replicates its circular chromosome at a speed of 1000 nucleotides per second. If it is able to completely replicate its chromosome in 45 minutes. How many base pairs of DNA are in the bacterial chromosome?

A	1.35 million.	
B	2.7 million.	
C	5.4 million.	✓
D	4.6 million.	

Question 4D Grade Responses (0)

Briefly explain your choice for Question 4C. (Maximum 3-4 sentences).

Given the rate and time of polymerization. A particular DNA polymerase can replicate 1000 x 60 x 45 bases = 2.7 million bases. However, at a given time, there are two replication forks operating in bacteria and, therefore, two polymerases will be active at a given time. Thus the total number is 2.7 x 2 = 5.4 million base pairs.

Question 5A Hide Correct Answer Show Responses

Bacteria do not have an end-replication problem because,

A	They have three DNA polymerases and one specifically replicates the ends.
B	They have Circular chromosome and 3' OH is available at the end of replication to fill the gap.
C	They have a unique enzyme called telomerase that replicates the ends.
D	Their DNA ends contain several repeat sequences to form a protective loop at the end.
E	None of the above.

Question 5B Hide Correct Answer Show Responses

Eukaryotes have linear chromosomes, and due to the end-replication problem, CANNOT fully replicate the following ends of DNA?

A	5' end
B	3' end

Question 5C Grade Responses (0)

Eukaryotes have the end-replication problem that leads to the recession of one strand of their DNA. However, eukaryotes use telomerase to solve this problem. But, telomerase only extends the 3' ends of chromosomes. Briefly explain how this strategy allows the extension of the 5' ends of the chromosome?

The 5' end of the chromosomes ends up to be shorter after every replication event due to the removal of the primer at the end. See below:
5' TEMPLATETEMPL 3'
3' NNNNNN PRIMER 5'
5' NNNNNNNNNNNN 3'
3' TEMPLATETEMPL 5'

5' TEMPLATETEMPL 3'
3' NNNNNN 5'
5' NNNNNNNNNNNN 3'
3' TEMPLATETEMPL 5'
The below sequence is the newly replicated DNA at the ends. The one with the primer is the lagging strand. After the primer is removed, it leaves a gap at the 5' end of the newly replicated DNA. However, the telomerase only extends the 3' end. But by this extension, it provides an additional template for the primer to bind to the lagging strand to extend this end as well.

Question 5D Grade Responses (0)

The telomerase adds multiple repeat sequences at the ends of the eukaryotic chromosome. Give TWO reasons why repeats

are added instead of a single stretch of some random sequence?

There are several reasons:

1. Template in the case of the telomerase is an RNA molecule which cannot be too long.
2. The telomerase adds multiple repeats and uses the previously added sequence as a way to find the template. Therefore, repeats are useful for telomerase to find the ends.
3. The long random sequence cannot be regulated. The repeats allow a feed back to control the extension of the ends of the chromosome.
4. Repeats allow the finding of a complementary sequence for the D loop formation to protect the ends.

Question 6. Fill in the blanks with T (for True) or F (for False).

Show Correct Answer Show Responses

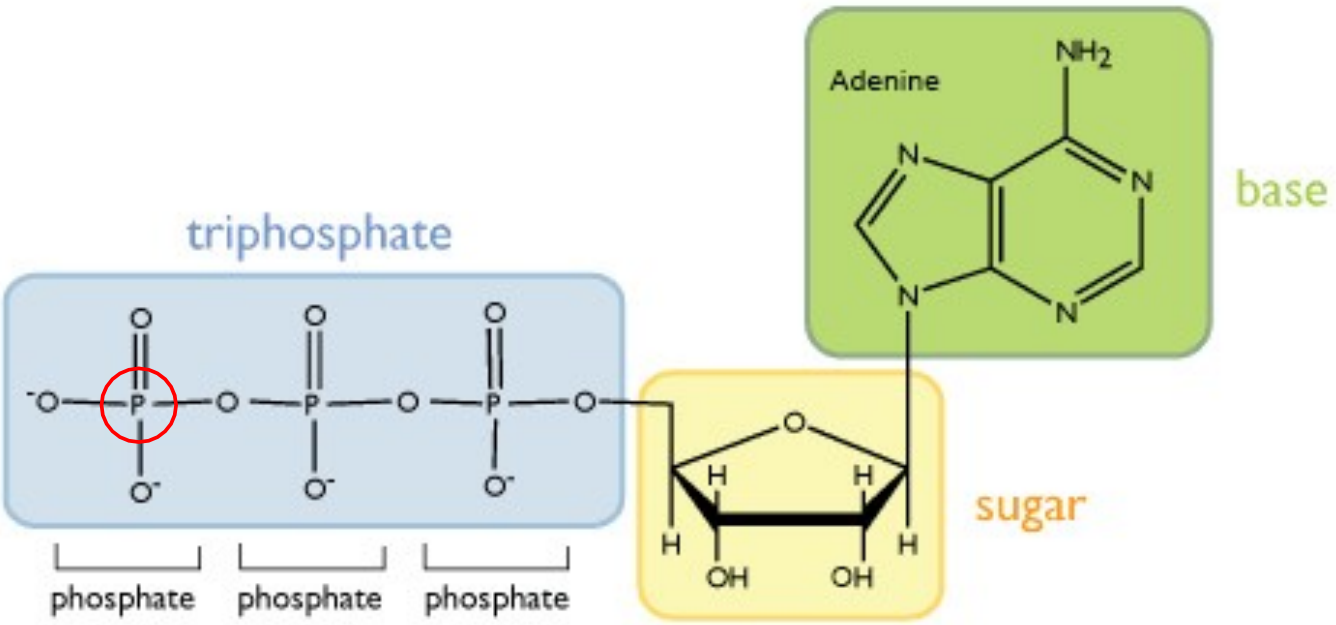
1. In eukaryotes, DNA replication starts at a single origin of replication but multiple times in S phase.
   _____ False - The origin fires only once
2. In Transcription, template strand is also called the coding strand of DNA. _____ False
3. Illumina sequencing requires new DNA synthesis. _____ True - for formation
4. In the case of high fidelity DNA polymerase, the 3' to 5' exonuclease activity is initiated only when a mismatch is detected. _____ False - The exonuclease activity occurs even in the absence of the mismatch
5. Griffith's experiments proved that DNA is the genetic material. _____ False
6. Hershey and Chase used S35 to label viral DNA and P32 to label viral proteins. _____ False
7. DNA molecule of identical sequence and size can be separated by CsCl gradient. _____ True - topoisomers & heavy isotopes
8. In eukaryotes, Okazaki fragments allow the proper functioning of DNA mismatch machinery.
   _____ True
9. In PCR, RNA oligos are used as primers for DNA replication. _____ False
10. Maxam-Gilbert & Nanopore DNA sequencing methods DONOT require new DNA synthesis.
    _____ True

Question 7A

Hide Correct Answer Show Responses

The following is a structure of a Adenosine triphosphate (ATP). Click on the phosphate (P) that should be radioactive (P32) such that only the 5'end of the DNA can become radioactive (using polynucleotide kinase).

Gamma phosphate added to the 5' ends of the DNA by PNK.



Question 7B

Show Correct Answer Show Responses

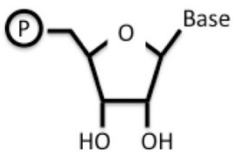

Shown are the two DNA double helix. Fill in the blanks with "LEFT" or "RIGHT".

1. The DNA shown in (a) is Right -handed DNA.
2. The DNA shown in (b) is Left -handed DNA.

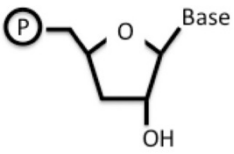
Question 7C Hide Correct Answer Show Responses

From the following structures. the dideoxyribose nucleotide is depicted by:

A.

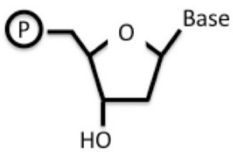


B.



C.

D.



A	A
B	B
C	C
D	D