<u>Dashboard</u> / <u>Courses</u> / <u>Science II - Section A2</u> / Topic 1 / <u>Endsem</u>

Started on	Tuesday, 20 April 2021, 3:39 PM
State	Finished
Completed on	Tuesday, 20 April 2021, 4:36 PM
Time taken	56 mins 24 secs
Grade	38.00 out of 50.00 (76 %)

Question 1
Complete
Mark 1.00 out of 1.00
In PCR sequencing by Sanger's method, the sequence of nucleotides reaching the other end of the gel electrophoresis reads 5'
TGACGATTA 3'. Give the sequence of the template strand in the correct orientation.
5' ACTGCTAAT 3'
Comment:

Question 2
Complete
Mark 0.00 out of 2.00
Give approximate values of window size and stringency (for matches) you would use for dot plot analysis to identify multiple copies of domains.
Window Size: 15
Stringency: 10
Comment:



Correct

Mark 1.00 out of 1.00

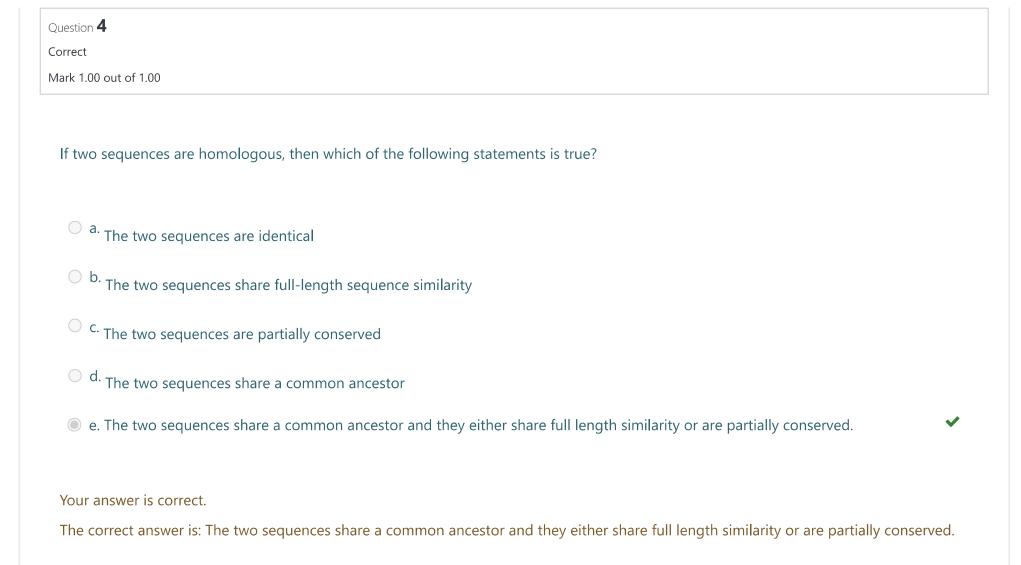
In double-stranded DNA, which of the following base ratios always equals 1?

- a. G/C
- b. C/T
- c. (A+T)/(G+C)
- od. G/A
- e. (A+G)/(C+T)

Your answer is correct.

The correct answer is:

(A+G)/(C+T)



Question **5**

Complete

Mark 2.00 out of 2.00

Construct a restriction map of a linear fragment of DNA, using the following data. Give the fragment lengths and their positions on a linear scale.

DNA	Sizes of Fragments (bp)
uncut DNA	10,000
DNA cut with EcoRI	8000, 2000
DNA cut with BamHI	5000, 5000
DNA cut with EcoRI + BamHI	5000, 3000, 2000

When cut with EcoRI:

location : length

1-8000 : 8000

8001-10000 : 2000

When cut with BamHI:

location : length

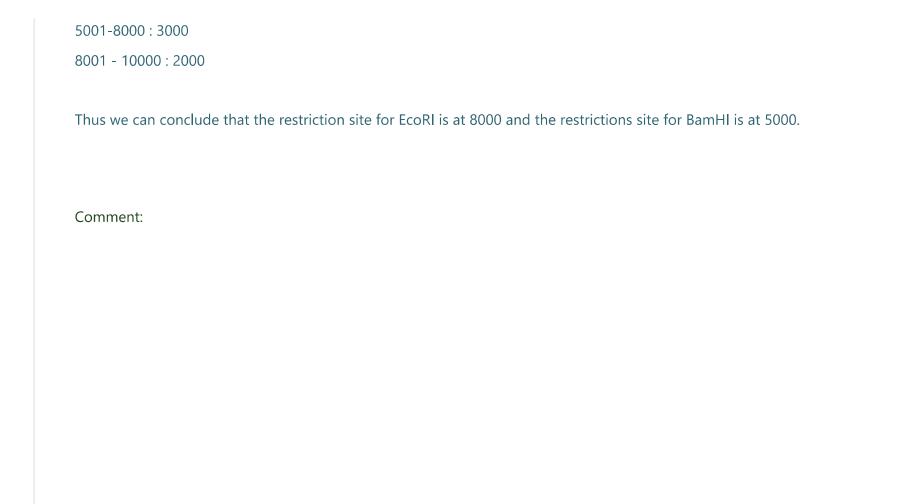
1-5000 : 5000

5001-10000 : 5000

When cut with Both:

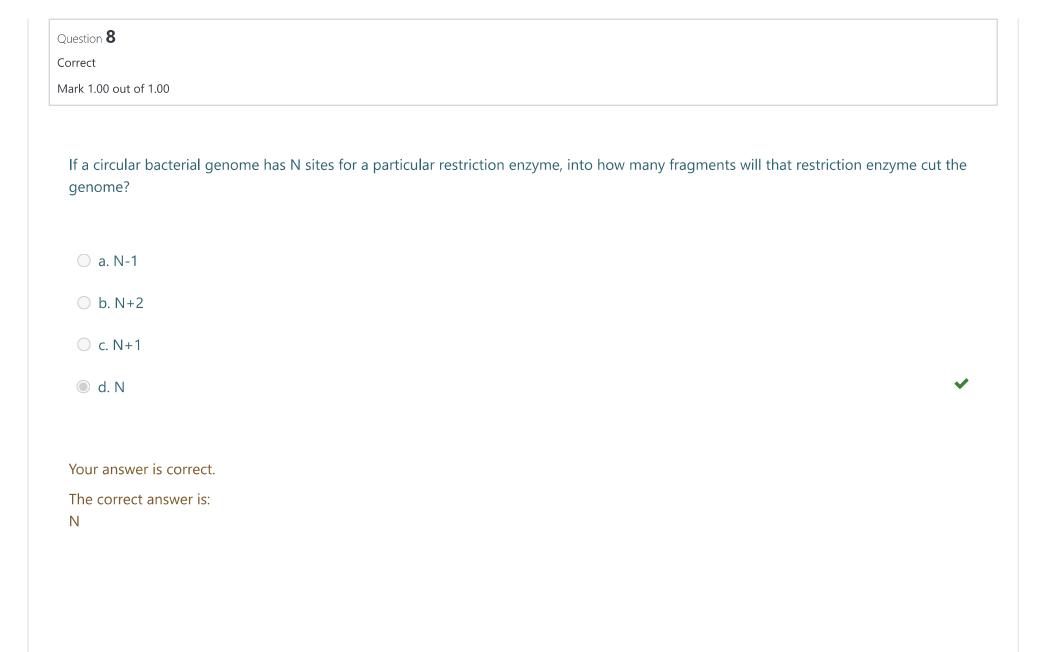
location : length

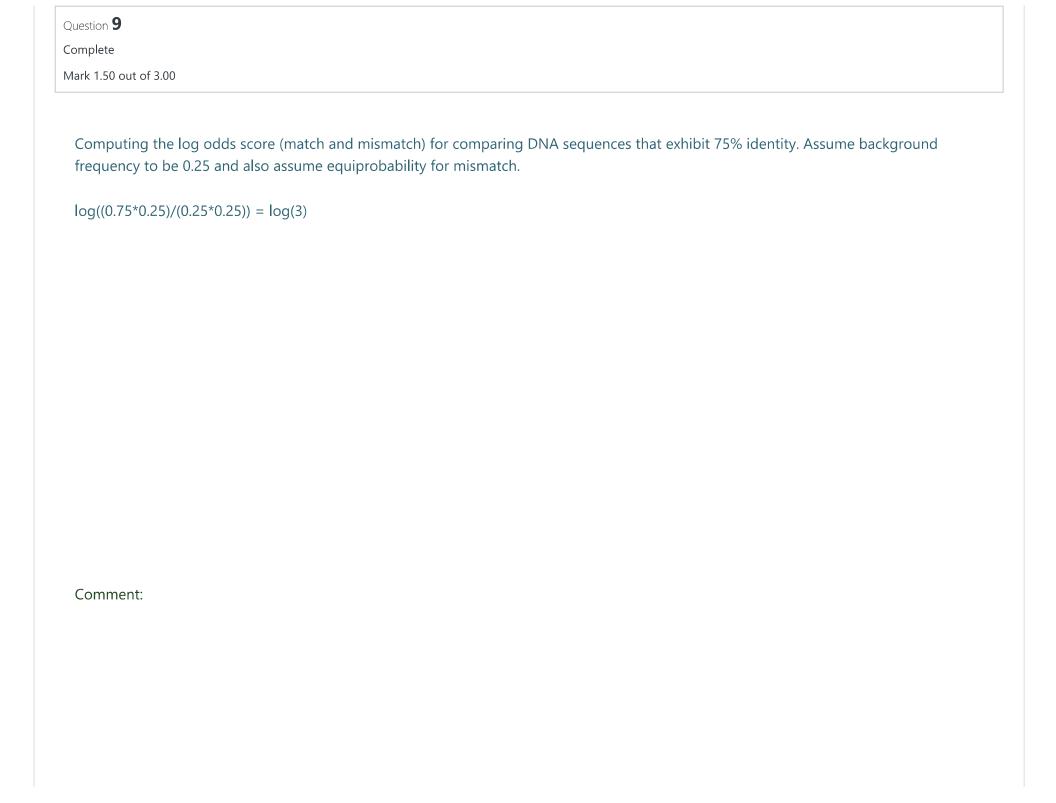
1-5000 : 5000



Question 6
Complete
Mark 1.00 out of 1.00
Which of the two scoring matrices, PAM250 and PAM125 would you use for comparing (i) closely related sequences and (ii) evolutionarily
distant sequences?
(i) PAM125
(ii) PAM250
Comment:

Question 7					
Correct					
Mark 1.00 out of 1.00					
The E-value in the	BLAST program depe	ends on database siz	e. True/False.		
Select one:					
True ✓					
○ False					
The correct answe	r is 'True'.				





Question 10	
Correct	
Mark 1.00 out of 1.00	
Which variant of the dynamic programming algorithm would you use if the two sequences are closely related:	
 a. does not matter, as both will give same results 	~
O b. global alignment	
C. local alignment	
Your answer is correct.	
The correct answer is:	
does not matter, as both will give same results	



Protein sequence database search is better than DNA sequence search for finding remote homologies. What are the possible reasons? [Note: List all the correct options]

a. Because of degeneracy in the code, a change at DNA level may not always lead to a change at the amino acid level, making it possible to find distant homologies using protein database search

b. Scoring matrices for proteins are more sensitive compared to those used for comparing DNA sequences

C. Only 4 characters in DNA compared to 20 in proteins, this leads to more hits by random chance at DNA level.

d. Computationally, protein sequence is one-third the size of the corresponding DNA sequence.

Your answer is correct.

The correct answers are:

Because of degeneracy in the code, a change at DNA level may not always lead to a change at the amino acid level, making it possible to find distant homologies using protein database search,

Only 4 characters in DNA compared to 20 in proteins, this leads to more hits by random chance at DNA level.,

Scoring matrices for proteins are more sensitive compared to those used for comparing DNA sequences

Question 12 Correct				
Mark 1.00 out of 1.00				
Base pairing between the two strands of DNA is formed by				
Answer: Hydrogen Bonds ✓				
The correct answer is: H-bonds				
Question 13 Correct				
Mark 2.00 out of 2.00				
Give the expected frequency of observing GC boxes, GCCGCC in a genome of length 10MB and $G = 0.2$?				
Answer: 640 ✓				
The correct answer is: 640				

Question 14	
Partially correct	
Mark 1.50 out of 2.00	
The SARS-CoV-2 virus genome is being continuously sequenced across the world from infected people. What is the advantage of resequencing? [Note: List all the correct options]	
a. demographic distribution of various strains of the virus	~
b. to understand the migration pattern	~
C. to know if the virus is mutating	~
\Box d. to know if the virus is becoming more virulent or loosing its virulence	
Your answer is partially correct.	
You have correctly selected 3. The correct answers are:	
to know if the virus is mutating,	
to understand the migration pattern,	
to know if the virus is becoming more virulent or loosing its virulence,	
demographic distribution of various strains of the virus	

Question **15**

Incorrect

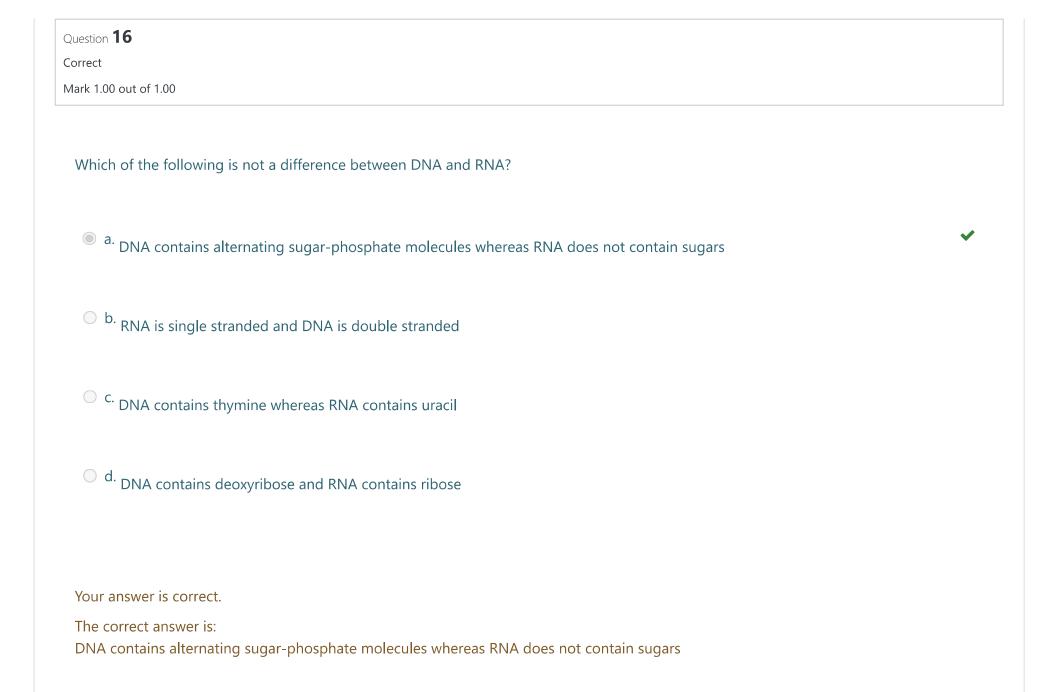
Mark 0.00 out of 1.00

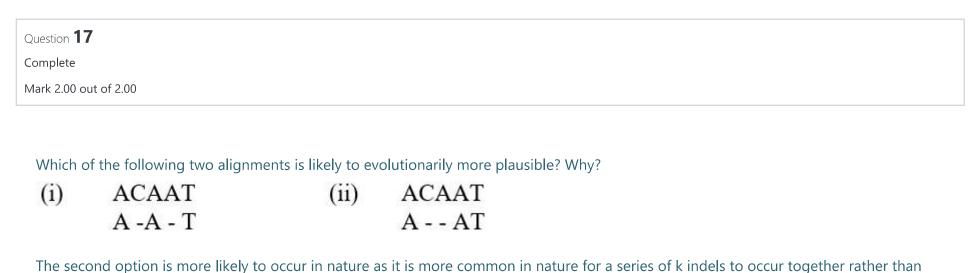
Homology is implied if

- a. both sequence and structure are similar
- b. two sequences are > 50% identical
- oc. two sequences are similar
- d. two structures are similar

Your answer is incorrect.

The correct answer is: both sequence and structure are similar





The second option is more likely to occur in nature as it is more common in nature for a series of k indels to occur together rather than separately.

Comment:

Question 18

Complete

Mark 3.00 out of 3.00

Compute the score of the following pairwise alignments:

Global alignment: Match = +1, Mismatch = 0, Gap: opening = -5, extension = -1

GAGG - - - TGAC - TGGGCA

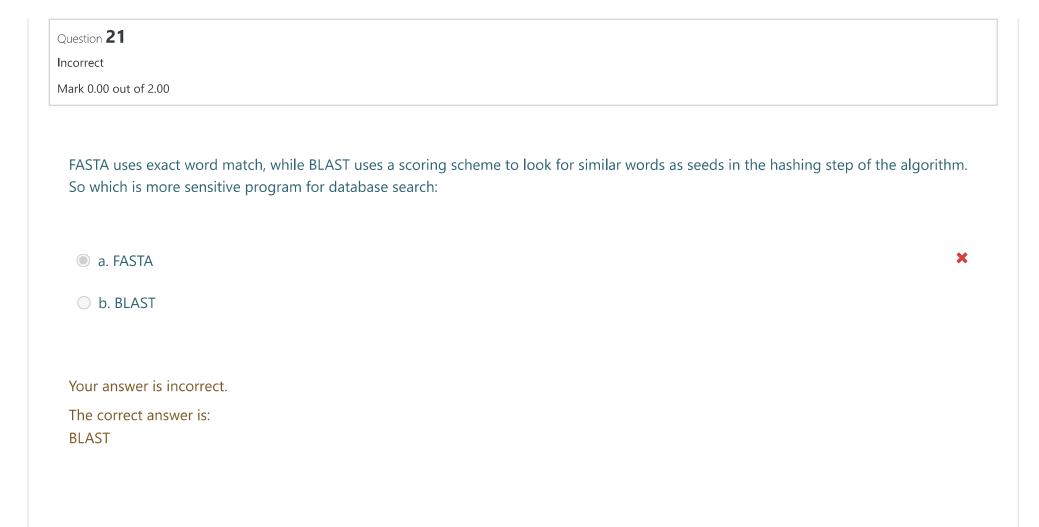
GTGGATGCGGCAAGGG - -

= -10

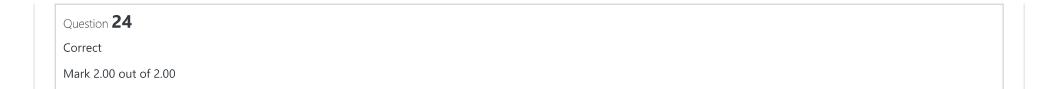
Comment:

Question	n 19
Correct	
Mark 1.0	00 out of 1.00
الم معد	easing the Cap Costs will requit in aborton local clippersonts?
IIICIE	easing the Gap Costs will result in shorter local alignments?
Sele	ct one:
© T	rue ✔
○ F	False
The	correct answer is 'True'.

Question 20
Complete
Mark 2.00 out of 2.00
BLAST program misses some good biological homologies below the accepted statistical cut off value. How would you identify these
distant homologies?
I would use PSI-BLAST to identify these distant homologies. It is useful because it is specifically made to find sequences that are similar and have 15-20% similarity.
Comment:



Question 22	
Incorrect	
Mark 0.00 out of 1.00	
The two strands of DNA molecule are:	
a. run antiparallel, i.e., are reverse of each other	
○ b. mirror images of each other	
C. reverse complement of each other	
d. complement each other	K
Your answer is incorrect.	
The correct answer is:	
reverse complement of each other	



If the length of sequence read is 200bases, and 10x coverage is desired, give the number of reads that will be required to sequence a human genome.

Answer: 150,000,000

The correct answer is: No. of Reads required = GenomeLength DesiredCoverage / ReadLength = $3 \times 109 \times 10/200 = 1.5 \times 108 = 150$ Million reads

Comment:

Question 25 Correct	
Mark 1.00 out of 1.00	
Polymerase Chain Reaction can be used for	
 a. amplification of DNA sequences 	
 b. both amplification and sequencing of DNA sequences 	~
C. sequencing of DNA sequences	
Your answer is correct. The correct answer is: both amplification and sequencing of DNA sequences	

Question 26
Correct
Mark 1.00 out of 1.00
Cloning can be used for of an unknown DNA sequence
a. storing
O b. expression
c. storing and amplification
O d. amplification
e. storing, amplification and expression
Your answer is correct.
The correct answer is: storing, amplification and expression

Question **27**Incorrect

Mark 0.00 out of 2.00

Which approach would you use for amplification of an unknown DNA sequence: (i) cloning, or (ii) PCR? Give reasons.

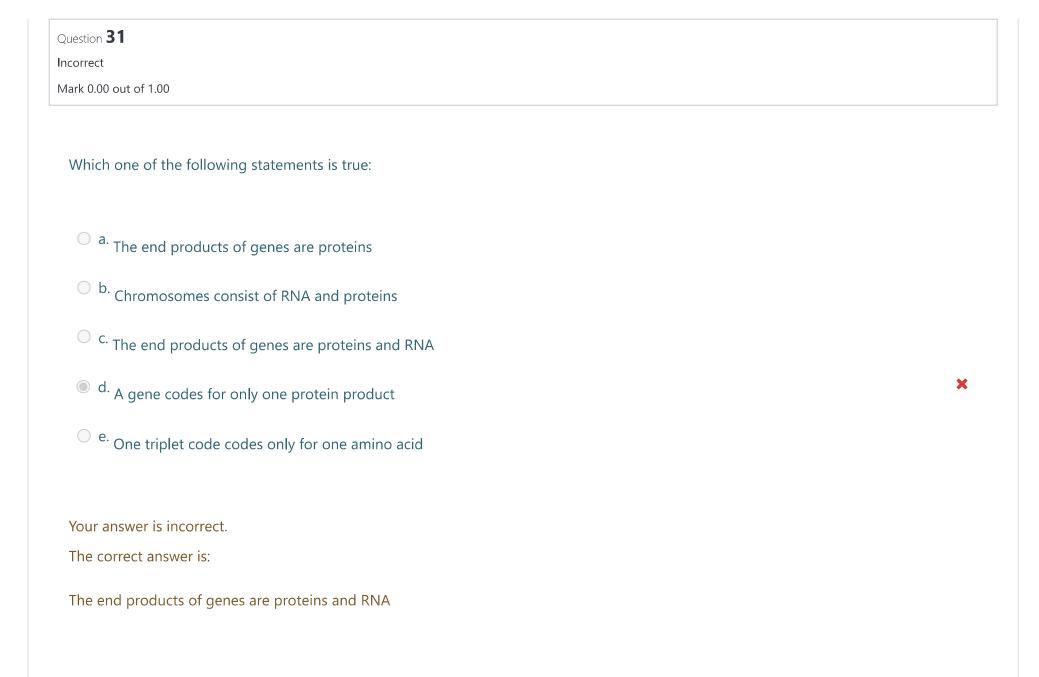
Answer: I would use PCR because PCR is faster, doesn't require an RE, requires a smaller si

The correct answer is: Cloning. For an unknown sequence we do not know the primers.

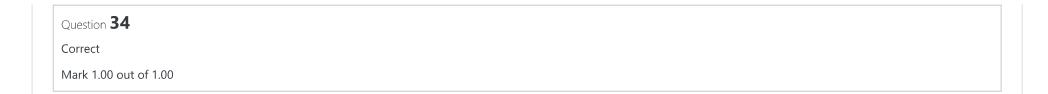
Question 28
Complete
Mark 2.00 out of 2.00
The recognition site for Sau3A I is GATC and is contained in the recognition site of BamH I, GGATCC. Will the two REs give the same results? If not, which one will give larger number of fragments?
No. Sau3A will give a higher number of fragments since wherever BamHl cuts, Sau3A will also cut, but Sau3A can cut where BamHl cannot.
Comment:

Question 29	
Correct	
Mark 1.00 out of 1.00	
Sequences in DNA that restriction enzymes bind to and cut are mostly:	
^{a.} Antiparallel	
b. Not symmetrical about the midpoint	
C. Random sequences	
© d. Symmetrical about the midpoint	~
Your answer is correct.	
The correct answer is:	
Symmetrical about the midpoint	

Question 30					
Correct					
Mark 1.00 out of 1.00					
Homologous sequend	ces are not always high	nly similar. True / Fa	ilse		
Select one:					
True ✓					
○ False					
The correct answer is	'True'.				



Question 32
Correct
Mark 1.00 out of 1.00
A single scoring matrix can be used for aligning sequences at different evolutionary distances.
Select one:
○ True
■ False
The correct answer is 'False'.
Question 33
Incorrect
Mark 0.00 out of 1.00
If ATATATAT is the sequence in the forward strand, give the sequence of the other strand in the correct orientation.
Answer: TATATATA **
The correct answer is: ATATATAT



Genes are stable entities and inherited from generation to generation. Are mutated genes also stable entities and inherited in the same way as normal genes? **[Yes/No]**

Answer:	Yes	~
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The correct answer is: Yes

Question 35
Correct
Mark 1.00 out of 1.00
The bond linking adjacent nucleotide building blocks in DNA is called:
a. An ether bond
O b. A polynuclieotide bond
c. A phosphate bond
d. A phosphodiester bond
Your answer is correct.
The correct answer is:
A phosphodiester bond
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