

Minor Exam

BBL231 (Molecular Biology and Genetics)

MM 30

November 9th, 2020

Duration: 1 h

Q. 1.

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a) Which of the following DNA sequences could most likely be cleaved by a restriction endonuclease?

5'-TATACC-3'

3'-ATATGG-5'

5'-GGAACC-3'

3'-CCTTGG-5'

5'-CGATTA-3'

3'-GCTAAT-5'

5'-CGTAGG-3'

3'-GGATGC-5'

b) Calculate how frequently a given restriction site would be expected to occur in a stretch of DNA of a specific base composition (%GC).

Recognition Sequence: AGCT

GC: 35%

c) Draw the restriction map

Restriction Enzyme(s)	Number of base pairs			
Bam HI	52.0			
Hind III	26.0	12.0	8.0	6.0
Hind III & Bam HI	14.0	12.0	8.0	6.0

Q. 2 You have isolated a new bacterium which glows in the dark. You would like to identify the gene responsible for that glow. Describe all the steps in detail about identification and isolation of the gene from the bacterium.

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Q. 3 You are working on an uncharacterized enzyme. You would like to enhance the thermostability of this enzyme. Describe the method you will use in this case. 3

Q. 4 Describe the technique that is used for studying the localization of heterochromatin and euchromatin region in the chromosome in eukaryotes. Differentiate between heterochromatin and euchromatin. 5

Q. 5 You would like to clone a gene for cell division from a eukaryote. Describe in detail the method you will use for obtaining the gene. 3

Q. 6 Design PCR primers 6

Calculate the T_m of each of the primers. Write the PCR cycle conditions. Design PCR primers for performing site directed mutagenesis at the bolded T and change it to G.

A **T** TGCAGACTTCTATGTAACCGAAAAATGCTGCAACACTTTATTAAGCAAGTTCATGATAATAGTGTAC
TGAAACCAAGCCCTCGTGTGTTTTGGTATGTGTCCCTTGTGGTTCTACTCAGGTTGAGCGTCGTGCCATTTCG
TGAGTCTGCACTGGGAGCAGGCGCACGTGAGGTCTATTTGATTGATGAGCCAATGGCGGCTGCAATTGGT
GCTGGCCTGCGAGTTTTAGAGCCTACTGGCTCTATGGTTGTTGACATCGGTGGCGGTTACTACAGAAGTCG
CGGTGATCTCTTTAAACGGCGTGGTTTTACTCCTCGTCAGTACGCATTGGTGGTGACCGTTTTGATGAGGC
CATTATCAACTACGTTTCGTTCGTAACACTACGGTAGCTTGATCGGTGAAGCGACGGCAGAGAAAATCAAACAC
GAGATTGGTTCAGCATAACCCAGGTGATGAAGTTGAAGAAAATTGAAGTGCGTGGCCGTAACCTTGCTGAAG
GTGTGCCACGAAGCTTTAGCCTGAATTCAAATGAAATTTCTCGAAGCTCTACAAGAGCCTCTGACTGGTAT
CGTGTCTGCTGTGATGGTCGCCTTGGAGCAGTGTCCACCAGAACTTGGCTCTGATATTTAGAAAATGGT
ATGGTTCTGACCGGCGGCGGTGCGTTACTTAAAGATCTCGATCGCCTTCTCACTGAAGAAACAGGCATTC
CAGTCGTTATTGCTGAAGATCCACTGACTTGTGTAGCTCGTGGTGGCGGTAAAGCTCTAGAAATGATCGA