This question paper consists of 2 printed pages, each of which is identified by the Code No.
BIOC 370001

An approved basic translation dictionary is allowed.

BIOC 370001

FACULTY OF BIOLOGICAL SCIENCES UNDERGRADUATE SCHOOL

BIOCHEMISTRY AND MICROBIOLOGY

May 2010

BIOC 3700: Molecular Genetics and Biotechnologies

Time allowed: 3 hours

This examination paper comprises two sections, A (*Molecular Genetics*) and B (*Biotechnologies*).

You should attempt **THREE** questions with at least **ONE** question from **SECTION A** and **ONE** question from **SECTION B.**

Use a **separate answer book** for each question.

SECTION A

A1. Discuss how epigenetic changes in gene control may contribute to human disease.

A2. With reference to the maternal effect, describe the role of the protein Pumilio in the establishment of the anterior-posterior axis in Drosophila embryogenesis.

A3. Discuss how human gene mutations can be detected at the molecular level. Giving appropriate examples, how have these techniques been applied to the study of human disease?

END OF SECTION A

TURN OVER

SECTION B

B1. The developments in structure determination and molecular biology have provided the protein engineer with all of the tools and knowledge that are required to create any new enzyme activity by rational design or redesign of existing enzymes. Discuss this claim.

B2. Answer **ALL** parts of this question.

(a) Describe the difference between an orthologue and a paralogue.

(b) Describe how a multiple sequence alignment is constructed using ClustalW. What are the strengths and weaknesses of ClustalW and why is it important to consider protein domain structure when using this program?

(c) Multiple sequence alignments form the basis of the secondary databases PROSITE, PRINTS and Pfam. Briefly discuss these databases and the advantages and disadvantages of using each one in bioinformatic analyses.

B3. Two identical batches of human epidermal cells were grown in culture. One batch of cells was treated with Epidermal Growth Factor (EGF), which interacts with the membrane-located EGF receptor (EGFR) and activates signalling processes leading to changes in protein expression; the other batch acted as a control. The two batches of cells were solubilised to generate two protein extracts. In order to identify the proteins that were over-expressed in response to EGFR activation, the control and experimental samples were individually labelled with Cy3 and Cy5 fluorescent dyes respectively. Samples were then analysed using Difference In-Gel Electrophoresis (DIGE).

(a) Describe the conventional 2-Dimensional Electrophoresis (2D-E) technique for the separation of complex protein mixtures, and outline how a set of gels would be analysed to enable the selection of proteins displaying an increased expression level.

(b) Outline the DIGE approach, highlighting the main differences from conventional 2D-E and commenting on the advantages and disadvantages of DIGE.

(c) Describe how MALDI-TOF peptide mass fingerprinting and MS/MS peptide sequencing could be used to identify a protein of interest in this experiment.

END