NTNU – Trondheim
Norwegian University of
Science and Technology

Department of Biology

Exam in Bi3013

EXPERIMENTAL CELL AND MOLECULAR BIOLOGY

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Examination date: 19th May, 2014
Examination time (from-to): 09.00 – 13.00 (4 hours)
Permitted examination support material: None

Other information: Language: English
Number of pages: 3 (including front page)
Number of pages enclosed: 0

Checked by:

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Date Signature

NOTICE THAT QUESTIONS 1, 2, 3, AND 4 ARE WEIGHTED EQUALLY, BUT SINGLE QUESTIONS MIGHT BE WEIGHTED DIFFERENTLY (INDICATED IN %). IF NO WEIGHTING IS GIVEN THE SUB-QUESTIONS ARE WEIGTHED EQUALLY.
PLEASE START ANSWERING EACH QUESTION (1, 2, 3, and 4) ON A NEW SHEET OF PAPER.

Question 1

In your lab exercises you learnt how to isolate RNA and quantify gene expression by quantitative RT-PCR (qPCR). Based on the knowledge you gained during these exercises, answer following questions.

- **(a)** Name different methods that you can you use to check integrity of RNA and describe any one of them (30 %)
- **(b)** What are the important points for RNA isolation and handling? (15 %)
- **(c)** Describe the different steps of column based RNA isolation (20 %)
- **(d)** Use a workflow chart to describe the different steps of a qPCR analysis (20 %)
- **(e)** Briefly compare semi-quantitative PCR and Real-time PCR (qPCR) (15 %)

Question 2

Mass spectrometry (MS) is the most common method used for the detection of analytes in proteomic and metabolomics research and has become an indispensable platform in biology, biotechnology and medicine.

- **(a)** How can you identify proteins from a 2D gel by mass spectrometry? (30 %)
- **(b)** What are the advantages of MALDI TOF MS? (20 %)
- **(c)** Describe briefly the second generation proteomics LC-MS/MS technique. (25 %)
- **(d)** Explain why derivatization of analytes in GC-MS metabolomics analyses often is necessary. (25 %)

Question 3

High throughput sequencing (HTS) technologies have an array of applications for both genome and transcriptome studies.

- **(a)** List some important applications of the HTS technology
- **(b)** What are the advantages / disadvantages with the HTS technology compared to DNA microarray technology?
- **(c)** Explain the principle behind sequencing by synthesis which is used by the Illumina platform.

Question 4

Explain or describe 4 of the 5 following terminologies/techniques, use figures wherever necessary (not more than 200 words for each).

(a) Capillary electrophoresis
(b) The shielding/chemical shift concept of Nuclear Magnetic Spectroscopy (NMR)
(c) Allyl isothiocyanate (Allyl ITC).
(d) Schematic diagram of the light path in brightfield microscopy.
(e) Köhlers illumination principle.