BIRLA INSTITUTE OF TECHNOLOGY & SCIENCE, PILANI – DUBAI
DUBAI INTERNATIONAL ACADEMIC CITY
SECOND SEMESTER 2011 – 2012
BIOT C344 PROTEOMICS
COMPREHENSIVE EXAMINAITON (CLOSED BOOK)

Duration: 3h. **Date: 5.6.2012** **Max. Marks: 40**

Note: a) Answer all questions, b) answer to the point and c) draw schematic diagram if required.

1. Describe the peptide mapping for protein identification? Mention the importance of *in silico* protein sequence data and the peptide mass library. Give schematic diagram. [3.0]

2. Explain the following peptide ionization for protein identification with suitable diagrams and mention advantages of each method. (a) MALDI and (b) ESI [4.0]

3. Differentiate between the Time-of-Flight Mass spectrometer and the Quadrupole Time-of-Flight Mass spectrometer. Draw suitable diagrams. [4.0]

4. How many different types of pH gradients normally available for 2D PAGE and mention the applications of pH gradients? Differentiate between conventional IEF and Immobilized pH gradients. [4.0]

5. What are functional proteomics and comparative proteomics and mention how the NMR and X-ray crystallography is used in the analysis? [3.0]

6. How isotope-coded affinity tags (ICAT) are used in quantitative proteomics for protein identification? Explain with a suitable diagram. [4.0]

7. What are the different types of post translational modifications occur in an eukaryotic cell and mention their functions? Explain in detail any one PTM and its role in cellular functions in eukaryotes. [3.0]

8. Write a short note on multidimensional protein identification (MudPIT) technology in proteomics. Explain in detail any one applications of MudPIT for the analysis of protein samples. [3.0]

9. Write a short note on the following: [3.0]
   a. Calmodulin (Cmd1)
   b. Protein partners of calmodulin (Cmd1) (functions and examples)
   c. FRET

10. Write a short note on the following protein complexes composition and functions. [3.0]
    a. Degradosome
    b. RNA Polymerase complexes

11. Describe the development of protein microarrays for protein analysis? List advantages and disadvantages of each application in proteome and genome analysis. [3.0]

12. Briefly discuss on Biomarkers, characteristics and weaknesses of current cancer biomarkers [3.0]

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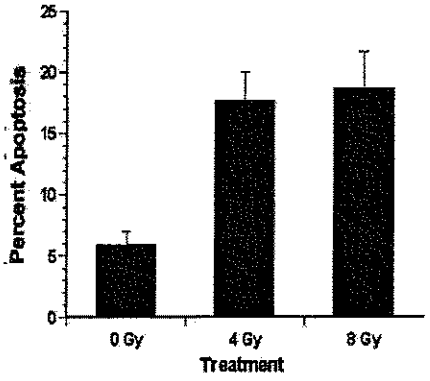
SECOND SEMESTER 2011 – 2012
BIOT C344 PROTEOMICS
TEST-II (OPEN BOOK)

Duration: 50 min. **Date: 16.5.2012** **Max. Marks: 20**

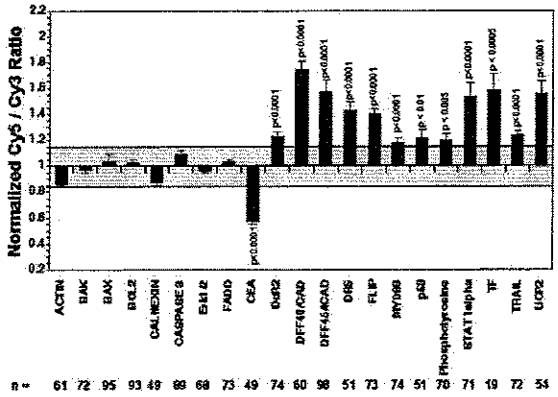
Note: a) Answer all questions, b) answer to the point and c) draw schematic diagram if required.

1. Radiation-induced alterations of protein levels and activity in LoVo cells as monitored using microarrays profiling of cancer cells using protein microarrays and discovery of novel radiation-regulated proteins is shown below. A) LoVo cells treated with 4 or 8 Gy radiation begin to undergo apoptosis within 4 h after irradiation. B) Differential expression of selected proteins in response to radiation treatment in LoVo cells. C) Validation of protein microarray data by fluorescent dye-reversal and immunoblot analysis.
   a. Describe the methods you will be using to analyze the above samples as per your understanding of protein microarray analysis of proteins. [3.0]
   b. Why do you need to validate protein microarray data with immunoblot assays? [2.0]
   c. List the advantages and disadvantages of protein microarrays. [2.0]
   d. Interpret the real-time protein assays of C with respect to radiation treatment in A and the microarray data in B. [3.0]

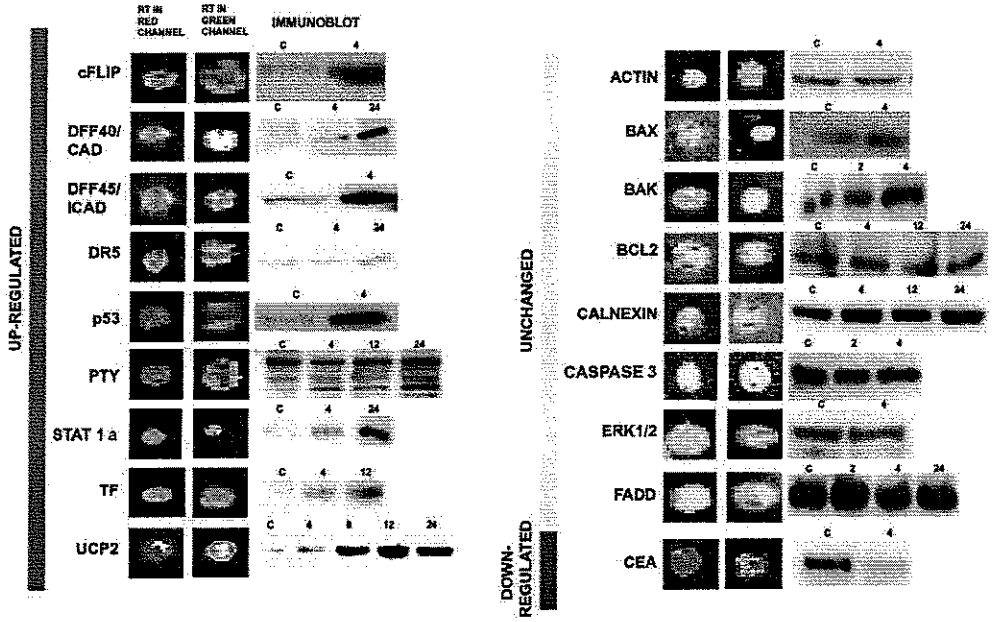
A



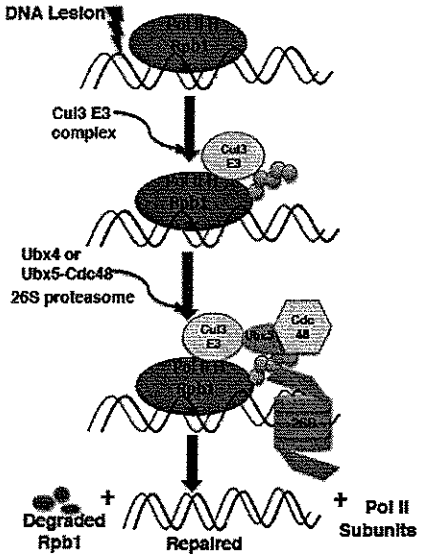
B



C



2. The UV induced DNA damage to the cell and its response to repair in cells is given below. The Rpb1 subunit of RNA Pol II holoenzyme (H) irreversibly stalled at sites of DNA lesions is ubiquitinated by the Cul3–RING ligase complex. UbRpb1 can independently recruit proteasome and Ubx5-Cdc48 complexes. UbRpb1 is extracted from its binding partners in an unfolding reaction dependent on Ubx4 or Ubx5-Cdc48 and is threaded into the 26S proteasome. It is observed that there are numerous proteins accumulated on proteasomes in *cdc48-3* mutants. Based on your understanding, how will you proceed for protein complex identification and answer the following: [6.0]



a. What are the protein complexes you will be identifying based on MS and mention brief outline on the procedure you follow for protein complexes identification?
b. How will you purify the protein complexes for MS analysis and reason out why you need to instead of total cell lysate?
c. What is your understanding on the above pathway and explain mechanisms?

3. The noninvasive therapy with chemotherapeutic strategies has great potential for improving the quality of life of patients. Early determination of therapeutic efficacy would allow for discontinuation of ineffective therapy, improving the chances of selecting an alternate treatment with favorable outcome and sparing the patient from side effects. Therapy induced decreases in choline-containing metabolites measured by localized NMR spectroscopy is being used as a biomarker for therapy response.
   a. What are the methods you will follow to study the response of choline metabolites to docetaxel based cancer therapy to quantify *in vivo* human breast cancer xenografts and *in vitro* by high-resolution NMR spectroscopy of cell extracts. Give an outline of the methods you will follow for NMR studies. [2.0]
   b. Mention the type of radioisotope you may choose to study the cellular response. [2.0]

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BIOT C344 PROTEOMICS TEST-I (CLOSED BOOK)

Duration: 50 min. **Date: 28.3.2012**
Weightage: 25% **Max. Marks: 25**

Note: a) Answer all questions, b) answer to the point and c) draw schematic diagram if required.

1. What are the differences between 1D PAGE and 2D PAGE for protein analysis? Outline in terms of principles involved and applications. [2+2=4.0]

2. Explain with suitable examples on any one method describing incorporation of labeled amino acids for protein identification. How the ICAT is different from the detection of labeled proteins as above? Draw a suitable diagram. [2+3=5.0]

3. What is Ligand Blot overlay assays? Explain with any two examples for the detection of specific groups of proteins through ligand blot overlay technique. [2+2=4.0]

4. What are the two major post translational modifications occur in a eukaryotic cell and mention their significance? Give a brief account on identification of each type of PTM proteins in a cell. [3+3=6.0]

5. Briefly explain the principle of MudPIT with a suitable diagram? Mention functionalities of any two protein complexes in a cell and why MudPIT is a preferred technique over other protein detection methods. [3+3=6.0]

9c

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SECOND SEMESTER 2011 – 2012
BIOT C344 PROTEOMICS
QUIZ-II (CLOSED BOOK)

Duration: 20 min. **Date: 13.5.2012** **Max. Marks: 7**

Name:

ID No:

Note: Answer to the point

1. What are the different parameters which determine the choice of the microscope for localization of fluorescent proteins in cells? Mention any four factors. [1.0]

2. Mention any two reasons why the blue fluorescent protein is not in much use than other GFP variants in protein localization. [1.5]

3. What are GRID and OSPREY and mention differences and their applications? [1.5]

4. Mention any two genes/ protein partners of stress response and protein synthesis with Cmd1 . [1.5]

5. What are the two major principle by which FRET measurement is carried out, mention which is most widely used and mention applications? [1.5]

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BIO C241 MICROBIOLOGY
QUIZ-I (CLOSED BOOK)

Duration: 20 min. **27.2.2012** **Marks: 5.0** **Weigtage: 5.0%**

Name: **ID No:**

1. Why the anaerobes are sensitive to Oxygen and mention how anaerobic environment can be made? [1.0]

2. What are endospores as per the Pasteur's experiment and mention his conclusions? [0.5]

3. What are antibiotics and how it acts on microbial growth? Give examples. [0.5]

4. What is the basic difference between the simple staining and negative staining? [1.0]

5. Briefly write a note on the following and give example media for each: [1.5]
   a. Selective media

   b. Differential media

   c. Enrichment media