Unit 2 - Week 1: Proteomics introduction and sample preparation

Course outline

How to access the portal

Week 1: Proteomics introduction and sample preparation

- Introductory lecture
- Lecture 1: Introduction to proteomics
- Lecture 2: Proteomics and sample preparation
- Lecture 3: Bacterial protein extraction
- Lecture 4: In-gel digestion
- Lecture 5: Fundamentals of mass spectrometry
- Lab Session-1.1: Protein/peptide pre-fractionation using OFFGEL FRACTIONATOR
- Lab session 1.2: Demonstration of Q-TOF MS technology
- Assignment-I Answer key
- Quiz : Assignment-1

Assignment-1

The due date for submitting this assignment has passed. Due on 2016-03-29, 05:15 IST.
As per our records you have not submitted this assignment.

1) Find the best suitable technique and the application it is best suited for *0.5 points*

a) Mass spectrometry	i) Protein sequencing
b) Realtime PCR	ii) DNA sequencing
c) Edman degradation	iii) Gene Expression Analysis
d) ELISA	iv) Protein identification
e) Sanger's method	v) Quantitation of an analyte

- a-i; b-iii; c-ii; d-v; e-iv
- a-iv; b-ii; c-v; d-i; e-iii
- a-iv; b-ii; c-i; d-v; e-iii
- a-iv; b-iii; c-i; d-v; e-ii

No, the answer is incorrect.
Score: 0

Accepted Answers:
a-iv; b-iii; c-i; d-v; e-ii

2) The central dogma of life which states that the information coded by the genome is transcribed and translated is best described by which of the following *0.5 points*

- DNA to RNA to DNA
- RNA to DNA to Protein
- Protein to RNA to DNA
- DNA to RNA to Protein

No, the answer is incorrect.
Score: 0

Accepted Answers:
DNA to RNA to Protein

3) Cell or tissue lysis is an essential technique which enables extraction of several cellular components including protein;which of the following lysis methods is gentle lysis method? *0.5 points*

- Sonication
- Freeze-thaw
- Bead Beater homogenization
- French-press

No, the answer is incorrect.
Score: 0

Accepted Answers:

Week 2: Basics of mass spectrometry

Week 3: Quantitative proteomics

Week-4: Proteomics and systems biology

Freeze-thaw

4) Pair the chemical reagents with its respective role **0.5 points**

a) Urea	i) Reducing agent
b) Iodoacetamide	ii) Cysteine blocking
c) Dithiothreitol	iii) Protein precipitation
d) Acetone	iv) DNA precipitation
e) Ethanol	v) Protein denaturation
f) Isoproponaol	vi) RNA precipitation

- a-iv; b-i; c-ii; d-v; e-iii; f-vi
- a-v; b-ii; c-i; d-iii; e-iv; f-vi
- a-v; b-ii; c-iv; d-i; e-iii; f-vi
- a-iv; b-i; c-iii; d-ii; e-v; f-vi

No, the answer is incorrect.
Score: 0

Accepted Answers:
a-v; b-ii; c-i; d-iii; e-iv; f-vi

5) Protein mixture having five different proteins namely P, Q, R, S and T. If they are separated using SDS-PAGE, find the separation of proteins from high to low mobility **0.5 points**

Protein Name	Mol. wt.
P	25 kDa
Q	17 kDa
R	36 kDa
S	64 kDa
T	45 kDa

- T, Q, S, R, P
- Q, S, R, T, P
- S, T, R, P, Q
- Q, P, R, T, S

No, the answer is incorrect.
Score: 0

Accepted Answers:
Q, P, R, T, S

6) What is the advantage of TRIzol based protein extraction protocol? **0.5 points**

- Add salts to protein essential for ionization
- TRIzol digest the protein used for mass spectrometry analysis
- Protein extraction is free from nucleic acid contamination
- All of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
Protein extraction is free from nucleic acid contamination

7) In the process of in-gel digestion you forgot to add cysteine blocking agent to the protein sample. The data analysis of MALDI-TOF/TOF data has showed poor results. What might be the reason? **0.5 points**

- The protein sample might not be denatured
- The protein sample might not be having disulphide bonds, which resulted in improper protein digestion followed by its identification in MS/MS analysis with low protein score
- The protein sample might be having disulphide bonds, which resulted in improper protein digestion followed by its identification in MS/MS analysis with low protein score
- All of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
The protein sample might be having disulphide bonds, which resulted in improper protein digestion follow by its identification in MS/MS analysis with low protein score

8) In-the process of in-gel digestion, which of the following reagent act as dehydrating agent to remove the CBB stain? ***0.5 points***

- 50 mM Iodoacetamide solution
- Ammonium bicarbonate solution
- 10 mM DTT solution
- Acetonitrile solution

No, the answer is incorrect.
Score: 0

Accepted Answers:
Acetonitrile solution

9) Match the following ***0.5 poi***

a) Electron ionization	i) Solid phase
b) Fast atom bombardment	ii) Liquid phase
c) Electrospray ionization	iii) Gas phase
d) MALDI	iv) Singly charged ion species

- a-iii; b-i; c-ii; d-iv
- a-iv; b-ii; c-i; d-iii
- a-iii; b-ii; c-i; d-iv
- a-iv; b-i; c-ii; d-iii

No, the answer is incorrect.
Score: 0

Accepted Answers:
a-iii; b-i; c-ii; d-iv

10) A protein mixture contains 5 different proteins namely P, Q, R, S and T. They were separated using gel filtration chromatography. Find the order of mobility (High to low) of these proteins in gel filtration chromatography. ***0.5 points***

Protein Name	Mol. wt.
P	13 kDa
Q	17 kDa
R	86 kDa
S	44 kDa
T	10 kDa

- R, S, Q, P, T
- T, P, Q, S, R
- P, T, S, R, Q
- Q, R, S, T, P

No, the answer is incorrect.
Score: 0

Accepted Answers:
R, S, Q, P, T

11) You have been given a solution having glutamic acid, aspartic acid and lysine amino acids. If you want to purify lysine amino acid using strong cation exchange chromatography. What is the pH of the buffer that you will use for the experiment? ***0.5 points***

- pH 3
- pH 7
- pH 8
- pH 10

No, the answer is incorrect.
Score: 0

Accepted Answers:
pH 7

12) If you are purifying the protein on Cation Exchange Chromatography, What will be the salt used in elution buffer? ***0.5 points***

- High concentration of phosphate buffer
- Low concentration phosphate buffer
- A buffer made with KCl
- Very low concentration imidazole solution

No, the answer is incorrect.
Score: 0

Accepted Answers:
A buffer made with KCl

13) Match the following techniques with their respective principles/ advantages ***0.5 points***

a) 2DE	i) Separation based on mol. Wt.
b) SDS-PAGE	ii) Separation based on pI
c) 2D-DIGE	iii) Less gel to gel variations
d) Offgel fractionation	iv) Separation based on pI & mol. wt.
e) Native PAGE	v) Separation based on charge to mass ratio

- a-iv; b-i; c-ii; d-v; e-iii
- a-v; b-ii; c-i; d-iii; e-iv
- a-v; b-ii; c-iv; d-i; e-iii
- a-iv; b-i; c-iii; d-ii; e-v

No, the answer is incorrect.
Score: 0

Accepted Answers:
a-iv; b-i; c-iii; d-ii; e-v

14) Which one of the following method is used for ionization of volatile compounds? ***0.5 points***

- Electrospray ionization
- MALDI
- Electron ionization
- FAB

No, the answer is incorrect.
Score: 0

Accepted Answers:
Electron ionization

15) There are many ionization sources that has been tried and tested for various applications. The ionizations sources are categorized into gas phase, solid phase and solution phases. Which of the falls under the gas phase ionization source? ***0.5 points***

- ESI
- MALDI
- Electron ionization
- All of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
Electron ionization

16) What is the basic principle of OFFGEL fractionator for fractionation of the proteins? ***0.5 points***

- Based on Molecular weight
- Based on isoelectric pH

- Both Molecular weight and isoelectric pH
- Based on charge

No, the answer is incorrect.
Score: 0

Accepted Answers:
Based on isoelectric pH

17) OFFGEL fractionator is used for fractionation of **0.5 points**

- Proteins
- Peptides
- Both
- DNA

No, the answer is incorrect.
Score: 0

Accepted Answers:
Both

18) Which of the following is tandem mass spectrometry **0.5 points**

- Q-TOF
- TOF-TOF
- Q-TRAP
- All of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
All of the above

19) What is advantage of Chip cube integrated with QTOF mass spectrometry? **0.5 points**

- Superior sensitivity
- Integrated RP column
- Low sample injection
- All of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
All of the above

20) What are the major application of chip cube QTOF instrument? **0.5 points**

- Metabolomic analysis
- iTRAQ based quantitation
- Label-free quantization
- All of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
All of the above

Previous Page End