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NPTEL

Courses » **Mass spectrometry based proteomics**

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Unit 4 - Week 3: Quantitative proteomics

Assignment-III

The due date for submitting this assignment has passed. **Due on 2016-04-12, 05:20 IST.**
As per our records you have not submitted this assignment.

1) You want to treat a human cell line with drug Imatinib and analyze its proteomic   **0.5 points**
alterations using SILAC. Which of the following radio-labeled amino acid could be used for SILAC experiment?

○ Leucine

○ Glycine

○ Proline

○ Lysine

No, the answer is incorrect.
Score: 0

Accepted Answers:
Lysine

2) You want to perform an in vitro labeling method for quantitative proteomics experiment.   **0.5 points**
Which of the following method could NOT be preferred for in vitro labeling?

○ Quest

○ CDIT

○ GIST

○ ICAT

No, the answer is incorrect.
Score: 0

Accepted Answers:
CDIT

3) In an iTRAQ experiment, the quantification of peptides could be performed by measuring   **0.5 points**
intensity of reporter ion in MS/MS spectra. Which of the following chemical group is reporter ion in iTRAQ?

○ N, N-dimethyl peperazine

○ N, N-peperazine

○ N, N- methyl peperazine

○ N-methyl peperazine

No, the answer is incorrect.
Score: 0

Accepted Answers:
N, N-dimethyl peperazine

○ Quiz :
  Assignment-III

**Week-4:
Proteomics and
systems biology**

4) After proteolysis using trypsin, peptides are labeled with iTRAQ for quantitative proteomic **0.5 points**
analysis. Which of the following amino acids could be involved in iTRAQ labeling?

○ Only lysine
○ Lysine and N-terminal amino acid
○ Both lysine and Arginine
○ Only Arginine

No, the answer is incorrect.
Score: 0

Accepted Answers:
Lysine and N-terminal amino acid

5) In iTRAQ based quantitative analysis, we always rely on MS/MS spectral data rather than **0.5 points**
MS data. What is the information that we could obtain from MS/MS spectrum during iTRAQ analysis?

○ Provide amino acid sequence information
○ Provide the quantitative information
○ Both A & B
○ Provide the sample injection to ensure ionization

No, the answer is incorrect.
Score: 0

Accepted Answers:
Both A & B

6) You want to grow bacterial sample in a media having N15 heavy labels for quantitative   **0.5 points**
proteome analysis. Though metabolic labeling of the proteins in bacteria is considered to be highly
robust method but still it has some disadvantages. What is the drawback of N15 labeling?

○ Quantification using MS
○ In vivo labeling for quantitation
○ Used for microorganism
○ Unequal incorporation of isotopes in protein

No, the answer is incorrect.
Score: 0

Accepted Answers:
Unequal incorporation of isotopes in protein

7) Match the reporter ion to the respective balancer ion in iTRAQ labeling method   **0.5 points**
a. 113   i. 184
b. 114   ii. 192
c. 115   iii. 31
d.116   iv. 30
e. 121   v. 29

○ a-ii, b-I, c-iv, d-v, e-iii
○ a-ii, b-iii, c-iv, d-v, e-i
○ a-ii, b-iii, c-I, d-v, e-iv
○ a-iii, b-ii, c-iv, d-v, e-i

No, the answer is incorrect.
Score: 0

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

8) Which one of the following statements is not correct with regards to SILAC?   **0.5 points**

○ 100% incorporation of labeled isotope
○ SILAC can be used for comparing up to 5 states in a single experiment
○ Cells behave exactly like control cell population grown in the presence of normal
amino acid

○ SILAC can be used for tissue and body fluid samples

No, the answer is incorrect.
Score: 0

Accepted Answers:
SILAC can be used for tissue and body fluid samples

9) In Tandem Mass spectrometry, the peptides are resolved using two mass analyzers,   ***0.5 points***
separated by collision cell. What is the function of mass analyzer-I, collision cell and mass analyzer-II?

○ Select fragment, fragmentation, select parent
○ Select parent, fragmentation, scans fragment ions
○ Select parent ion, select fragment ion, fragmentation
○ Fragmentation, parent ion selection, fragment ion selection

No, the answer is incorrect.
Score: 0

Accepted Answers:
Select parent, fragmentation, scans fragment ions

10) Different types of mass analyzers are available to resolve the ions based on its respective ***0.5 points***
principle. Which of the following mass analyzer has highest resolution?

○ Triple Quadrupole
○ Fourier Transformer
○ Fourier Transformer Ion Cyclotron Resonance
○ Electron-positron cyclotron collider

No, the answer is incorrect.
Score: 0

Accepted Answers:
Fourier Transformer Ion Cyclotron Resonance

11) Many protein labeling methods are available for the mass spectrometry based protein   ***0.5 points***
quantitation. Which of the following labeling method, which is also first gel-free quantitative labeling
method, depends on cystine residue for labeling of protein?

○ iTRAQ
○ TMT
○ iCAT
○ SILAC

No, the answer is incorrect.
Score: 0

Accepted Answers:
iCAT

12) During the in vitro labeling, tagging of the protein is either by N-terminal, C-terminal or   ***0.5 points***
amino acid based. Which of the following method is an amino acid based labeling method?

○ iTRAQ
○ Esterification
○ MCAT
○ GIST

No, the answer is incorrect.
Score: 0

Accepted Answers:
MCAT

13) Match the following labeling method with its respective statement   ***0.5 points***
a.   VICAT   i. In vivo labeling
b.   TMT   ii. Amino acid based in vitro labeling
c.   Proteolysis O16/O18   iii. N-terminal peptide in vitro labeling

d. CDIT iv. C-terminal peptide in vitro labeling

○ a-iv, b-iii, c-ii, d-i
○ a-i, b-iii, c-iv, d-ii
○ a-iii, b-iv, c-i, d-ii
○ a-ii, b-iii, c-iv, d-i

No, the answer is incorrect.
Score: 0

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

14) Which of the following is the proteomic data management database? *0.5 points*

○ PRIDE
○ Ensembl
○ HapMap
○ None of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
PRIDE

15) You wish to study effects of Doxorubicin on cancer patients post chemotherapy using *0.5 points* Serum samples. Which one of the following labeling methods could be used for quantification of serum proteome?

○ N15 Labeling
○ C13 Labeling
○ iTRAQ Labeling
○ All of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
iTRAQ Labeling

16) You have been given a peptide digest to run on MALDI-TOF. How will you be confident *0.5 points* that the peptide mass fingerprinting data is accurate?

○ By considering threshold score
○ By considering the peptide number
○ Sequence coverage
○ All of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
All of the above

17) Key feature of Selective Reaction Monitoring (SRM) is best described by which of the *0.5 points* following?

○ Full fragment ion spectrum of each precursor in target list is recorded continuously
○ Selectively monitors desired transitions
○ Relative quantitation of samples
○ Selected sample monitoring to obtain transitions

No, the answer is incorrect.
Score: 0

Accepted Answers:
Selectively monitors desired transitions

18) You have run two peptides (X and Y) on LC MS/MS instrument and obtained same MS spectra for both peptides. How will you distinguish these two peptides?   *0.5 points*

- ○ By considering score
- ○ By considering the quantity of the protein
- ○ By acquiring MS/MS data
- ○ All of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
By acquiring MS/MS data

19) You have a complex protein mixture from serum and you want to quantify the protein of interest. Which of the following techniques will fit best?   *0.5 points*

- ○ Shotgun proteomics
- ○ MALDI -TOF/TOF analysis
- ○ Quantitative analysis using TMT
- ○ Multiple reaction monitoring

No, the answer is incorrect.
Score: 0

Accepted Answers:
Multiple reaction monitoring

20) There are many vendor specific software to build and run the MRM assays. Which of the following is an open source software widely used for MRM assays to generate peptide transition list?   *0.5 points*

- ○ Multiquant
- ○ Skyline
- ○ Lab Solutions
- ○ Proteome Discoverer

No, the answer is incorrect.
Score: 0

Accepted Answers:
Skyline

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