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NPTEL

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Courses » Mass spectrometry based proteomics

Announcements **Course** Ask a Question Progress

Unit 5 - Week-4: Proteomics and systems biology



Course outline

How to access the portal

Week 1: Proteomics introduction and sample preparation

Week 2: Basics of mass spectrometry

Week 3: Quantitative proteomics

Week-4: Proteomics and systems biology

- Lec 16: Quantitative proteomics data analysis
- Lec 17: Proteomics and Systems biology I
- Lec 18: Proteomics & Systems biology II
- Lec 19: Proteomics applications
- Lec 20: Advances and challenges in proteomics
- Lab session 4.1: Protein-protein interaction using label-free biosensors

Assignment-IV

The due date for submitting this assignment has passed. **Due on 2016-04-19, 11:30 IST.** As per our records you have not submitted this assignment.

1) Systems biology involves a holistic approach of understanding several facets of biology and is best described the best by which of the following: **0.5 points**

- Computational and mathematical modelling of complex biological systems.
- Chip based storage of bioinformation.
- Systematic documentation of living species on earth.
- Tools for exploring databases

No, the answer is incorrect.
Score: 0

Accepted Answers:

Computational and mathematical modelling of complex biological systems.

2) Which one of the following is a primary database that is used for Peptide Mass Fingerprinting (PMF) analysis of mass spectrometry data? **0.5 points**

- Pubmed
- EXPASY
- SWISSPROT
- DAVID

No, the answer is incorrect.
Score: 0

Accepted Answers:

SWISSPROT

3) You have run a BSA sample on MALDI TOF/TOF; What does 'Protein score' refer in MASSCOT? **0.5 points**

- It is the measure of protein amount ionized.
- It is the highest ion score multiplied by ionization time.
- It is the sum of the best ion scores which is seen for each spectrum.
- All of the above.

No, the answer is incorrect.
Score: 0

Accepted Answers:

It is the sum of the best ion scores which is seen for each spectrum.

4) A protein hit is only significant (reliable) if it has an expect value below **0.5 points**

Assignment-IV
answer Key

Quiz :
Assignment-IV

- 0.01
 0.05
 0.50
 0.25

No, the answer is incorrect.

Score: 0

Accepted Answers:

0.05

5) You want to analyze your data file using MASCOT software what would the format of the data file? **0.5 points**

- .xml
 .mgf
 .rar
 .csv

No, the answer is incorrect.

Score: 0

Accepted Answers:

.mgf

6) The major aim of Human Plasma Proteome Project is best depicted by which of the following **0.5 points**

- To characterize the enzyme involved in physiological processes involved in oxygen transport
 To characterize human serum and plasma by sequencing in high throughput manner using Illumina sequencers
 To characterize the entire alterations in human serum/plasma proteome in different disease conditions.
 All of the above.

No, the answer is incorrect.

Score: 0

Accepted Answers:

To characterize the entire alterations in human serum/plasma proteome in different disease conditions.

7) Which of following statement is NOT true about systems biology? **0.5 points**

- Understanding metabolism and cellular networks is one of the major applications
 It cannot create predictive model of cells, organs, biochemical processes
 It can build models from experimental data
 Research focuses on data mining and data integration

No, the answer is incorrect.

Score: 0

Accepted Answers:

It cannot create predictive model of cells, organs, biochemical processes

8) The glycosylated peptides could be enriched prior to Mass Spectrometric analysis by which of the following method(s)? **0.5 points**

- Affinity based chromatography using Lectin Columns
 IMAC based purification
 Rapid fragmentation prior to MS/MS
 All of the above

No, the answer is incorrect.

Score: 0

Accepted Answers:

Affinity based chromatography using Lectin Columns

9) Which of the following large-scale quantitative proteomic technique enables greater coverage of the proteome and helps to overcome several limitations of mass spectrometry-based **0.5 points**



quantitative proteomics?

- Sanger sequencing
- Super SILAC
- Surface Plasmon Resonance
- All of the above.

No, the answer is incorrect.

Score: 0

Accepted Answers:

Super SILAC

10) Systems biology integrates several aspects of biology, omics and bioinformatics techniques. Which of the following approaches can be used for systems biology investigation? 0.5 points

- Elucidation of Transcription factors
- Network building using bioinformatics tools
- Metabolite profiling and metabolomics
- All of the above

No, the answer is incorrect.

Score: 0

Accepted Answers:

All of the above

11) The advantages of label-free detection techniques include which of the following? 0.5 points

- Enables the monitoring of the sample with minimalistic modification
- Doesn't use kinetic assays and can give molecular structural information
- Uses light sensitivity and energy transfer
- All of the above

No, the answer is incorrect.

Score: 0

Accepted Answers:

Enables the monitoring of the sample with minimalistic modification

12) Human proteome reference map is very important to understand the physiology. The proteomics field has advanced over the years and the proteomic scientists are able to publish the human proteome references map. Recent draft protein reference maps have been published so far using which proteomic technologies? 0.5 points

- Gel-based platforms
- Label-free biosensors
- Mass Spectrometry
- All of the above

No, the answer is incorrect.

Score: 0

Accepted Answers:

Mass Spectrometry

13) MASCOT server is an open source online server used for mass spectrometry data analysis. What type of data analysis can be done using MASCOT server? 0.5 points

- PMF
- MS/MS
- Sequence Query
- All of the above

No, the answer is incorrect.

Score: 0

Accepted Answers:

All of the above



14A MS/MS file is provided for data analysis, which could be downloaded 0.5 points
<http://www.bio.iitb.ac.in/~sanjeeva/itpws/wp-content/uploads/2016/04/File3.txt>). This file was generated using MALDI-TOF/TOF MS system. Please analyze the file using online MASCOT server (http://www.matrixscience.com/search_form_select.html). What is the species of the sample which was analyzed using MALDI-TOF instrument?

- Yeast
- Human
- E. coli
- Bos Taurus

No, the answer is incorrect.

Score: 0

Accepted Answers:

Bos Taurus

15A MS/MS file is provided for data analysis, which could be downloaded 0.5 points
<http://www.bio.iitb.ac.in/~sanjeeva/itpws/wp-content/uploads/2016/04/File3.txt>). This file was generated using MALDI-TOF/TOF MS system. Please analyze the file using online MASCOT server

- Yeast
- Human
- Bacillus pumilus*
- Bos taurus*

No, the answer is incorrect.

Score: 0

Accepted Answers:

Bacillus pumilus

16A MS/MS file is provided for data analysis, which could be downloaded 0.5 points
<http://www.bio.iitb.ac.in/~sanjeeva/itpws/wp-content/uploads/2016/04/File3.txt>). This file was generated using MALDI-TOF/TOF MS system. Please analyze the file using online MASCOT server (http://www.matrixscience.com/search_form_select.html). What is the protein sequence coverage for the significant protein identified using MASCOT analysis?

- 10-15%
- 20-25%
- 30-35%
- 40-45%

No, the answer is incorrect.

Score: 0

Accepted Answers:

10-15%

17What is the approximate mass of a protein containing 200 amino acids? (Assume there 0.5 points
 are no other protein modifications). MALDI-TOF analysis has given the peak at 22,000 Da whereas ESI-Q-TOF have produced peak at 11,000 Da. What is the reason for this?

- MALDI leads to breakage of the protein
- ESI leads to fragmentation of the protein
- MALDI produce single charge whereas ESI produce double charge
- Protein is degraded before injection

No, the answer is incorrect.

Score: 0

Accepted Answers:

MALDI produce single charge whereas ESI produce double charge

18What are the advantages of using label free quantitation techniques like BLI (Bio Layer Interferometry) 0.5 points

- Gives molecular information of the binding
- Doesn't rely on tags or chemical labels that sometimes can occlude in binding



- Gives kinetics details of the binding
- All of the above

No, the answer is incorrect.

Score: 0

Accepted Answers:

All of the above

19A binding event via the Interferometry technique is measured by the following

0.5 points

- Intensity of the precursor ions after binding happens is calculated
- Kinetic assays rapidly give amount of thermal energy spent after interference
- Change in number of molecules bound causes shift in the in the interference pattern
- All of the above

No, the answer is incorrect.

Score: 0

Accepted Answers:

Change in number of molecules bound causes shift in the in the interference pattern

20 Which of the following can be done using BLI technology?

0.5 points

- Protein-protein interaction studies
- Glycan-protein binding
- Antibody subtyping
- All of the above

No, the answer is incorrect.

Score: 0

Accepted Answers:

All of the above

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Funded by

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