

## Questions – Chapter 04

1- Why is MS-based proteomics not inherently quantitative?

- ☐ There are losses of peptides during analysis and differences in the ionization efficiency of peptides
- ☐ The intensity of a peak in a mass spectrum is not a good indicator of the amount of the analyte in the sample, although differences in peak intensity of the same analyte between multiple samples accurately reflect relative differences in its abundance
- ☐ Detection efficiencies for ions with different  $m/z$  values are unequal
- ☐ The relationship between the amount of analyte present and measured signal intensity is complex and incompletely understood

2- What technique(s) can provide comparison of each individual peptide between experiments/samples?

- ☐ Label-free techniques
- ☐ SILAC
- ☐ Isobaric labelling
- ☐ MS gives directly the concentrations of analytes, which can be compared between the samples

3- What does the spectral counting approach compare in different analyzed samples?

- ☐ The number of all spectra associated with a specific protein
- ☐ The sum of all precursor intensities of peptides associated with a specific protein
- ☐ The precursor intensities of the 3 most intense detected peptides
- ☐ The count of observed peptides *versus* all possible peptides

4- What are some advantages of the label-based techniques?

- ☐ As the labeling occurs during sample preparation, quantitative artifacts are minimized
- ☐ The techniques are usually very cheap
- ☐ Multiplexing of samples is possible
- ☐ They can be performed at protein or peptide level

5- What does SILAC stand for?

- ☐ Selective *In-vivo* Labeling After Chemical reaction
- ☐ Nothing in particular
- ☐ Static Isoforms Labels for Affinity Capture
- ☐ Stable Isotope Labeling with Amino Acids in Cell Culture

6- At what MS level does SILAC quantification occur?

- ☐ MS<sup>1</sup>                      ☐ MS<sup>2</sup>                      ☐ MS<sup>3</sup>                      ☐ MS<sup>n</sup>

7- At what MS level does TMT or ITRAQ quantification occur?

- ☐ MS<sup>1</sup>                      ☐ MS<sup>2</sup>                      ☐ MS<sup>3</sup>                      ☐ MS<sup>n</sup>

8- How is it possible to compare the liver proteome of two mice?

- ☐ Using *in-vivo* SILAC      ☐ Using SILAC                      ☐ Using isobaric labeling                      ☐ Using a label-free approach

9- In general, how many generations of animals are needed at least to completely label all organs in a SILAC mouse?

- ☐ 1                      ☐ 2                      ☐ 10                      ☐ 5

10- What amino acids are generally available to perform a SILAC experiment?

- ☐ Lysine and arginine      ☐ Glycine and Leucine      ☐ Lysine and proline      ☐ Leucine and isoleucine

11- What is called a super-SILAC mix?

- ☐ A mixture of samples labelled with TMT      ☐ A mixture a cell lines labelled by SILAC      ☐ A mixture of non-labeled healthy tissues

12- What multiplexing capabilities are available with TMT?

- ☐ 2-plex                      ☐ 4-plex                      ☐ 6-plex                      ☐ 10-plex

13- What amino acid(s) is/are labeled with TMT or iTRAQ?

- ☐ Lysine                      ☐ Arginine                      ☐ N-terminus                      ☐ Cysteine

14- At what level is TMT or iTRAQ labeling generally performed?

- ☐ Amino acid level      ☐ Peptide level                      ☐ Protein level                      ☐ Cell culture level

15- In order to decipher subtle changes in phosphorylation regulation in two cell lines, what quantitative approach(es) would you recommend?

- ☐ SILAC                      ☐ *In-vivo* SILAC                      ☐ Isobaric labeling                      ☐ Spectral counting

16- What mass spectrometer is commonly used for targeted protein quantification with stable isotope dilution?

- ☐ FT-ICR
- ☐ QqQ
- ☐ Ion trap
- ☐ MADLI-TOF

17- How are peptides selected for their use as heavy AQUA standards?

- ☐ They need to be proteotypic
- ☐ They need to contain more than 25 amino acids
- ☐ They need to be heavily modified post-translationally
- ☐ They need to fragment efficiently

18- What does PSAQ stand for?

- ☐ Protein Standard Absolute Quantification
- ☐ Protein for Stable Accurate Quantification
- ☐ Peptide Standard for Absolute Quantification
- ☐ None of these

19- How is abbreviated multiple selected reaction monitoring?

- ☐ SRM
- ☐ MRM
- ☐ mSRM
- ☐ MSM

20- What type of mass spectrometer is used for parallel reaction monitoring?

- ☐ QqQ
- ☐ FT-ICR
- ☐ Orbitrap
- ☐ Ion trap

21- What does PRM required for its development?

- ☐ Selection of transitions
- ☐ Optimization of collision energies
- ☐ Selection of peptides to be used as heavy standards
- ☐ An LC system