Questions – Chapter 02

1- In what workflow(s) are peptides analyzed?

□ Top-down □ Shotgun □ Bottom-up □ Native MS

2- What is the most common enzyme used for protein digestion in MS-based proteomics?

□ Lys-C □ Trypsin □ Chymotrypsin □ Pepsin

3- Explain the principle of peptide mass fingerprinting (PMF)?

4- What is the difference between PMF and MS/MS ion search?

5- For what does DDA stand?

□ Data-derived acquisition □ Data-dependent acquisition □ Data-independent acquisition □ None of these

6- In DDA, typically how many tandem mass spectra are recorded after an MS survey scan?

□ One □ Ten □ One hundred □ It depends

7- In shotgun proteomics, how proteins are finally identify?

□ By comparing experimental tandem mass spectra with theoretical *in silico*-generated tandem mass spectra □ By using DNA sequence databases □ By using mass information only □ By *de novo* annotating every tandem mass spectrum

8- Why top-down is relevant?

□ Every proteomic lab is using top-down workflows □ Proteoforms can be characterized □ Protein sequence coverage is comprehensive □ Entire proteins are easier to separate

9- In what application(s) is top-down particularly employed?

□ Characterization of biosimilars □ Study of post-translational modifications □ Study of sequence variants □ Protein identification

10- For what step(s) of sample preparation are DTT or TCEP used?

□ Protein digestion | □ Cell lysis | □ Disulfide bridge reduction | □ Sample fractionation

11- What reagent(s) can be used for cell lysis?

□ Several detergent | □ Iodoacetamide | □ Sodium dodecyl sulfate | □ Acetone

12- What method(s) is(are) used for protein/peptide enrichment?

□ Antibody-based capture | □ Depletion of abundant proteins | □ Lysis | □ Alkylation

13- Where does trypsin hydrolyze the peptide bonds?

□ The carboxyl terminal side of arginine and glycine amino acid residues | □ The carboxyl terminal side of arginine and lysine amino acid residues | □ The carboxyl terminal side of arginine and tryptophan amino acid residues | □ The carboxyl terminal side of cysteine and methionine amino acid residues

14- Why using different enzymes for protein digestion?

□ Increase protein coverage | □ Generate proteotypic peptides | □ Trypsin is unspecific and additional enzymes are needed | □ Digestion efficiency is not enough

15- You have received a gel piece in a tube. You want to identify the protein(s) present in the sample. What workflow(s) would you recommend?

□ A top-down approach | □ In-gel digestion | □ A enrichment of the protein of interest | □ Use of chymotrypsin for protein digestion

16- You have received human blood plasma to analyze. You want to identify the maximal number of protein present in the sample. What workflow(s) would you recommend?

□ A top-down approach | □ A shotgun proteomic workflow | □ Not using mass spectrometry-based workflow | □ Depletion of abundant proteins

17- You have received a purified protein to analyze. You want to characterize it. What workflow(s) would you recommend?

□ A top-down approach | □ A bottom-up approach | □ Use of different enzymes for protein digestion | □ An initial separation with 1D-gel electrophoresis