Questions – Chapter 05

1- What is UniprotKB?

☐ A DNA database

☐ A search engine

☐ A database of functional information on proteins with accurate, consistent and rich annotation

☐ A TV program about proteins on the Discovery Channel

2- What is a protein FASTA file?

☐ A file containing the DNA sequences coding for specific proteins

☐ A file containing protein sequences

☐ A result of protein identifications

☐ All functional information available in UniprotKB

3- Is all spectral information used for database search?

☐ Yes, directly from the raw spectral files

☐ No, raw spectral files are converted into filtered peak lists

☐ No, the user defines which spectra he wants to keep for database search

☐ None of these

4- What entries are necessary for an MS/MS ion search?

☐ A protein database

☐ A file containing tandem mass spectra as a peak list

☐ A chromatographic elution order file

☐ A mass spectrometry method file

5- What parameters are usually indicated for the search?

☐ The used enzyme

☐ The mass tolerances for MS and MS/MS levels

☐ The fixed and variable amino acid modifications

☐ The type of chromatography used

6- What would be the effect to specify too stringent mass tolerances?

7- Explain the principle of estimating FDR with the target-decoy method?

8- What is the characteristics of the following quantitative measurement?

☐ It is imprecise
☐ It is accurate
☐ It is precise
☐ It is inaccurate

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10- What is often abbreviated as FC?

☐ Quantitative fold change
☐ False change
☐ Free count
☐ Free cells

11- What is commonly used to express FC?

☐ Log_2
☐ Log_{10}
☐ 10^n

12- What does CV stand for?

☐ Coefficient of variation
☐ Coefficient of variability
☐ Change of variance
☐ None of those