

Questions – Chapter 04

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
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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