

BMG744/PHR744 Qualitative and quantitative burrowing of the proteome

1. Why is SELDI or MALDI-TOF mass spec alone insufficient for the identification of biomarkers?
2. Name the four major classes of post-translational modifications of proteins.
3. Give one example of proteolytic processing of a proprotein.
4. Identify four examples of enzymatically-induced, post-translational modifications of proteins.
5. Which are the three sites of phosphorylation on proteins?
6. Give three ways of showing that a peptide contains a phosphate group
7. Why does a parent ion scanning method help in the identification of phosphopeptides?
8. Why is it necessary to methylate peptides containing aspartate and glutamate residues when using metal ion affinity chromatography isolation of phosphopeptides?
9. What is MuDPIT? How can it be used to detect post-translationally modified peptides?
10. Name five isotope labeling methods used in quantitative proteomics.
11. What is the method of quantification that has won the last two ABRF competitions? Why does it work so well?
12. What is the value of multiple reaction ion monitoring in proteomics?