Q: What is m/z:

A) mass/zeta

B) mass/charge

C) ion/charge

D) distance/intensity

Answer: B

Q: What model organism was used to highlight the last decade of proteomics?

A) Schizosaccharomyces pombe

B) Danio rerio

C) Saccharomyces cerevisiae

D) Drosophila melanogaster

Answer: C

Q: Which is not a method for Quantitative Mass Spectrometry?

A) SILAC

B) Spectral Counting

C) MRM

D) Yeast Two Hybrid Assay

Answer: Yeast Two Hybrid Assay

Q: What is a major problem in determining a crystal structure?

A) Phase

B) Recombinant Protein Expression

C) Crystallization Conditions

D) All of the above

Answer: D

Q: Can a modern, fully equipped MS lab collect sequence data from peptides spanning the entire human proteome in a single sample and in a single 60 minute LC-MS experiment?

Answer: NO

Q: Can a phosphopeptide be unambiguously identified and the site of phosphorylation determined by mass spectrometry?

Answer: Yes

Q: Atomic level protein structures at 1.5 Angstroms are determined with:

A) Visible Light

B) X-Rays

C) MRM

D) Gamma Rays

Answer: **B**

Q: Which electron density map is at the highest resolution?

A) 

B) 

C) 

Answer: **B**