Questions for January 13, 2009 class

1. What is MALDI-TOF mass spectrometry? Why is it largely a friend of the biochemist?
2. How can MALDI-TOF-MS help in monitoring modification of antibodies?
3. For MALDI-TOF-MS, what does the fine structure of the spectrum reveal? Over what *m/z* range can the fine structure be observed?
4. What is a *monoisotopic mass* and an *average mass*?
5. What is *peptide mass fingerprinting*? And how is it done on my sample?
6. Why is the choice of protease dependent on the sequence of my protein?
7. What is MASCOT database searching? How do I do this?
8. Practical issues in peptide mass fingerprinting?
9. How do I get the crystal structure of a protein I've discovered on a gel?

There are homework questions embedded in the slides – **the answers are due on Jan 20**

10. What is *electrospray ionization* (ESI)? Is it a friend of a biochemist?
11. What are the differences in mass accuracy between ESI-MS and MALDI-TOF-MS and why?
12. Where do peptides carry their positive charge? How many positive charges are on a peptide or protein?
13. What is *deconvolution* of protein mass spectra?
14. How does the formation of *protein complexes* alter the observed ionization states of proteins? What is needed to exploit this outcome?
15. *Fourier transform-ion cyclotron resonance mass spectrometry* improves the fine structure of a protein mass spectrum – how?
16. What is nanoLC-ESI tandem mass spectrometry and why is it so important in proteomics? What is *MuDPIT*?
17. What is *tandem mass spectrometry* and what "*flavor*s" does it come in?