Questions for BMG/PHR 744 class on January 16, 2009

1. What does peptide fragmentation offer when performing proteomics experiments?
2. What are the four major types of peptide fragmentation methods?
3. What are *a, b, c, x, y* and *z ions*?
4. Are all the theoretical ions observed in a tandem mass spectrum?
5. Why are computational methods essential for peptide sequencing in proteomics experiments?
6. What was the important “adjustment” in computational methods that was necessary for meaningful proteomics?
7. Why is mass accuracy so important to proteomics analysis?
8. What is the b_1-ion fallacy?
9. Which posttranslational modifications can be analyzed by collision-activated dissociation?
10. Why are electron capture dissociation (ECD) and electron transfer dissociation (ETD) valuable in identifying PTMs? What are their strengths and weaknesses?