Questions for January 23rd class

1. What are the principal goals in isolating analytes for mass spectrometry analysis?
2. Why are drugs (most of them) extractable into organic solvent? How can we make them soluble?
3. How can buffers and freezing be a problem in proteomics/protein chemistry?
4. Why can homogenization of tissue lead to problems?
5. Does SDS-PAGE analysis improve contamination issues?
6. What's to be done to get samples ready for 2D-electrophoresis?
7. How can similar samples be readied for mass spectrometry?
8. What are the approaches that can be used to simplify a proteome?
9. Outline the pros and cons of using recombinant expression of a protein.