

Questions for the January 25th BMG/PHR 744 class

1. How many separation methods are needed to purify a protein?
2. Is ammonium sulfate fractionation compatible with mass spectrometry?
3. How does a protein's amino acid composition determine the conditions for ion exchange chromatography?
4. What are the differences between ion exchange chromatography and chromatofocusing?
5. Is hydroxyapatite chromatography a good method for all proteins?
6. Why is gel filtration less compatible with mass spectrometry?
7. What is the value of purification tables when purifying proteins?
8. How can we analyze intact proteins and protein complexes by ESI-MS?