Questions for class on Feb 22, 2008 – Mass spec and enzymology

1. Do enzymes have the same molecular weight throughout the catalytic cycle?
2. Are substrates covalently or non-covalently bound to an enzyme? How would ensure that you could detect a non-covalently bound substrate?
3. How would you discover the site on an enzyme of a covalently bound suicide inhibitor?
4. Which species would be absent if you electrosprayed under neutral conditions the reaction mixture of an enzyme that had a Ping-Pong reaction?
5. Why are pharmaceutical companies so interested in converting enzyme kinetics experiments to ones based on mass spectrometry?
6. If an enzyme transiently binds a substrate into a binding, what are the expected changes in H/D exchange at (a) the global level, and (b) the peptide level after pepsin hydrolysis (in the cold)?
7. Can mass spectrometry observe the start of enzyme reactions in the millisecond time scale? If so, how is this done and what type of mass spectrometer is required?