

**Colorado State University
Fall Session 2015**

**CHEM 431
Instrumental Analysis Laboratory**

**Notes for
Identification of Proteins from Molecular Mass
Using Electrospray Ionization Mass Spectrometry**

The following is a set of short notes to outline the experiment in question and to provide helpful guidance to those executing the experiment.

- A.** Mass spectrometry is an analytical technique used to identify and, in some cases, quantify different chemical species. Until the advent of electrospray ionization (ESI-MS) in the early 1980s, the analyte(s) being measured using mass spectrometry had to be ionized in the gas phase. The development of this ionization technique was paramount in establishing the large-scale study of proteins in a field called Proteomics.
- B.** You will assign an identity to an unknown protein using ESI-MS through analysis of the resulting mass spectra. Identify proteins through calculations associated with the multiple charging phenomenon.
- C.** Compare the resolution and mass accuracy of the Time of Flight instrument to the Linear Trap Quadrupole instrument from the spectrum of a singly charged compound.
- D.** Given some structural information and a potential amino acid inventory determine the primary structure of an unknown peptide through the use of tandem mass spectrometry.