

## CHARACTERIZATION OF PHOSHOPEPTIDES BY ELECTRON TRANSFER DISSOCIATION ION TRAP MASS SPECTROMETRY

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Phosphorylation of proteins is an important post translational modification that plays important roles in many cellular functions, such as cell signalling, metabolism – protein activation/deactivation, transcription, cell differentiation and apoptosis. Analysis of peptide phosphorylation is complicated due to the low stoichiometry of phosphorylation. In addition classical CID MSMS cleaves the phosphate group from the peptide backbone and the resulting spectra have limited structural data on the phosphate location and it is often difficult to differentiate these spectra from non phosphorylated peptides particularly in ion trap mass spectrometers

Electron transfer dissociation (ETD) uses a radical anion to transfer an electron to a typical even electron protonated molecule produced by electrospray ionization. This gas phase reaction when applied to peptides results in an odd electron charged peptides. The fragmentation process of odd versus even electron species are quite different. Even electron species typically fragment through thermal processes producing B and Y type fragment ions in addition to numerous side chain cleavages. In contrast odd electron fragments are thought to fragment via an electronic excitation that produces primarily C and Z cleavages i.e. fragments of the peptide amide backbone. This process is less dependant on the amino acid components of the backbone and typically produces even degradation across the entire backbone chain with little side chain fragmentation. This can be used for improved sequence coverage and also the determination of post translation modifications such as phosphorylation

In this study we present results of peptide and phosphopeptides analysis by ETD MSMS on a Agilent 6130 Ion trap mass spectrometer equipped with ETD capabilities. Comparison is made between results from ETD, CID and combined ETD/CID.