

Using Electronic Transfer Dissociation to Identify Multiple Post-Translational Modifications on a Single Histone H3 Molecule

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Background and Objectives: In eukaryotes DNA is wrapped around histones to form nucleosomes and is condensed into chromatin. At the core of each nucleosome is a complex of four histones H2A, H2B, H3 and H4. Post-translational modifications (PTMs) on these histones can help control the regulation of gene expression.

Methods: We show how four of our mass spectrometers: a MALDI-prO-TOF, a vMALDI-LTQ, an ETD-enabled ESI-LTQ-XL and an ESI-LTQ-Orbitrap are being used for PTM analysis.

Results: Using the ETD mass spectrometer we were able to identify multiple fragment ions from the N-terminal GluC peptide of a recombinant form of H3. These fragment ions indicate both K18 acetylation and K36 trimethylation/acetylation on the same H3 molecule.

Discussion and Conclusions: The ability of ETD to fragment randomly along the peptide backbone allows more complete coverage of peptides as well as aiding in keeping PTMs intact. This has allowed us to conclude that a mutant strain contains altered K36 methylation/acetylation as well as acetylation of K18 which is not found in the wild-type. These changes in modifications may have gene expression implications.

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