

## [Individual Abstract Info](#)

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### **Structural and Post Translational Modification Analysis by MALDI Orthogonal-TOF MS**

[Chris Lynch](#)<sup>1</sup>; Scott Kuzdzal<sup>1</sup>; Lisa Sapp<sup>1</sup>; Tillmann Ziegert<sup>1</sup>; Alexandre Lobada<sup>2</sup>; Suzanne Ackloo<sup>2</sup>;

<sup>1</sup>PerkinElmer, Shelton, CT; <sup>2</sup>MDS SCIEX, Concord, ON, Canada;

#### **Introduction:**

Matrix-Assisted Laser Desorption/Ionization (MALDI) has become an important tool for proteomics researchers. A commercial MALDI Orthogonal-TOF mass spectrometer with collisional cooling has demonstrated the ability to analyze intact ions of very fragile molecules, including gangliosides. We herein demonstrate the ability to obtain information on post-translational modifications as well as the primary sequence by reducing the cooling flow or increasing the voltage difference between the quadrupole and the cone. Structural information may be obtained easily, without the need for traditional CID experiments.

#### **Methods:**

The commercially available MALDI Orthogonal-TOF mass spectrometer has precise control over ionization conditions; the pressure of the gas (N<sub>2</sub>) used for 'collisional cooling gas', the potential difference between the QO region and the cone, and the potential difference between the cone and target plate (declustering potential). 'Cool' ionization conditions generate spectra that are relatively free of fragment ions. These spectra are very simple to interpret but lack (valuable) structural information. Reducing the gas pressure in the target area and increasing the declustering potential provides structural information. Alternatively and preferably, structural information is also obtained by increasing the voltage difference between the quadrupole and the cone. Such 'hot' ionization conditions accommodate CID-type analyses.

#### **Abstract:**

A mixture of Glu-Fib and the oxidized B-chain of insulin was subjected to these CID conditions and the fragments (y and b series ions) are annotated. Sequence analysis is also presented for other peptides, including substance P and FLAG. . Myoglobin was digested with trypsin (20 min), subjected to an LC separation, and the eluant was deposited on a plate for MALDI analysis. The VEADIAGHGQEVLR ion was subjected to CID conditions. The analysis of phosphopeptides under CID conditions is also demonstrated.

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