**Overview**

**Purpose:** To overcome low mass limits on ion traps, a new activation method has been developed, called pulsed-Q dissociation, PQD.

**Methods:** Peptides from a protein digest were analyzed using NanoLC-MS/MS on a Thermo Electron LTQ mass spectrometer using Data Dependent MS/MS on the 114, 115, 116 and 117 iTRAQ reporter ions. The intensity ions are constant with the peptide sequence. The four iTRAQ reporter ions have the same charge, with a relative standard deviation of 4.7% for the new intensities, which is comparable. If not better than previously reported data.

**Results:** The average deviation of the iTRAQ reporter ions was within 10% of the theoretical value of 1:1:1:1. The ratios range from a low of 0.55 to a high of 1.22. However, the average ratio for each tag ranged from 0.93 to 0.95. This demonstrates the value of averaging the ratios of all peptides from a given protein to determine an overall level for a given protein.

**Conclusions**

The new PQD fragmentation technique generates low mass ions below 150 m/z which are detectable and quantifiable:

- iTRAQ reporter ions are detectable with PQD
- y1 and b2 ions are detectable with PQD
- iTRAQ reporter ions are detectable with PQD
- iTRAQ reporter ions are quantifiable with PQD

**References**


2. iTRAQ reporter ions are detectable with PQD

3. Acalay is a registered trademark of Aqent Technologies, Inc. SEQUEST is a registered trademark of Thermo Electron Corporation. All other trademarks are the property of Thermo Electron Corporation and its subsidiaries.