Finnigan LTQ FT

Ultra High Performance Mass Spectrometer
Finnigan LTQ FT – Ultra High Performance

- Ion Trap based Fourier Transform ICR Mass Spectrometer
- FTICR (FTMS) at LC timescale
- Accurate Mass
- High Sensitivity
- Ultra-high Resolution
- Above All - Simple to Operate
Finnigan LTQ FT – Ultra High Performance

- Surveyor HPLC
- API, MALDI Sources
- 2-D Linear Ion Trap
- ICR Cell
- Actively Shielded Superconducting Magnet

- For details – have a look at the dummy
Finnigan LTQ FT – Ultra High Performance

• First Routine FTMS Mass Spectrometer
  – Fast
  – Automated
  – Data dependent scanning
  – Robust technology

• Most Advanced Mass Spectrometer Available
  – Proteomics
  – Metabolomics
  – Pharmaceutical and Drug Discovery
  – Small Molecule Analysis, Structural Elucidation
Finnigan LTQ FT – Combination of Performance

- All Useful Ion Trap Features
  - API with APCI, ESI and MALDI Ion Sources
  - MS, MS/MS and MS^n Analysis
  - AGC Control
  - Data Dependent Scanning
  - Secondary Electron Multiplier Detector

- Combined w. FT Features
  - High Mass Accuracy
  - High Resolution
  - High Dynamic Range
  - ICR Cell Detector

Linear Ion Trap Data

FTMS Data

Actively Shielded 7 Tesla Magnet

60 m^3/hr  200L/sec  220L/sec  210L/sec  210L/sec
Finnigan LTQ FT – Experiment Description

- Generate Ions
  - API: ESI, APCI, APPI, MALDI Source
- Store and Prepare Ions in 2-D Linear Trap
  - MS, MS\(^n\)
  - AGC to regulate number of ions
- Transfer Ions to ICR Cell
  - RF ion guides
- Excite Ions in ICR Cell
  - RF frequency sweep or SWIFT excitation
- Detect Ion Transient Signal
- Fourier Transform Data Processing
  - Data dependent information passed to 2-D Linear Trap
Finnigan LTQ FT – Performance Specifications

- **Resolution**
  - 100,000 resolution at m/z 400 at 1 Hz repetition rate
  - >500,000 resolution broadband mode

- **Mass Range**
  - m/z 50-4000 (standard range)
  - 1-order-magnitude in single scan (e.g. m/z 200-2000)

- **Mass Accuracy**
  - 2 ppm RMS, external mass calibration
  - <1 ppm RMS, internal mass calibration

- **Dynamic Range**
  - 5,000 within mass spectrum
  - >500,000 between mass spectra
Finnigan LTQ FT – Accurate Mass

- The magnetic field is very stable, therefore mass calibration is valid for several days

- Accurate Mass with External Calibration
  - Must control the number of ions in ICR cell - Ion cyclotron frequency varies with ion density
  - Number of ions controlled with AGC on the 2-D Linear Trap
  - Mass accuracy of 2 ppm RMS for MS and MS/MS mode

- Accurate Mass with Internal Calibration
  - A reference substance of known mass is analyzed with the unknown substance and used as a mass calibrant
  - Mass accuracy of better than 1 ppm RMS
Finnigan LTQ FT – High Resolution

- Resolution Varies with Mass
  - Resolution is inversely proportional to mass

- Resolution Depends on Detection Time
  - Double the detection time to double the resolution
  - Detect time of 745 ms for 100,000 resolution at m/z 400

- Resolution Depends on Magnet Field Strength
  - Double the magnet field to double the resolution
  - Magnet price increases immensely with field strength!
Calibration Mixture
m/z 195 to 1922

1024 k Word transient
Acquisition rate 1 Hz

MRFA – $^{13}$C and $^{34}$S Isotopes resolved

Res. Power at m/z 526:
90,000 (FWHM)

This is equivalent to

Res. Power at m/z 400:
118,000 (FWHM)
Finnigan LTQ FT – Ultra High Resolution

NRVYVHPFHL (3+) 427.89988 (Angiotensine from Goosefish)

Resolution m/Δm 547,000
Finnigan LTQ FT – MS/MS Analysis

MS/MS Angiotensin I DRVYIHPFHL m/z 432.9 (3+), single Scan
Finnigan LTQ FT – Productive Software

- Known and Accepted Software Platform
  - *LCQ TUNE PLUS enhanced for FTICR analysis*
  - *Data dependent scanning*
  - *Xcalibur enhanced for accurate mass*
  - *Bioworks*
  - *DeNovoX*
  - *Metabolite ID*
  - *Mass Frontier*
Xcalibur™ Software

Xcalibur 1.4

- Extended functions for high resolution and accurate mass

TunePlus

- Simple to use
- Intuitive GUI
Finnigan LTQ FT – Productive Software

Known Platform
- LCQ TUNE PLUS, enhanced for FTICR analysis
- Method Editor, with data dependent scanning
- Xcalibur
- Bioworks, DeNovoX, Metabolite ID, Mass Frontier
- Accurate Mass Data Evaluation Software

If you can run a Finnigan LCQ you can run an LTQ FT
LTQ FT – Tune Plus Window

Define Scan Button

ICR Cell Button

Cryo Button
Method Setup for Data Dependant Scanning

Method Editor

Additions made to standard method editor
MS/MS of MRFA – Scan Setup and Tune Plus

Additions made to standard 'Define Scan' editor

Define Scan Button
Finnigan LTQ FT – Comparison

- Unlike Other FTICR Instruments…
  - *no trapping gas is pulsed into the ultra-high vacuum region to trap ions in the ICR cell*
    - don’t need to wait several seconds to pump away gas before detecting ICR signal
  - *no collision gas is pulsed into the ICR cell for MS/MS*
    - MS/MS performed in 2-D Linear Trap
    - again, don’t need to wait to pump away gas prior to detection
  - *minimized transmission discrimination*
    - short path length between 2-D Linear Trap and ICR cell and octopole ion optics, reduces mass discrimination
  - *ultra High Speed Signal Processing*
    - Fourier Transformation performed in real time
Finnigan LTQ FT – What About?

- High Resolution Parent Ion Isolation?
  - possible in ICR cell with SWIFT isolation

- Collision Activated Dissociation in the ICR Cell?
  - need pulsed gas inlet. Not planned
  - MS/MS performed in 2-D Linear Trap

- IRMPD?
  - possible, and in progress

- ECD?
  - possible, and in progress
High Resolution and Accurate Mass

Peptides: [Val5]-Angiotensin II
Sequence: DRVYVHPF
Formula: C_{49}H_{69}N_{13}O_{12}
Exact mass: [M+2H]^{2+} = 516.76671

Lys-des-Arg^{8}-Bradykinin
Sequence: KRPPGFSPF
Formula: C_{50}H_{73}N_{13}O_{11}
Exact mass: [M+2H]^{2+} = 516.78490

Δm (mmu): 18.2
Δm (ppm): 35 ppm
Required Resolution: 56,700 (FWHM)

RP = 15,000

RP = 56,700
Entering the exact mass of a peptide into a program to calculate the elemental composition will yield different numbers of proposals. These numbers only depend on the maximum allowed mass errors and limits for the elements in use. The below listed limits of elements is for an average peptide composed of common amino acids. The mass error differs with instrument type and is not directly related to the resolution if a single compound is analyzed.

Example Peptide: [Val$^5$]-Angiotensin II, [M+2H]$^{2+} = 516.77671$
Limitation for Elements: C 35-70, H 45-100, N 8-16, O 9-16, S 0-2

<table>
<thead>
<tr>
<th>Instrument</th>
<th>QqTOF</th>
<th>LTQ-FT</th>
<th>LTQ-FT</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mass Error</td>
<td>10 ppm</td>
<td>5 ppm</td>
<td>2 ppm</td>
</tr>
<tr>
<td># of Proposals for m/z 516.76671</td>
<td>49</td>
<td>23</td>
<td>10</td>
</tr>
</tbody>
</table>
Finnigan LTQ FT – Angiotensin I

Sample Concentration: 40 fmol/µl
Nano-spray Flow Rate: ~ 30 nl/min
Sample Consumption: ~ 20 amol/s
Single Scan
Injection Time: ~ 1 ms

Sample Concentration: 40 fmol/µl
Nano-spray Flow Rate: ~ 30 nl/min
Sample Consumption: ~ 20 amol/s
Single Scan
Injection Time: ~ 1 ms
Finnigan LTQ FT – MS/MS Angiotensin I

Angiotensin I
MS/MS 433 (3+)
Single Scan
Injection Time: 65 ms
Scan Cycle Time: < 1 s

B9 (2+)
Theoretical Mass: 583.2987 (error 0.09 ppm)
Finnigan LTQ FT – MS/MS Angiotensin I

+ p ESI Full ms2 433.00@28.00 [195.00-2000.00]

Angiotensin I
MS/MS 433 (3+)
Injection Time: 65 ms
Scan Cycle Time: < 1 s

<table>
<thead>
<tr>
<th>B8 (1+)</th>
<th>1028.53123</th>
<th>(0.61 ppm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>B6 (1+)</td>
<td>784.41005</td>
<td>(0.57)</td>
</tr>
<tr>
<td>B5 (1+)</td>
<td>647.35114</td>
<td>(0.06)</td>
</tr>
<tr>
<td>B9 (2+)</td>
<td>583.29871</td>
<td>(-0.15)</td>
</tr>
<tr>
<td>B7 (2+)</td>
<td>441.23504</td>
<td>(-0.36)</td>
</tr>
<tr>
<td>B6 (2+)</td>
<td>392.70866</td>
<td>(-0.35)</td>
</tr>
<tr>
<td>Y4 (1+)</td>
<td>513.28199</td>
<td>(-0.02)</td>
</tr>
<tr>
<td>Y3 (1+)</td>
<td>416.22923</td>
<td>(-0.17)</td>
</tr>
<tr>
<td>Y2 (1+)</td>
<td>269.16082</td>
<td>(-0.67)</td>
</tr>
<tr>
<td>Y9 (3+)</td>
<td>394.55746</td>
<td>(-0.35)</td>
</tr>
</tbody>
</table>
Finnigan LTQ FT – MS³ Angiotensin I

+ p ESI Full ms3 433.00@32.00 583.00@14.00 [195.00-2000.00]

Angiotensin I
MS³
433(3+) → 583(2+) → O
Scan Cycle Time: 1.16 s
Using the two MS detectors (Linear ion trap and FTMS) for post-translational modification assignment
Using the two MS detectors to pinpoint the PTM – phosphopeptides

Using the accurate mass and high resolution on FTMS full MS mode (0.8 ppm mass accuracy and 2+ charge confirmed HPO3 addition to the peptide (note: it will be 3.8ppm if it’s SO3 addition)
Using the two MS detectors to pinpoint the PTM – phosphopeptides

The neutral loss of the previous ion (1031 m/z) is the major peak (982 m/z) on MS/MS spectrum as shown. Using the accurate mass and high resolution on the FTMS in MS/MS mode (confirmed that’s a doubly charge ion with the loss of H3PO4 – it’s not the loss of Pro or Val or the loss of sialic acid in 3+ charges)
Using the two MS detectors to pinpoint the PTM – disulfide-linked peptides

Using the accurate mass and high resolution on FTMS full MS mode (0.1 ppm mass accuracy and 3+ charge) confirmed the two cysteine-containing peptides are linked.
Using the two MS detectors (Linear ion trap and FTMS) for intact protein assignment
Human Growth Hormon (intact): FTMS Spectrum

Zoom-in

[M+16H]\(^{16+}\)
M.W. ca. 22125
Resolution ca. 70000

16+ charge resolved

[Image showing a zoomed-in FTMS spectrum with m/z values and relative abundance percentages]

- [M+16H]\(^{16+}\)
- M.W. ca. 22125
- Resolution ca. 70000
- 16+ charge resolved

Thermo Electron Corporation
Finnigan LTQ FT

Recent Results
AP-MALDI on the Finnigan LTQ FT

MALDI

Full scan MS
20 Laser shots
Masstech AP-MALDI
RP= 100,000
AP-MALDI MS/MS with the Finnigan LTQ FT

MALDI_030524182253  # 418-438  RT: 10.68-12.08  NL: 1.72E2
FTMS +p ESI w Full ms2 1386.80@45.00 [200.00-2000.00]

MALDI

Full scan MS/MS
40 Laser shots
Masstech AP-MALDI
RP= 100,000

Peptide sequence : FPPHHLTVILGR

<table>
<thead>
<tr>
<th>Peptid-ID</th>
<th>B [M+1H]1+</th>
<th>Y [M+1H]1+1</th>
</tr>
</thead>
<tbody>
<tr>
<td>F</td>
<td>148.07569</td>
<td>1386.80046</td>
</tr>
<tr>
<td>P</td>
<td>245.12845</td>
<td>1239.73205</td>
</tr>
<tr>
<td>P</td>
<td>342.18121</td>
<td>1142.67928</td>
</tr>
<tr>
<td>H</td>
<td>479.24013</td>
<td>1045.62652</td>
</tr>
<tr>
<td>H</td>
<td>616.29904</td>
<td>908.56761</td>
</tr>
<tr>
<td>L</td>
<td>729.38310</td>
<td>771.50870</td>
</tr>
<tr>
<td>T</td>
<td>830.43078</td>
<td>658.42463</td>
</tr>
<tr>
<td>V</td>
<td>929.49919</td>
<td>557.37695</td>
</tr>
<tr>
<td>I</td>
<td>1042.58326</td>
<td>458.30854</td>
</tr>
<tr>
<td>L</td>
<td>1155.66732</td>
<td>345.22448</td>
</tr>
<tr>
<td>G</td>
<td>1212.68879</td>
<td>232.14041</td>
</tr>
<tr>
<td>R</td>
<td>1386.80046</td>
<td>175.11895</td>
</tr>
</tbody>
</table>

MALDI	558x48
AP-MALDI MS/MS with the Finnigan LTQ FT

FTMS +p ESI w Full ms2 1386.80@45.00 [200.00-2000.00]
LC-MS Accurate Mass with the LTQ FT

RT: 22.00 - 34.55

C₁₈ H₁₉ O₇
0.99 ppm

C₂₀ H₁₇ O₆
0.03 ppm

C₂₀ H₁₅ O₈
0.05 ppm

C₁₈ H₁₁ O₇
339.05102
0.13 ppm

C₁₈ H₉ O₇
337.03537
0.14 ppm

C₂₀ H₁₉ O₇
371.11362
0.30 ppm

Negative ESI
Accurate Mass for Small Molecules

On-line HPLC measurements of 4 different compounds were performed on the LTQ FT at a resolution power of 200,000. AGC was used to control the number of ions.

<table>
<thead>
<tr>
<th>Compound</th>
<th>Scan Range</th>
<th>Accurate Mass:</th>
<th>Average:</th>
<th>Minimum:</th>
<th>Maximum:</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cinchonidine</td>
<td>55 to 155</td>
<td>295.18049</td>
<td>295.1802</td>
<td>295.1801</td>
<td>295.1804</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>-0.91 ppm</td>
<td>-1.24 ppm</td>
<td>-0.21 ppm</td>
</tr>
<tr>
<td>Lidoflazine</td>
<td>521 to 551</td>
<td>492.28210</td>
<td>492.2816</td>
<td>492.2813</td>
<td>492.2820</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>-1.02 ppm</td>
<td>-1.74 ppm</td>
<td>-0.31 ppm</td>
</tr>
<tr>
<td>Procainamide</td>
<td>55 to 155</td>
<td>236.17574</td>
<td>236.1756</td>
<td>236.1755</td>
<td>236.1757</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>-0.51 ppm</td>
<td>-1.1 ppm</td>
<td>0.0 ppm</td>
</tr>
<tr>
<td>Trimipramine</td>
<td>480 to 630</td>
<td>295.21688</td>
<td>295.2166</td>
<td>295.2165</td>
<td>295.2168</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>-0.97 ppm</td>
<td>-1.34 ppm</td>
<td>-0.31 ppm</td>
</tr>
</tbody>
</table>

\[\text{[M+H]}^+ = C_{19}H_{23}N_{2}O \quad 295.18049 \]

\[\text{[M+H]}^+ = C_{30}H_{36}F_{2}N_{3}O \quad 492.28210 \]

\[\text{[M+H]}^+ = C_{13}H_{22}N_{3}O \quad 236.17574 \]

\[\text{[M+H]}^+ = C_{20}H_{27}N_{2} \quad 295.21688 \]
Accurate Mass for Small Molecules

Resolution = 200,000

2 ppm window

TIC

NL: 4.93E6
m/z = 265.17900-265.18108

NL: 1.60E7
m/z = 265.21629-265.21747

NL: 2.34E6
m/z = 236.17527-236.17621

NL: 6.61E6
m/z = 492.28112-492.28308

C_{13}H_{22}N_3O
236.17574
-0.55 ppm

C_{19}H_{23}N_2O
295.18049
-0.71 ppm

C_{20}H_{27}N_2
295.21688
-1.22 ppm

C_{30}H_{36}F_2N_3O
492.28210
-0.85 ppm

C_{13}H_{22}N_3O
236.172
236.178

C_{19}H_{23}N_2O
295.18021

C_{20}H_{27}N_2
295.21652

C_{30}H_{36}F_2N_3O
492.28168

Procainamide

Cinchonidine

Trimipramine

Lidoflazine
The Advion NanoMate 100 on the Finnigan LTQ FT
Mass accuracy for repetitive measurements of the MH\(^+\) Peak of Bupropion on the LTQ FT with the NanoMate 100 attached. 13 injection were carried out giving the 2400 data points. Same results are obtained for 3 other small molecules, Threohydrobupropion, Hydroxybupropion (HB), D\(_6\)-BUP and D\(_6\)-HB. The red line indicates the theoretical mass. The average error is -0.20ppm.
Accurate Mass with the LTQ FT

The combination of the Advion Nanomate system with the LTQ FT mass spectrometer was used to make 13 repetitive measurements of Bupropion. Statistics for the molecular ion and its most abundant isotope peaks are shown in the graph. For each injection the Nanomate performed a nanospray at ca. 200 nL/min. The complete set of data was acquired in less than 1 hour.

Bupropion

\[ [M+H] = 240.11497 \]

\( \text{C}_{13} \text{H}_{18} \text{N O Cl} \)

Ca. 200 spectra per injection
Accurate Mass Statistics for Bupropion M+H

![Accurate Mass Statistics Graph](image)

- **M/z** values: 240.114700 to 240.115150
- **# of Injection**: 1 to 13
Accurate Mass Statistics for Bupropion M+H+1

<table>
<thead>
<tr>
<th># of injection</th>
<th>m/z</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>241.118000</td>
</tr>
<tr>
<td></td>
<td>241.118100</td>
</tr>
<tr>
<td></td>
<td>241.118200</td>
</tr>
<tr>
<td></td>
<td>241.118300</td>
</tr>
<tr>
<td></td>
<td>241.118400</td>
</tr>
<tr>
<td></td>
<td>241.118500</td>
</tr>
<tr>
<td></td>
<td>241.118600</td>
</tr>
<tr>
<td></td>
<td>241.118700</td>
</tr>
</tbody>
</table>

Thermo
Analyze • Detect • Measure • Control™
Accurate Mass Statistics for Bupropion M+H+2

Bupropion M+H+2 (37Cl)

<table>
<thead>
<tr>
<th># of injection</th>
<th>m/z</th>
<th>aver value</th>
<th>min value</th>
<th>max value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>10</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>11</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>13</td>
<td>242.111700</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
The acquired spectra were analyzed for the accurate masses of the four isotope peaks on the protonated molecule. The mass chromatogram for the MH⁺ ion of Threohydrobupropion is shown as well as one exemplary spectrum. Again, the first four isotope peaks on the MH⁺ ion were evaluated. As expected, the mass accuracy for all different concentrations are equally good and there is no trend visible with regard to mass accuracy. The errors are randomly distributed across the measurements, all results are better than 0.5 ppm.
Ubiquitin at Very High Resolution

Settings: 1e-6 M, infusion @ 1 ul/min, 5 transients averaged, 4.5 ms inject time / transient

Blow up
Ubiquitin at Very High Resolution – A Comparison

Settings: 1e-6 M, infusion @ 1 ul/min, 5 transients averaged

`IonSpec Experiment`: Resolution 200,000 @ m/z 779
Sample consumption 30 fmol
S/N 115 : 1
Inject time 360 ms

Finnigan LTQ-FT:
Resolution 200,000 @ m/z 779
Sample consumption 408 amol
S/N 270 : 1
Inject time 24.5 ms

Blow up
On-line Nano HPLC-MS at Ultra High Resolution

Sample: very complex crude cell extract (non digested) from human blood platelets
Amount: unknown, but very low conc.
Flow: 200 nl / min

Resolution: 400,000 @ m/z 400
Workshop
Finnigan LTQ FT

Thermo Electron’s Annual Customer Forum
Sunday, June 9, 2003
Montreal, Canada
Agenda

• Welcome and Introduction
  Helmut Muenster, Thermo Electron Corp., Bremen, Germany

• Finnigan LTQ FT – A Technical description of the new Hybrid FTMS
  Stevan Horning, Thermo Electron Corp., Bremen, Germany

• High Resolution FTMS for Quantitative Proteomics Measurements
  Thomas P. Conrads, National Cancer Institute (NCI) Frederick, NC

• First Results with the new LTQ FT
  Michael Linscheid, Humbold University, Berlin, Germany
Jens Griep-Raming
Bremen, Germany
+49-421-5493-219

Poster MPI 182
Fully Automated High-Throughput Accurate Mass Determination using FT-ICR Mass Spectrometry

Jens.Griep-Raming@Thermo.com
Poster TPX 449
An Integrated LC-MS Platform for Rapid and Precise Identification of Proteins and their Post-Translational Modifications using a Linear Ion Trap coupled with a FT-ICR Mass Spectrometer

Wolfgang.Metelmann-Strupat@Thermo.com
Demo Chemist – Billy Wu

Shiaw–Lin (Billy) Wu
San Jose, USA
+1-408-965-6308

Poster TPE 091
Fourier Transform Ion Cyclotron Resonance (FT-ICR) Mass Spectrometry – A Rapid Method for Metabolite Identification

Billy.Wu@Thermo.com
Additional LTQ FT Posters at ASMS

Poster MPI 189

Timo Hagemeister, Humbold Univ. Berlin, Germany
Fragmentation Pathways of Cisplatin Adducts to Dinucleotides Determined by FT-ICR-MS

Poster MPX 457

Michael Linscheid, Humbold Univ. Berlin, Germany
Structure Elucidation of Structural Proteins from Yersina Phages using MALDI-ToF and ESI-FTMS Data
Finnigan LTQ FT

Installation Requirements
Superconducting Magnet – Requirements

• Transportation
  – Cold shipping possible

• Positioning in Laboratory
  – Active shielding so no influence on lab equipment
  – Must not be positioned near elevator, large electric motor or massive steel structural supports

• Maintenance
  – Autofill for LN2

• Safety
  – Venting
  – Oxygen depletion sensors
Finnigan LTQ FT

Conclusion
Highlights

- High resolution @ 1 Hz repetition rate
- Automation
- High mass accuracy
- On-line LC-MS
- MS, MS/MS and MS\(^n\)
- Low maintenance
- Small footprint
- And overall – **simple to use**
Bremen Development Team

... plus R&D Team in San Jose !!!