

NEW! vMALDI Ion Source for the Finnigan LTQ

High Throughput Protein ID MALDI-MS/MS

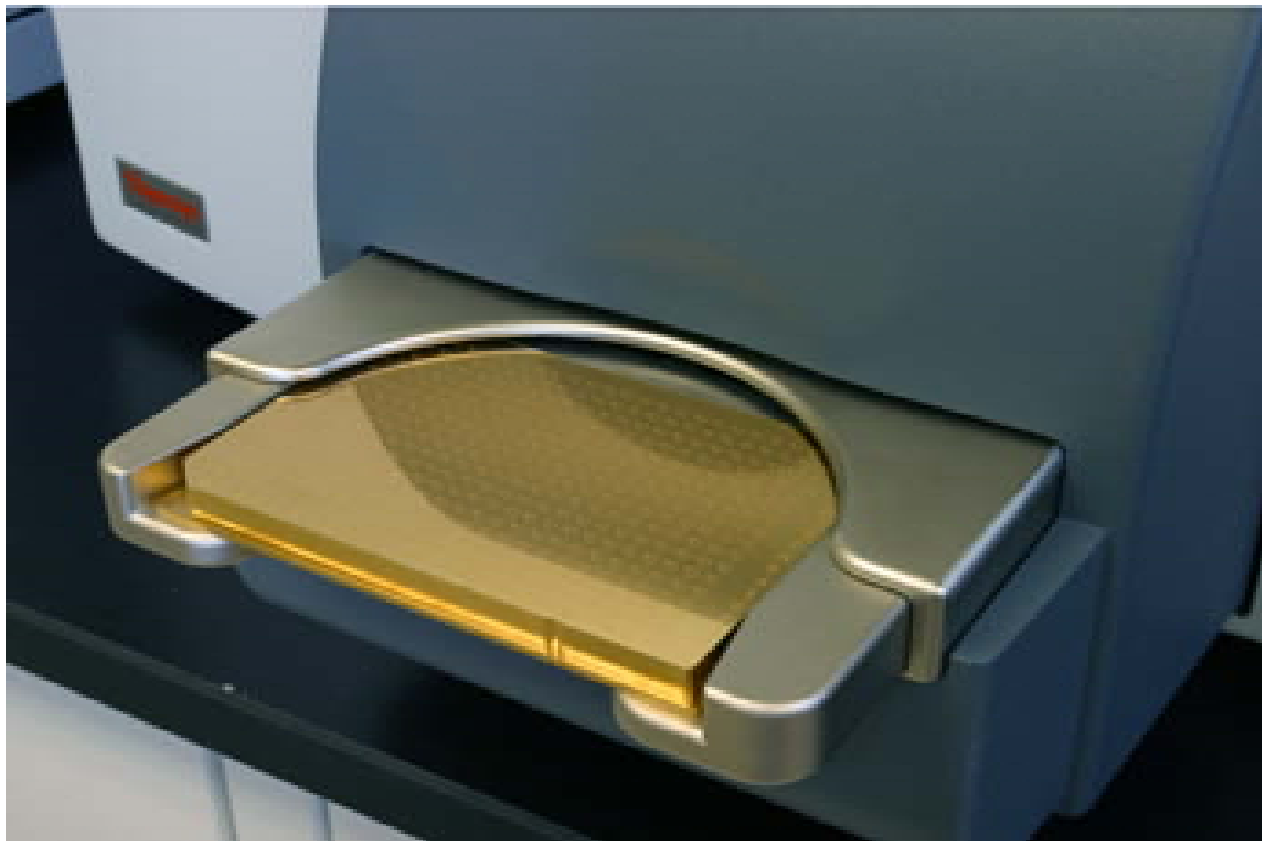


Laser/Electronics Box

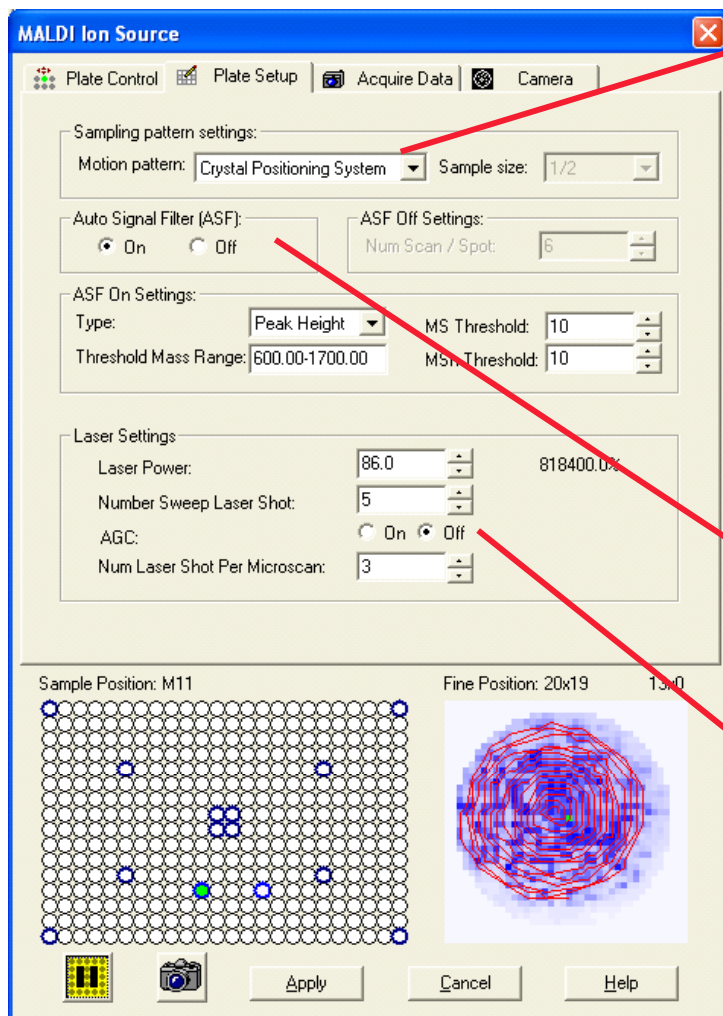
LTQ w/ vMALDI Ion Source

- Sample Plates
 - 96- and 384-position plates
 - “Bruker style”
- Laser
 - Nitrogen, 337nm, 20Hz
- Software
 - MALDI Calibrate, Tune & Operation
 - Plate View
 - Spot View
 - Acquisition
 - CPS
 - AGC
 - ASF
 - BioWorks
 - PMF – ProFound
 - MS/MS – PlateID
- Switchable with ESI* (*requires service call)

vMALDI Ion Source – Plate Loading



vMALDI Ion Source Software: Set Up

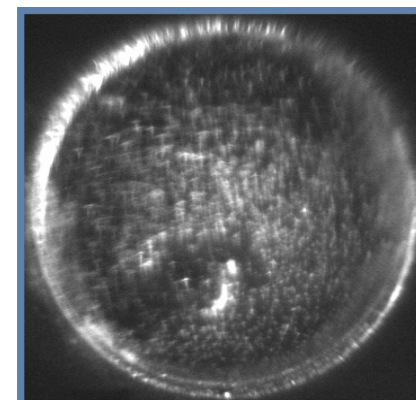


- **CPS: Crystal Positioning System**
– *Determine spot sampling pattern*

GPS



CPS

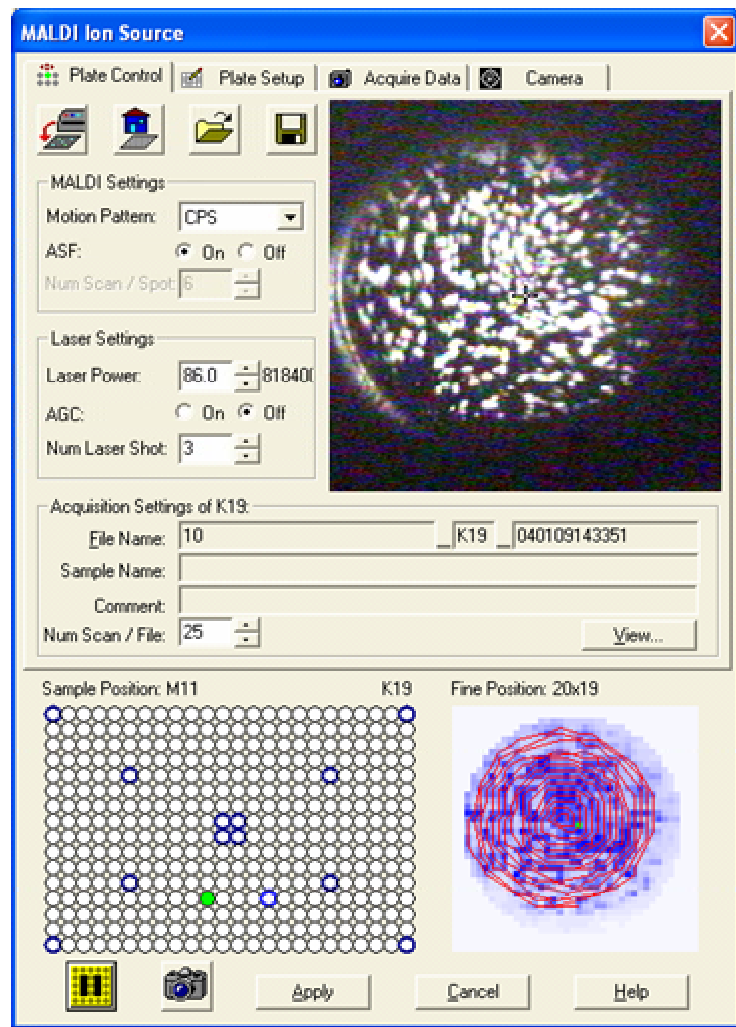


- **ASF: Automatic Spectral Filter**
– *Make sure there is signal*

- **AGC: Automatic Gain Control**
– *Optimize linear trap filling*

- Sensitivity
- Spectral Quality

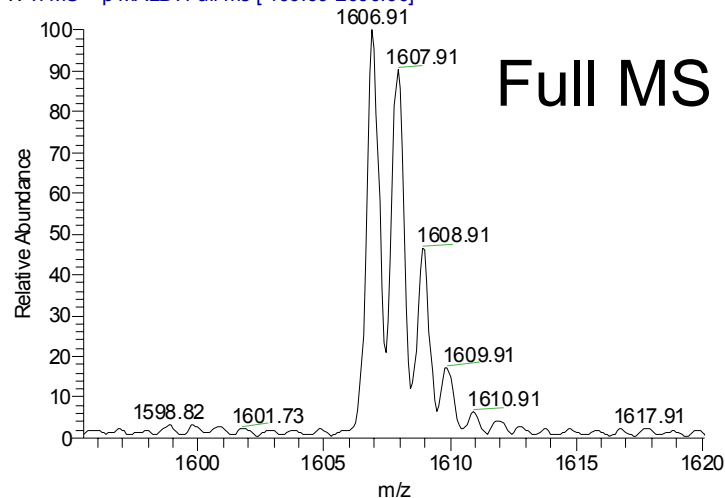
vMALDI Ion Source Software: Operation



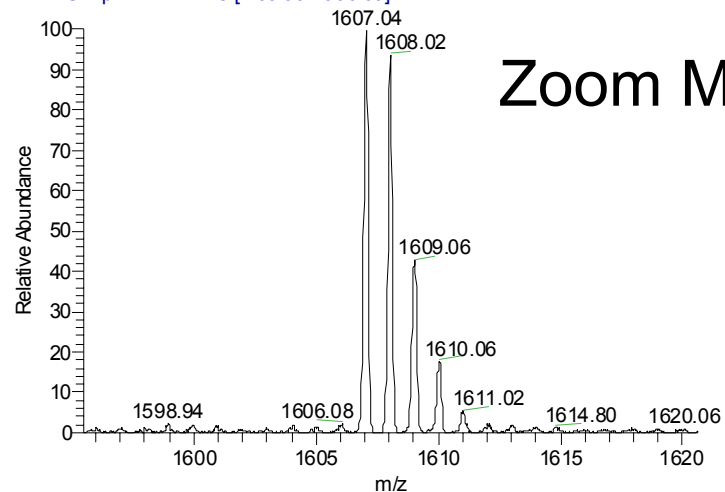
- Easy to Use
- “One Window” access to common operational Parameters / Control
 - Home/Load/Fire Laser
 - Sample Plate Position
 - Camera
 - Sampling Pattern
 - Laser Power
 - Acquisition Set Up

vMALDI Ion Source: Performance

Myo 5 fmol_test_C5_040114081341 #2-10 RT: 0.05-0.09 AV: 9 NL: 8.68E1
T: ITMS + p MALDI Full ms [400.00-2000.00]



Myo 5 fmol_test_C5_040114080742 #1-10 RT: 0.06-0.32 AV: 10 NL: 5.57E1
T: ITMS + p MALDI Z ms [400.00-2000.00]

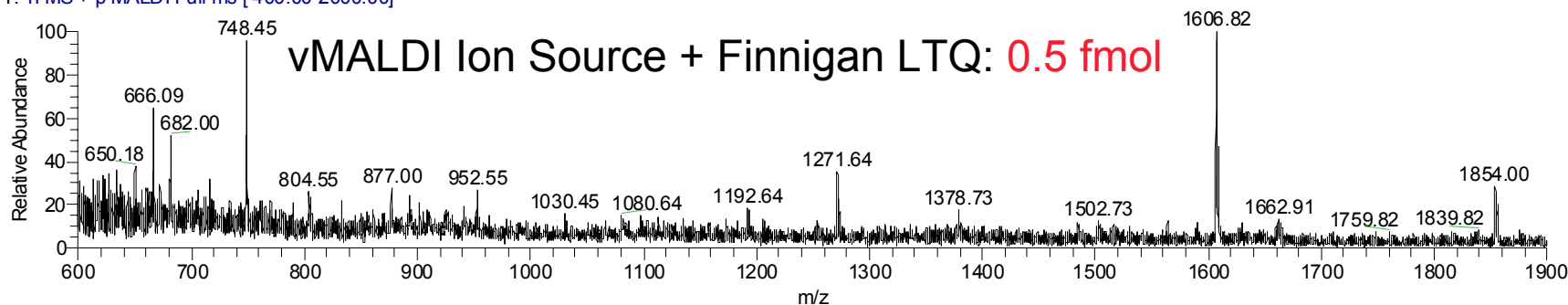


- **Mass Accuracy and Resolution**
~30ppm **10,000?**

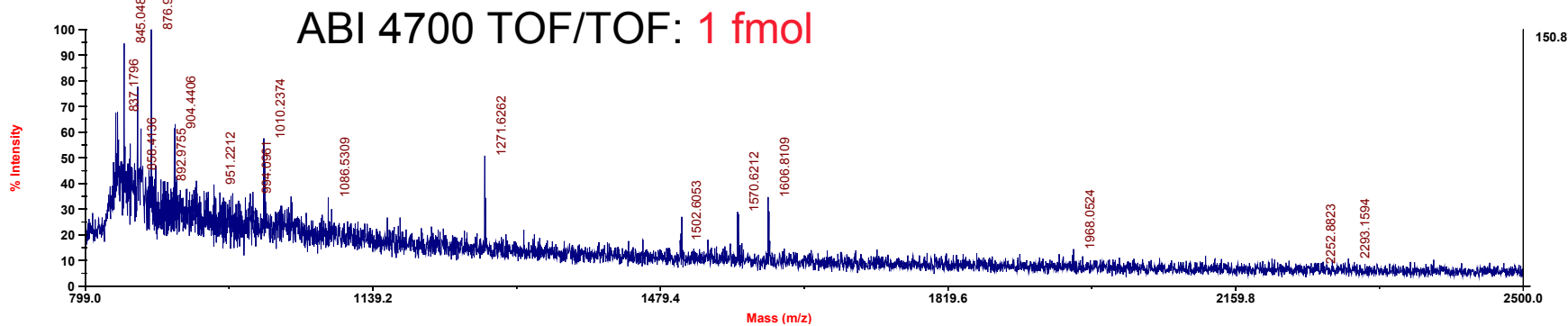
vMALDI Ion Source: Sub-fmol Protein Digests

Myoglobin Digest

Myo_0_5 fmol ms_C6_040113095519 #1-10 RT: 0.04-0.10 AV: 10 NL: 1.06E4
T: ITMS + p MALDI Full ms [400.00-2000.00]

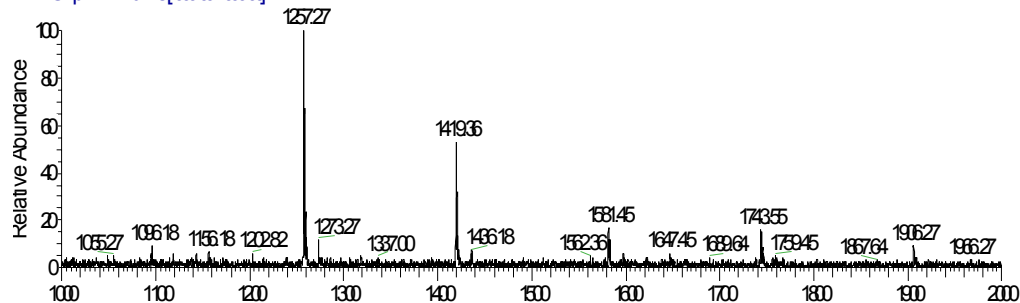


4700 Reflector Spec #1 MC[BP = 877.0, 151]

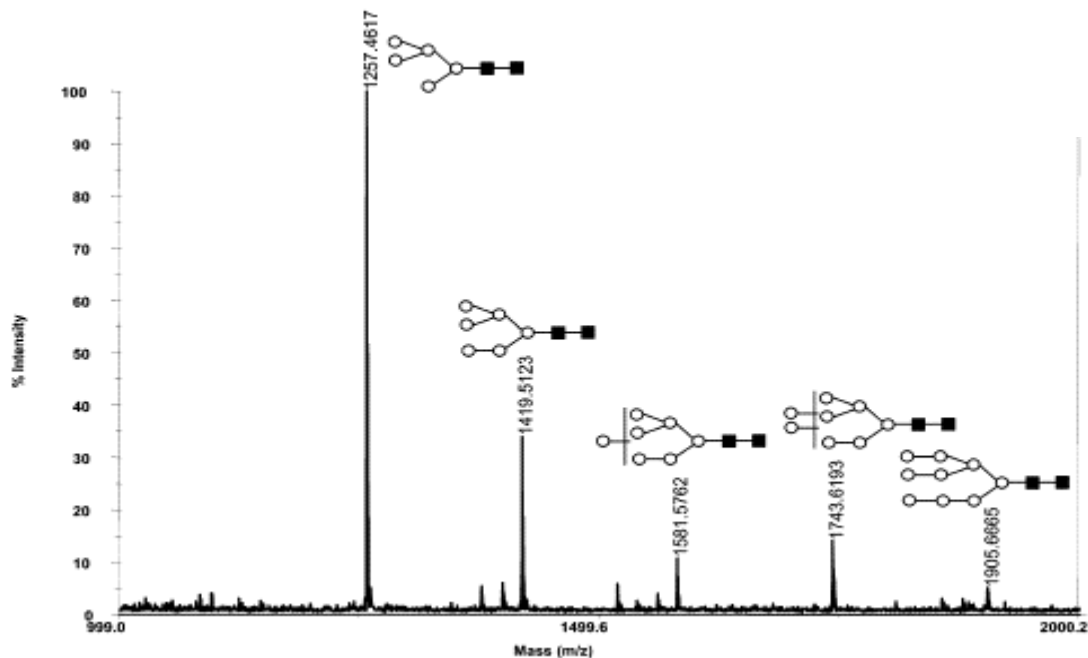


vMALDI Ion Source: Carbohydrate Analysis

N-glycan100.probes.AC#19 RF:011026 A/9 NL:939
T:IMS+pMALDI Full ms[600.00-2000.00]



Anal. Chem. 2003, 75 4895-4903

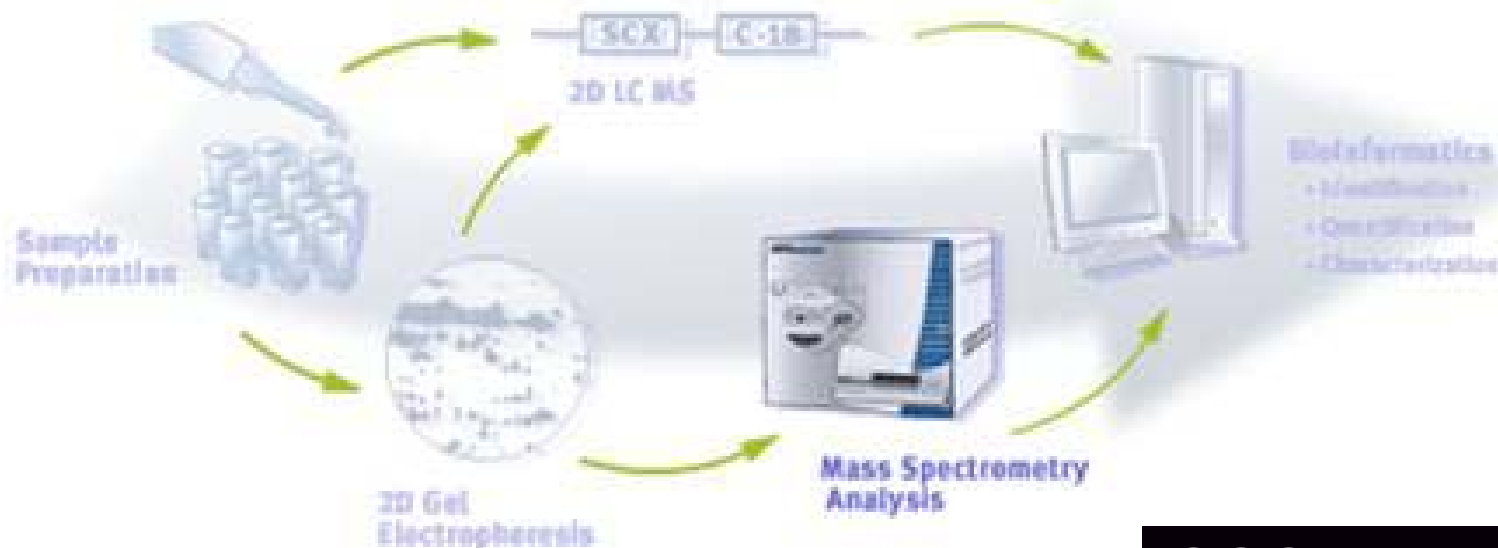


N-Glycan from Ribonuclease B

vMALDI Ion Source + Finnigan LTQ vs. ABI 4700

FEATURE	ABI 4700 TOF/TOF	MALDI LTQ
Ion gate	± 5 Da	± 0.5 Da
Sensitivity	MSMS on 5 fmol digest	MSMS on 0.5 fmol digest; single peptide 250 attomole
Stages of MS	MS ₂	MS _n
Calibration	External calib needs be spatially close to sample or use internal calib	Stable calibration since desorption decoupled from analysis
High mass	7100 m/z, pmoles concentration (reflectron)	2000 m/z
Mass accuracy	5 ppm-internal; 10 ppm external	30 ppm (avg mass range, digest 700-1900 m/z); min 4 ppm, max 132 ppm
Plate format	Fits only ABI plate	Universal plate format: 96, 384
Speed data acquisition	10 sec (20 laser shots X 100 averaged spectra)	1.5 sec (3 laser shots X 10 averaged spectra)
Camera	Poor quality	Good quality

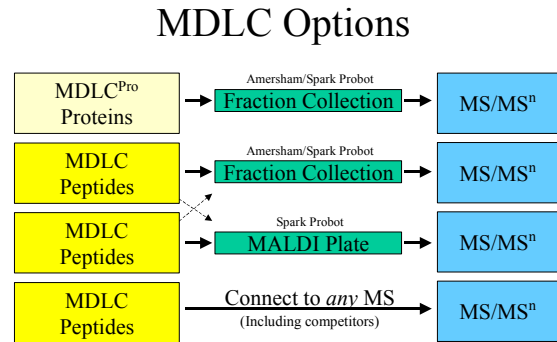
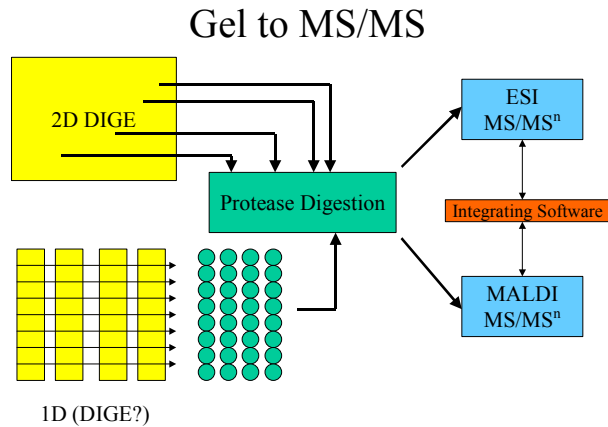
Workflow - Proteomics



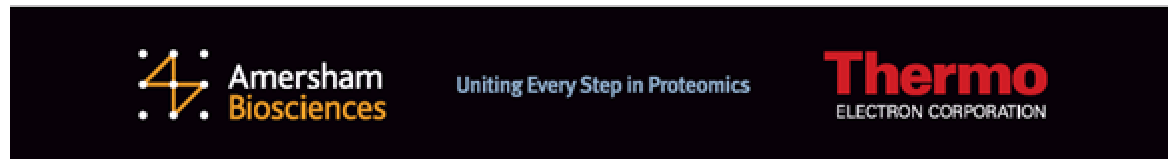
1. Sample Prep
2. Gels / Chromatography
3. Mass Spectrometry
MALDI-TOF
LC/MS
4. Data Analysis



Amersham Proteomics Alliance



- Joint Marketing Activities



- Focus on Solutions

- Gel to MS
- LC/MS
 - Intermediate fraction collection
 - High-yield PTM solutions
- Biological Sample Prep (e.g. plasma analysis)

