

International Journal of Mass Spectrometry 259 (2007) 205-207



www.elsevier.com/locate/ijms

Subject index Volume 259

Acetylation

Assigning *in vivo* carbamylation and acetylation in human lens proteins using tandem mass spectrometry and database searching, 161

Ambient ionization

Development of capabilities for imaging mass spectrometry under ambient conditions with desorption electrospray ionization (DESI), 8

Aminoacyl-tRNA synthetases

Laying the groundwork for proteomics. Mass spectrometry from 1958 to 1988, $\boldsymbol{1}$

Antigen processing

The contributions of mass spectrometry to understanding of immune recognition by T lymphocytes, 32

Atmospheric pressure ionization

GC/MS on an LC/MS instrument using atmospheric pressure photoionization, 57

Bacillus anthracis

Specific identification of Bacillus anthracis strains, 140

Bioinformatics

Comparative bioinformatics analyses and profiling of lysosome-related organelle proteomes, 147

Biomarker

Identification of peptidase substrates in human plasma by FTMS based differential mass spectrometry, 174

Brain

Characterization of neurohistone variants and post-translational modifications by electron capture dissociation mass spectrometry, 184

Carbohydrate sequencing

Glycoproteomics: Past, present and future, 16

Chromatir

Deciphering the histone code using mass spectrometry, 46

Deglycosylation

Rapid removal of N-linked oligosaccharides using microwave assisted enzyme catalyzed deglycosylation, 117

Differential mass spectrometry

Identification of peptidase substrates in human plasma by FTMS based differential mass spectrometry, 174

Donald Hunt

"Hunt"-ing for post-translational modifications that underlie the histone code, 40

Electron capture dissociation (ECD)

Deciphering the histone code using mass spectrometry, 46

Characterization of neurohistone variants and post-translational modifications by electron capture dissociation mass spectrometry, 184

Electron transfer dissociation

Deciphering the histone code using mass spectrometry, 46

Electrospray ionization

Monolithic column plastic microfluidic device for peptide analysis using electrospray from a channel opening on the edge of the device, 65

Laser flash photochemical oxidation to locate heme binding and conformational changes in myoglobin, 124

Electrospray ionization mass spectrometry

Microfluidic electrocapture interfaced with electrospray mass spectrometry, 73

ETD

Analysis of intact proteins on a chromatographic time scale by electron transfer dissociation tandem mass spectrometry, 197

FAIMS

Peak deconvolution in high-field asymmetric waveform ion mobility spectrometry (FAIMS) to characterize macromolecular conformations, 87

Fast photochemical oxidation of proteins (FPOP)

Laser flash photochemical oxidation to locate heme binding and conformational changes in myoglobin, 124

FTMS

Identification of peptidase substrates in human plasma by FTMS based differential mass spectrometry, 174

Gas chromatograhy

GC/MS on an LC/MS instrument using atmospheric pressure photoionization, 57

Glycoproteomics

Glycoproteomics: Past, present and future, 16

G-tes

Differential quantitative proteomics of *Porphyromonas gingivalis* by linear ion trap mass spectrometry: Non-label methods comparison, *q*-values and LOWESS curve fitting, 105

H/D exchange

Improving digestion efficiency under H/D exchange conditions with activated pepsinogen coupled columns, 130

Histone

Characterization of neurohistone variants and post-translational modifications by electron capture dissociation mass spectrometry, 184

Histone code

"Hunt"-ing for post-translational modifications that underlie the histone code. 40

Histone post-translational modification

Deciphering the histone code using mass spectrometry, 46

History of mass spectrometry

Development of capabilities for imaging mass spectrometry under ambient conditions with desorption electrospray ionization (DESI), 8

Holomyoglobin

Laser flash photochemical oxidation to locate heme binding and conformational changes in myoglobin, 124

Human pituitary

Linear ion-trap mass spectrometric characterization of human pituitary nitrotyrosine-containing proteins, 96

Human plasma

Identification of peptidase substrates in human plasma by FTMS based differential mass spectrometry, 174

Hydroxyl radical footprinting

Laser flash photochemical oxidation to locate heme binding and conformational changes in myoglobin, 124

206 Subject index

Identification

Specific identification of Bacillus anthracis strains, 140

In vivo carbamylation

Assigning *in vivo* carbamylation and acetylation in human lens proteins using tandem mass spectrometry and database searching, 161

Interface

Microfluidic electrocapture interfaced with electrospray mass spectrometry, 73 Ion mobility

A novel surface-induced dissociation instrument for ion mobility-time-of-flight mass spectrometry, 79

LC-MS/MS

Assigning *in vivo* carbamylation and acetylation in human lens proteins using tandem mass spectrometry and database searching, 161

Liquid chromatography

GC/MS on an LC/MS instrument using atmospheric pressure photoionization, 57

Lysosome-related organelle (LRO)

Comparative bioinformatics analyses and profiling of lysosome-related organelle proteomes, 147

Lysozyme

Peak deconvolution in high-field asymmetric waveform ion mobility spectrometry (FAIMS) to characterize macromolecular conformations, 87

MALDI

Development of capabilities for imaging mass spectrometry under ambient conditions with desorption electrospray ionization (DESI), 8

Mass spectrometry

Laying the groundwork for proteomics. Mass spectrometry from 1958 to

Glycoproteomics: Past, present and future, 16

"Hunt"-ing for post-translational modifications that underlie the histone code, 40

GC/MS on an LC/MS instrument using atmospheric pressure photoionization, 57

Monolithic column plastic microfluidic device for peptide analysis using electrospray from a channel opening on the edge of the device, 65

Improving digestion efficiency under H/D exchange conditions with activated pepsinogen coupled columns, 130

Characterization of neurohistone variants and post-translational modifications by electron capture dissociation mass spectrometry, 184

Matrix assisted laser desorption/ionization

A novel surface-induced dissociation instrument for ion mobility-time-of-flight mass spectrometry, 79

MHC molecules

The contributions of mass spectrometry to understanding of immune recognition by T lymphocytes, 32

Microfluidic electrocapture

Microfluidic electrocapture interfaced with electrospray mass spectrometry, 73 Microwave

Rapid removal of N-linked oligosaccharides using microwave assisted enzyme catalyzed deglycosylation, 117

Monolithic column

Monolithic column plastic microfluidic device for peptide analysis using electrospray from a channel opening on the edge of the device, 65

MudPIT

Specific identification of Bacillus anthracis strains, 140

Nitroproteomics

Linear ion-trap mass spectrometric characterization of human pituitary nitrotyrosine-containing proteins, 96

Oligosaccharide

Rapid removal of N-linked oligosaccharides using microwave assisted enzyme catalyzed deglycosylation, 117

Organelle proteome

Comparative bioinformatics analyses and profiling of lysosome-related organelle proteomes, 147

PEG

Peak deconvolution in high-field asymmetric waveform ion mobility spectrometry (FAIMS) to characterize macromolecular conformations, 87

28111

Improving digestion efficiency under $\mbox{H/D}$ exchange conditions with activated pepsinogen coupled columns, 130

Pepsinogen

Improving digestion efficiency under H/D exchange conditions with activated pepsinogen coupled columns, 130

Peptide separation

Microfluidic electrocapture interfaced with electrospray mass spectrometry, 73

Peptide sequencing

Laying the groundwork for proteomics. Mass spectrometry from 1958 to 1988. 1

Glycoproteomics: Past, present and future, 16

Peptides

The contributions of mass spectrometry to understanding of immune recognition by T lymphocytes, 32

Photoionization

GC/MS on an LC/MS instrument using atmospheric pressure photoionization, 57

Plastic microfluidic device

Monolithic column plastic microfluidic device for peptide analysis using electrospray from a channel opening on the edge of the device, 65

PNGase F

Rapid removal of N-linked oligosaccharides using microwave assisted enzyme catalyzed deglycosylation, 117

Poly(ethylene glycol)

Peak deconvolution in high-field asymmetric waveform ion mobility spectrometry (FAIMS) to characterize macromolecular conformations, 87 *Porphyromonas gingiyalis*

Differential quantitative proteomics of *Porphyromonas gingivalis* by linear ion trap mass spectrometry: Non-label methods comparison, q-values and LOWESS curve fitting, 105

Post-translational modifications

The contributions of mass spectrometry to understanding of immune recognition by T lymphocytes, 32

"Hunt"-ing for post-translational modifications that underlie the histone code 40

Characterization of neurohistone variants and post-translational modifications by electron capture dissociation mass spectrometry, 184

Profiler

Specific identification of Bacillus anthracis strains, 140

Protein conformation

Peak deconvolution in high-field asymmetric waveform ion mobility spectrometry (FAIMS) to characterize macromolecular conformations, 87

Laser flash photochemical oxidation to locate heme binding and conformational changes in myoglobin, 124

Protein database

Comparative bioinformatics analyses and profiling of lysosome-related organelle proteomes, 147

Protein sequencing

Laying the groundwork for proteomics. Mass spectrometry from 1958 to 1988, 1

Proteomics

Laying the groundwork for proteomics. Mass spectrometry from 1958 to

Rapid removal of N-linked oligosaccharides using microwave assisted enzyme catalyzed deglycosylation, 117

Comparative bioinformatics analyses and profiling of lysosome-related organelle proteomes, 147

Identification of peptidase substrates in human plasma by FTMS based differential mass spectrometry, 174

PTR

Analysis of intact proteins on a chromatographic time scale by electron transfer dissociation tandem mass spectrometry, 197

Subject index 207

Quantitative proteomics

Differential quantitative proteomics of *Porphyromonas gingivalis* by linear ion trap mass spectrometry: Non-label methods comparison, *q*-values and LOWESS curve fitting, 105

q-Value

Differential quantitative proteomics of *Porphyromonas gingivalis* by linear ion trap mass spectrometry: Non-label methods comparison, q-values and LOWESS curve fitting, 105

SEQUEST

Assigning in vivo carbamylation and acetylation in human lens proteins using tandem mass spectrometry and database searching, 161

Shotgun proteomics

Assigning in vivo carbamylation and acetylation in human lens proteins using tandem mass spectrometry and database searching, 161

SIMS

Development of capabilities for imaging mass spectrometry under ambient conditions with desorption electrospray ionization (DESI), 8

Spectral count

Differential quantitative proteomics of *Porphyromonas gingivalis* by linear ion trap mass spectrometry: Non-label methods comparison, *q*-values and LOWESS curve fitting, 105

Stable isotope labeling

Deciphering the histone code using mass spectrometry, 46 Strains

Specific identification of Bacillus anthracis strains, 140

Surface-induced dissociation

A novel surface-induced dissociation instrument for ion mobility-time-of-flight mass spectrometry, 79

Tandem mass spectrometry

Linear ion-trap mass spectrometric characterization of human pituitary nitrotyrosine-containing proteins, 96

Time-of-flight

A novel surface-induced dissociation instrument for ion mobility-time-of-flight mass spectrometry, 79

Tissue imaging

Development of capabilities for imaging mass spectrometry under ambient conditions with desorption electrospray ionization (DESI), 8

Two-dimensional Western blotting

Linear ion-trap mass spectrometric characterization of human pituitary nitrotyrosine-containing proteins, 96

7P3

Glycoproteomics: Past, present and future, 16