NEDERLANDSE VERENIGING VOOR MASSASPECTROMETRIE

PROGRAM SPRING MEETING

June 29, 2026, Leiden

Morning

09.30-10.00	**Coffee and Registration**
10.00-10.20	Rick Ursem, Leiden University Medical Center *Joining Forces: Correlating Metabolites, Lipids, and N-Glycans in Murine Kidney Microstructures via Integrative Mass Spectrometry Imaging*
10.20-10.40	Pascalle Deenekamp, Radboud University *Non-target screening of VOCs under field conditions by GC-IMS: headspace and in-stable detection of poultry red mite presence*
10.40-11.00	Luca Tutiš, VU Amsterdam *High-resolution impurity profiling of therapeutic oligonucleotides using advanced LC-MS approaches*
11.00-11.30	**Coffee / Poster Session *Even numbers***
11.30-11.50	Hendrik Krolle, VU Amsterdam *Native charge reduction in the gas-phase: An improved charge reduction workflow for native, high-mass proteins*
11.50-12.10	Raya Sadighi, VU Amsterdam | **Travel Award Winner** *Novel strategies for the characterization of the early-stages of aggregate formation of α-Synuclein using ion mobility mass spectrometry*
12.10-12.40	General Assembly (ALV)
12.40-12.45	IMSIS
12.45-13:45	**Lunch and posters** *13.05-13.25 Poster Session **odd numbers*** *13.25-13.45 Posters Session **even numbers***

Afternoon

13.45-14.05	Nienke Meekel, KWR Water Research Institute *Prioritization of very polar substances in groundwater sources using non-target screening-based hazard and exposure prediction*
14.05-14.25	Samiksha Sardana, Maastricht University *Automated mass spectrometry for mapping osteoarthritis molecular endotypes*
14.25-14.45	Niek Kijk in de Vegte, Leiden University Medical Center *LC-MRM-MS Reveals Value as an Add-On Test to Improve Detection of Antithrombin Deficiency Beyond Activity Assays*
14:45-15.30	**Coffee /Poster Session *Odd numbers***
15.30-15.50	Thomas Holmark, University of Amsterdam *Ion-exchange chromatography hyphenated to native mass spectrometry for detecting intact serum immunoglobulin G repertoires*
15.50-16.10	David Falck, Leiden University Medical Center *Glycopeptide-centered LC-MS approaches and stable isotope-labeled glycoproteins to comprehensively characterize antibodies in infection*
16.10-16.30	Linus Wollenweber, Utrecht University | **Travel Award Winner** *Plasma proteome diversity: the overlooked albeit dominant contribution of immunoglobulins*
16.30-16.50	Peter Horvatovich, University of Groningen *PASTAQ: Threshold-Avoiding Multidimensional LC–MS Data Processing for Robust and Scalable Quantification*
16.50-17.00	Closure + poster award(s)
17.00-17.45	**Drinks**

POSTERS

#	Presenter, affiliation *Poster title*
	Industry Sponsors
1	Saar van der Laarse, Thermo Fisher Scientific *Expanding plasma metabolome coverage with enhanced dynamic range and iterative MS/MS acquisition on a modified Orbitrap Hybrid mass spectrometer*
2	Michele Genangeli, Bruker Nederland BV *New ExD, MS^n and Ion Mobility Capabilities of the timsOmni Platform for Structural Analysis*
3	Perry Derwig, Waters *Profiling the lipidome of adrenal cancer*
	Glycoproteomics & Glycan Analysis
4	Amélie Willemse, Leiden University Medical Center *From Bulk to Precision: N-Glycan Mass Spectrometry Imaging at the Single-cell Level*
5	Karthika Korumadathil Shaji, University of Groningen *One sample, two glycomes: Optimizing Simultaneous N- and O-glycan Profiling by CE-MS*
6	Ifigeneia Skiada Papadogrigorakou, VU Amsterdam *Optimization of CID and Hybrid CID–EAD Fragmentation for N-Glycoproteomic Analysis of Human Plasma*
7	Shelley Jager, Utrecht University *Human hepatocyte organoids for the prognostication of blood glycoproteoform biomarkers*
8	Sigourney Karijodikoro, Leiden University Medical Center *Unraveling Proteoforms of the Heavily Glycosylated C1-INH by Nanoscale MS-Based Strategies*
9	Pedro Almeida, Leiden University Medical Center *Nasal Secretory Immunoglobulin A is Differentially Glycosylated to its Plasma and Saliva Counterparts: a comparative LC-MS study across biofluids*
10	Flavio Aragozzini, University of Amsterdam *Is there a pregnancy proteoform code? Intact human chorionic gonadotropin proteoform profiling from pregnant donors*
11	Raluca Teodorescu, University of Groningen *Impact of Hyperglycemia on the Serum N-Glycome in a Mouse Model of Colorectal Cancer*
	Antibody & immunoglobulin Analysis
12	Srishti Shah, Leiden University Medical Center *Topic: Antibody & immunoglobulin analysis* *Antigen-specific antibody glycosylation signatures are associated with increased risk to Crohn's disease*
13	Albert Bondt, Utrecht University *Topic: Antibody & immunoglobulin analysis* *Antibody biology unraveled by repertoire analysis with clonal resolution*
14	Despoina Mavridou, Leiden University Medical Center *Topic: Antibody & immunoglobulin analysis* *Longitudinal profiling of the ACPA IgG1 Fab repertoire in Rheumatoid Arthritis patients*
15	Rien Leuvenink, Utrecht University *Topic: Antibody & immunoglobulin analysis* *Extending serum IgG1 antibody repertoire coverage using DIA-PTCR*
16	Yue Li, Leiden University Medical Center *Topic: Antibody & immunoglobulin analysis* *Evaluating IgA endoproteases with different specificity for the characterization of IgA1 and IgA2 subunits by middle-up LC-MS*
17	Anastasia Tzasta, Radboud UMC *Feasibility of blood-based monoclonal quantitation for minimal residual disease monitoring by mass spectrometry in AL amyloidosis*
18	Lizaveta Yurkianets, Utrecht University *Toward Predicting Top-Down Antibody Fragmentation*
	Lipids, Metabolites & Spatial MS
19	Laura De Bruym Wölfel, Leiden University Medical Center *Optimization of glycosphingolipid detection and spatial analysis in brain tissue*
20	Rachel Pultoo, Leiden University Medical Center *Development and validation of a spatial MALDI imaging method for BMP lipids*
21	Golsa Nayeb Ghanbar Hosseini, Leiden University *DESI-MS: A High-Resolution Tool for Specialized Metabolite Identification, Chemical Diversity Profiling, and Spatial Localization in Soil Streptomyces Populations*
22	Yue Wang, Maastricht University *Global Proteomic Profiling Reveals Reduced Toxicity and Enhanced Cytoprotective Activity of a Quercetin-Derived Metabolite*
23	Jiaxing Liu, VU Amsterdam *A Workflow for Parent-Anchored Mass-Shift Screening and QSPR-Based Semi-Quantification of NPS Metabolites in Wastewater and Urine*
	PROTEOMICS, BIOMARKERS & CLINICAL MS
24	Anabel Torrente Lopez, Leiden University Medical Center *Multi-level characterization of apolipoprotein E by LC-MS*
25	Rimsha Saif, Maastricht University *Optimizing Serum Proteomics Workflows Using Evosep–timsTOF Pro 2 and diaPASEF for Enhanced Low-Abundant Biomarker Discovery in Osteoarthritis*
26	Nicolaas van Neer, Leiden University Medical Center *LC-MRM-MS based Reference Measurement Procedure for Global Standardization of Serum Apolipoprotein(a)*

27 Alexander Heijnis, Princess Maxima Center
Bottom-up LC-MS/MS Quantification and Validation of Pegaspargase and Crisantaspase in Human Plasma

28 Betzabeth Pereira Herrera, Maastricht University
Decoding tendon-infrapatellar fat pad crosstalk in osteoarthritis revealed by an SP3-based proteomics pipeline

29 Christopher Zala, Utrecht University
Stoichiometry-dependent specificity in biotin enrichment: a benchmarking framework for proximity labeling proteomics

NATIVE MS, ION MOBILITY & STRUCTURAL ANALYSIS

30 Georgia Stavara, Vrije Universiteit Amsterdam
Native Trapped Ion-Mobility Mass Spectrometry Reveals Mutation-Dependent Differences in Conformational Landscapes of Amyloid-β

31 Olivia Rusli, Vrije Universiteit Amsterdam
Unraveling the Role of PTMs on αSynuclein Aggregation Using Ion Mobility-Mass Spectrometry

32 Alexandra Charmani, Vrije Universiteit Amsterdam
Structural Characterization of Metallothionein-2 and Its Zinc-Binding Behavior Using IR Action Spectroscopy and Native Mass Spectrometry

33 Carley Hinrichs, Leiden University Medical Center
Nano-Reverse Phase Liquid Chromatography-Mass Spectrometry Methods for In-Depth AAV Capsid Characterization

34 **Emily Byrd, Vrije Universiteit Amsterdam**
30 nm Diameter Nanopipette nESI Emitters Significantly Enhances Desalting and Sensitivity for Native Mass Spectrometry of Large Proteins

METHOD DEVELOPMENT & INSTRUMENTATION

35 Fabrice Kusters, Utrecht University
Protein Language Model Decoys for Target Decoy Competition in Proteomics: Quality Assessment and Benchmarks

36 Kas Houthuijs, Vrije Universiteit Amsterdam
Data-Driven Filter for Detector Oscillation Artefacts in Time-of-Flight Mass Spectrometry

37 Guylain Cuiper, University of Amsterdam
Development of a RPLC–HILIC 2D-LC–HRMS Method for Expanding Chemical Space Measurability in Non-Target Analysis

38 Xiaoyi Zhang, Vrije Universiteit Amsterdam
Mass Spectrometry Guided Identification of Muscarinic Receptor Ligands from Snake Venoms

BREATH, ENVIRONMENTAL & VOC ANALYSIS

39 Joris Meurs, Radboud University
Monitoring hay fever response through exhaled breath VOC profiling using PTR-ToF-MS and TD-GC-MS

40 Marleen Huisman, Radboud University
Characterization of Gas-Phase Ion-Molecular Reactions for Chlorinated Compounds Using SRI-ToF-MS

OLIGONUCLEOTIDES & RNA ANALYSIS

41 Matthijs Dobbelaar, University of Amsterdam
2DLC-MS for impurity and diastereomer profiling of small interfering RNA

42 Merel Post, Charles River Laboratories
LC-HRMS Method Development for Low-Level Oligonucleotide Analysis in In Vitro DMPK Assays