|MC:SUBJECT|

MetaboNews

This month in metabolomics

July, 2025
Vol 15, Issue 7

MetaboNews is a monthly newsletter published in a partnership between The Metabolomics Innovation Centre (TMIC) and The Metabolomics Society

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|MC:SUBJECT|

Metabolomics Society News

The Metabolomics Society is an independent, non-profit organization dedicated to promoting the growth, use, and understanding of metabolomics in the life sciences.

General Enquiries

info@metabolomicssociety.org

Members Corner

Board of Directors

Message from Warwick (Rick) Dunn, President

Dear Metabolomics Society Members and metabolomics friends,

Thank you to all for the success of Metabolomics 2025 in Prague and I hope all who attended enjoyed the science, discussions with sponsors, food, alcohol and city as much as I did. My sincere thanks go to the local organisers (Tomas and David), conference committee chair (Natasa), scientific committee and SnapIT (conference organising company); without these we would not have a conference. My thanks also go to all the attendees who shared their high-quality science through presentations and posters. A large volume of photographs are available on the conference website, see if you can spot yourself.

We broke our attendance record with 1118 registrations. Congratulations to our 2025 award winners:

- 2025 Presidents Award winner: Tao Huan from the University of British Columbia
- 2025 Metabolomics Society Medal: Dr Hiroshi Tsugawa from the Tokyo University

of Agriculture and Technology
- 2025 Lifetime Honorary Fellowships: Prof. Marta Cascante from the University of Barcelona and Dr Jessica Lasky-Su from Harvard University

A number of new initiatives and news including our new ECR mobility grant to support Early Career Researchers and Technical Experts to go to a Host Institution to learn something new in metabolomics or lipidomics and to take this knowledge and know-how back to their home institution.

Other major news announced in Prague was that the journal Metabolomics will once again be the official journal of the Metabolomics Society. I am somewhat biased as an editor for the journal but this is good news for the society and its members including that the journal is moving to a full open access journal from 2026. Further news will follow. Importantly, the journal editors who sit on the board of directors were not involved in the process at any point so to provide neutrality and ensure no conflicts of interest. Thanks to Michael and the publications committee for driving this through to completion.

Our next annual conference will be in Buenos Aires in June 2026. I think this was the worst kept secret during the conference. The final date is to be decided and we will announce as soon as we know. One of my objectives as President was to reach out to the whole community globally and ensure they can engage with the society; this will be our first conference in South America and I look forward to seeing many of you there.

Finally, we are at the time of the year where we are requesting members to provide nominations and then vote for new Directors to join the board from October 1st. There are six positions available this year and we are requesting nominations and voting to provide diversity both geographically and in job type (academia, industry etc). Please provide your nominations by August 6th. You can submit nominees here: https://forms.gle/byvdjq5murm5EDuZ8.

All the very best,
Warwick (Rick) Dunn, University of Liverpool, UK
President, Metabolomics Society

Early-Career Members Network (EMN)

EMN Elections
We are inviting early-career researchers to join the committee of the Metabolomics

Society's Early-career Members Network (EMN). We welcome applications from members* of the Metabolomics Society that are graduate students (Masters or PhD) or within 5 years post PhD (graduation date after October 2020) while being in a training position (*e.g.* post-doc) in a metabolomics discipline or are actively engaged in metabolomics science. Applications to join the EMN committee will be open July 28 - Aug 10, 2025 (2359 Pacific Daylight Time (UTC/GMT -7)). Top candidates will be invited for an interview, which is expected to take place at the end of August/beginning of September. Successful candidates are expected to commence their EMN mandate in October 2025.

To apply, please visit this link. Please note that the form will not be accepting responses until July 28. Alternatively, we will be sharing the link on our LinkedIn, Bluesky and X accounts when applications open. As we strive for diversity and representation in our committees, we encourage applications from all corners of the globe and would strongly recommend ECRs from Asia, Africa and the Americas to apply. The full application call can be found here: Application Call 2025. Please follow the application guidelines carefully. Given the high number of applications we receive, applications that do not confer to guidelines will not be evaluated.

**current member or willing to become a member. EMN committee members receive a free Metabolomics Society membership for the time they serve on the committee.*

EMN at the MetSoc 2025 Conference in Prague

EMN Conference Workshop

A warm thank you to all participants of the EMN conference Workshop! The EMN is especially grateful to the invited panellists Erin Baker, Evelina Charidemou, Biswapriya Misra, Álvaro Fernández Ochoa, Nicholas Rattray, and Lynn Vanhaecke, who brought all the experience this workshop needed to be a success. Among the take-home messages to remember: (i) having several mentors is beneficial for both industry and academia, (ii) multiple strategies for initiating and maintaining a successful mentor-mentee relationship, (iii) mentors can be approached by e-mail or in person at conferences, (iv) and don't forget to follow mentoring programmes (FeMs, Sci.STEPS, RFMF and soon the MetSoc Mentoring Program). We hope to see you all at the next EMN Workshop at Metabolomics 2026 in Buenos Aires!

Career Night Roundtable Discussions
Sunday, June 22, 6:45 p.m. – 8:00 p.m.

We're incredibly grateful to the brilliant professionals who led engaging and insightful

conversations at our **Career Night Roundtable** event. Each session was a masterclass in experience, wisdom, and inspiration, helping participants navigate diverse career paths in metabolomics across academia and industry.

Here’s a special thank you to the discussion leaders:

Translating Research into Industry Applications
– Tomáš Pluskal (Czech Academy of Sciences, Czech Republic)
– Clary Clish (Broad Institute of MIT and Harvard, USA)

Career Transitions
– Kati Hanhineva (University of Turku, Finland)
– Liz Want (Imperial College London, UK)

Careers in Industry
– Biswapriya Misra (Enveda, India)
– Matej Orešič (Örebro University, Sweden)

International Employment Opportunities: Understanding Visas, Relocation, and Cultural Considerations
– Sastia Prama Putri (University of Osaka, Japan)
– María Eugenia Monge (CIBION – CONICET, Argentina)

Leadership and Management in Research Teams
– Erin Baker (University of North Carolina at Chapel Hill, USA)
– Fabien Jourdan (INRAE-MetaboHUB, France)

How to Be a Good Reviewer (Tips and Tricks for Peer Review)
– Roy Goodacre (University of Liverpool, UK)
– Michael Witting (Helmholtz Zentrum München, Germany)

Obtaining a Postdoctoral Fellowship
– Aurelia Williams (North-West University, South Africa)
– Tao Huan (University of British Columbia, Canada)

Grant Writing
– Jennifer Kirwan (Charité University Hospital, Germany)
– Lynn Vanhaecke (Ghent University, Belgium)

Science Communication

– Alice Limonciel (Biocrates life sciences ag, Austria)
– Olya Vvedenskaya (Lipotype GmbH, Germany)

Diversity, Equity, and Inclusion
– Millena Barros Santos (INRAE Avignon, France)
– Domenica Berardi (Yale University, UUSA)

Your contributions made this event a standout success. Thank you for fostering such a dynamic and supportive space for career exploration and growth.
Let's keep building on these conversations and connections!

EMN Reception and Treasure Hunt
A heartfelt thank you to everyone who joined the EMN reception and treasure hunt, making it such a fantastic success! It was wonderful to see so many motivated teams exploring the venue, scanning QR codes, and collaborating to solve all the questions. The competition was fierce, and every team performed impressively. We want to extend special congratulations to our winners: **"Girlsforce"** (first place), **"MetaBAUT"** (runner-up), and **"MetaboNerds"** (second runner-up). Kudos as well to all the other teams for their excellent scores and enthusiastic participation!
We hope you all had a great time, made new connections, and enjoyed the spirit of friendly competition.

MetaboART
Congratulations to our winners of the MetaboART competition, who were announced at the EMN Reception. Maicol Andrés Avellaneda Arciniegas was selected as the winner of the human-created category for their piece *'Diagnostic "machine"'*, while Jayden Lee Roberts won the AI-generated category with '*Lipoprotein profiling from a single droplet'.* Thank you to everyone who submitted their work; the quality of the entries was outstanding and made the final decision a challenging one.

International Affiliates' Corner

Latin American Metabolic Profiling Society (LAMPS)
Visit https://jwist.github.io/lamps/

Dear LAMPS members,

We have received nominations from seven of the Founding Members, who are eager to

continue serving in the Board of Trustees, which will be composed by:

Dr. Martín Arán (FIL-CONICET, Argentina);
Dr. Paula Burdisso (IBR-CONICET, Argentina);
Dr. Mónica Cala Molina (Universidad de los Andes, Colombia);
Dr. Ian Castro-Gamboa (UNESP, Brazil);
Dr. Pablo Hoijemberg (CIBION-CONICET, Argentina);
Dr. María Eugenia Monge (CIBION-CONICET, Argentina);
Dr. Guillermo Moyna, (Universidad de la República, Uruguay).

Based on our Charter, the current Board will last for three years. In case of a vacancy, an extraordinary election may be held virtually (online form).

We encourage you to continue participating in the activities promoted by LAMPS.

Together, we will endeavor to expand collaborative research, foster training opportunities, and consolidate LAMPS as a leading network for metabolomic science in our region.

Nordic Metabolomics Society
Visit www.nordicmetsoc.org

Save the date: Nordic Metabolomics Conference 2026
We are excited to announce that the **5th Nordic Metabolomics Conference** will be held in **Uppsala, Sweden,** from **September 28-30, 2026**. The event will take place at Uppsala University, hosted by local organizers Daniel Globisch, Ingela Lanekoff, and Wojciech Michno.

More details will follow soon- but for now, mark your calendars and get ready for what will be an outstanding conference covering a range of topics within metabolomics.

Nominations for new board members
Elections for all nine board positions in the Nordic Metabolomics Society will take place in October 2025.

Eligibility for nominations:

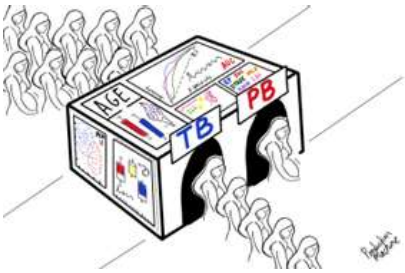
- Candidates must have been members for at least 12 months
- Must be based in one of the five Nordic countries

Board members serve a 2-year term (maximum of two consecutive terms)

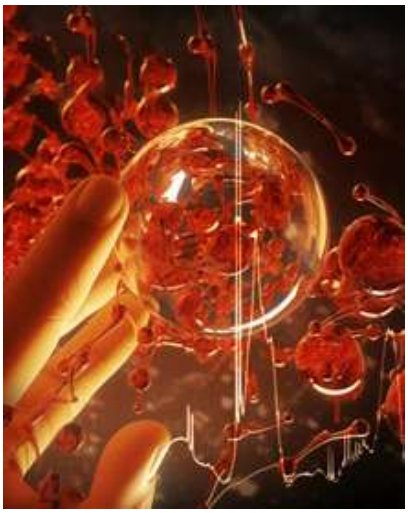
You may nominate a colleague or yourself by emailing **normetsoc@gmail.com** with the following:

1. Full name
2. Affiliation
3. Early-career status (within 5 years post-PhD, excluding career breaks)
4. Short profile (see examples from current board members: https://nordicmetsoc.org/board/
5. Portrait photo (for the website ahead of elections.)

Deadline for nominations: September 1, 2025, at 23:59



Diagnostic "machine"
By: Maicol Andrés Avellaneda Arciniegas
“My image illustrates how, by combining metabolomics with clinical variables, we can build a powerful 'machine' capable of diagnosing medical conditions such as preterm birth in women during their first trimester of pregnancy.”



Lipoprotein profiling from a single droplet
By: Jayden Lee Roberts
“Fingerprick microsampling redefines ^{1}H NMR lipoprotein analysis: A drop of blood is as informative as the oceans traditionally drawn through venepuncture. Created with AI using the Midjourney web app.”

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Spotlight Article

Sponsored Content

NIST Metabolomics and Microbiome Reference Materials Now Available!

Confidence in Data Quality

The National Institute of Standards and Technology (NIST) has launched two new reference material (RM) suites for the metabolomics communities to facilitate high quality measurements, promote reproducibility and reliability of results, and encourage data harmonization and comparability.

RM 8231 - Frozen Human Plasma Suite for Metabolomics

RM 8231 was created as a suite of three phenotypically distinct human plasma. Pooled Plasma 1, Diabetic Plasma: designed to represent a Type 2 diabetic plasma material with glucose >126 mg/dL and low/normal triglyceride (<150 mg/dL). Pooled Plasma 2, Hypertriglyceridemic Plasma: designed as a hypertriglyceridemic plasma material with glucose <100 mg/dL and triacylglycerols >300 mg/dL. Pooled Plasma 3, African-American Plasma: created as a young (ages 20-25 years of age), African American plasma material. A unit of RM 8231 consists of two vials each of the three phenotypes.

RM 8048 – Human Fecal Material

RM8048 was designed to assist scientists in improving the reproducibility of their data and advancing diagnostics and clinical tools that focus on the gut microbiome. The RM 8048 unit includes four vials from vegetarian cohorts and four vials from omnivores. This material has identified over 150 metabolites and more than 150 genetic signatures.

Requesting community input!
RGTM 10212 – Fecal Calibrant Solution

NIST is developing a fecal metabolite calibrant solution as a research grade test material (RGTM) designed specifically to evaluate the performance and precision of microbiome metabolomics measurements. This solution contains 70 compounds at biologically relevant concentrations, representing a diverse range of chemical classes found within

the gut microbiome including short-chain fatty acids (SCFAs), amino acids, phenols, and pyrimidines. We are offering **a unit free of charge** for community evaluation that will aid in assessing suitability for microbiome metabolomics and the data will provide NIST important feedback in the evolution of the RGTM to a reference material.

Materials can be acquired at the NIST Storefront!

Confidence in your data! Confidence in published results! Confidence in deposited data!

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MetaboInterview

Linda Nartey

Biography:

Ms. Linda Nartey is a final-year Ph.D. candidate in Microbiology at the University of Victoria, where she works under the supervision of Professor David R. Goodlett. Her research focuses on advancing rapid, culture-independent methods for microbial identification by directly analysing microbial lipidomes and proteomes from clinical and environmental samples. Her work leverages mass spectrometry techniques to profile species-specific lipid markers, with the goal of improving diagnostic speed and accuracy for infectious diseases.

Linda's scientific journey began with a B.Sc. in Botany from the University of Ghana, where she studied fungal and bacterial contaminants in food. She went on to earn M.Sc. in Biology from Zhejiang Sci-Tech University in China, researching fungal biocontrol agents. Before beginning her graduate studies, she gained hands-on experience at the Noguchi Memorial Institute for Medical Research, contributing to diagnostic research on neglected

tropical diseases such as Buruli ulcer and Schistosomiasis.

Her broader research interests include microbial pathogenesis, antimicrobial resistance, and clinical microbiology. Linda aspires to bridge the gap between research and real-world diagnostics by developing faster, more reliable tools to identify pathogens directly from samples, ultimately improving patient care and public health outcomes.

Could you share your journey into lipidomics and what initially sparked your interest in this field?

My journey into lipidomics began in the Goodlett lab UVic, where I first became fascinated by how membrane lipids influence microbial adaptation and survival in challenging environments. I was intrigued by the idea that something as small as a bacterial lipid could have such a significant impact on human health. Previous research by Prof. David Goodlett and collaborators showed that microbial membrane lipids could serve as ‘barcodes’ to identify microbes. Knowing that these lipids can be easily extracted means we can analyze them directly from clinical samples without the need for culture, which could greatly improve diagnostic speed, throughput, and ultimately patient care. This possibility drives my commitment to using lipidomics to answer clinically relevant questions and advance better solutions for patients.

What other key lipidomics projects are you currently pursuing or look forward to pursuing in the future?

Beyond my current work on urinary tract infections, I am expanding my lipidomics research to include environmental samples. I am particularly interested in how bacteria from diverse sources such as surface waters, wildlife, or cold environments like Antarctica adapt and how these environments influence their lipid profiles to help them persist in such conditions. A key area I’m investigating is how lipid A modifications contribute to membrane-associated antimicrobial resistance enabling pathogens to survive both in the environment and during infection. Alongside lipidomics, I am also advancing proteomics workflows that analyze bacterial proteins directly from clinical

specimens without the need for culture. By combining direct-from-specimen proteomics and lipidomics, I aim to build a more complete picture of how bacteria adapt in real world contexts, which could lead to new strategies for detecting resistance and understanding pathogen survival outside traditional lab conditions.

What aspects of lipidomics research do you find most exciting, both generally and in relation to your work on urinary tract infections?

What excites me the most about lipidomics is its ability to uncover hidden layers of microbial physiology that conventional methods often miss. Lipids are dynamic and sensitive to environmental pressures, making them powerful indicators of how bacteria adapt inside the human body. I find it fascinating how the lipid A structure of bacteria can shift in ways that affect immune recognition and influence treatment outcomes. Understanding these specific lipid modifications directly from patient samples could lead to faster, more precise diagnostics and targeted therapies.

Can you describe the key lipidomics initiatives you are currently involved in at your research centre or institute?

I am part of a team advancing rapid, culture-independent diagnostic methods using lipidomics and mass spectrometry. We are developing and validating a workflow, known as the Fast Lipid Analysis Technique (FLAT), to extract and profile bacterial lipids directly from clinical biofluids. I am also investigating the potential of lipid A modifications as biomarkers for antibiotic resistance and host adaptation.

How is lipidomics research evolving in your country, particularly in the context of infectious diseases?

In Canada, lipidomics is gaining traction as researchers and clinicians recognize its potential for addressing complex health challenges. While molecular studies and other ‘omics’ approaches such as proteomics and genomics have long been at the forefront, lipidomics is now being integrated into studies several studies such as infectious

diseases, antimicrobial resistance, and host-pathogen interactions. Research institutes are investing in advanced mass spectrometry platforms and fostering collaborations that combine multiple ‘omics’ approaches and strengthening the capacity of Canada to tackle emerging health threats through a more comprehensive biological understanding.

How do you see lipidomics being applied today and in the future, both in clinical metabolomics and in other areas of your research?

Lipidomics is already improving our understanding of disease mechanisms, pathogen phenotypes, and treatment responses. In the clinical setting, I see it evolving toward rapid, point-of-care diagnostics that profile pathogen-specific lipids directly from patient samples. Beyond infections, lipidomics offers great potential for discovering biomarkers related to metabolic disorders, cancers, and various inflammatory conditions. In my own work, I envision combining lipidomics with other ‘omics’ to build comprehensive diagnostic panels that not only identify pathogens but also detect key biomarkers and improve patient outcomes.

In your experience, what are the major strengths of lipidomics as a tool for understanding biological systems?

Lipidomics provides valuable insight into how living systems function and adapt. Unlike genes, which stay largely the same, lipids can change rapidly in response to stress, host interactions, or treatment, making them sensitive indicators of physiological changes. In infectious disease research, this is particularly valuable because lipid modifications can reveal how pathogens evade the immune system or develop resistance. Another strength is that lipidomics complements other ‘omics’ approaches and when combined with proteomics and genomics, it helps build a more complete understanding of complex biological systems

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What challenges have you encountered in your lipidomics research, especially regarding infectious disease applications, and how are you addressing them?

One of the biggest challenges in my lipidomics research is dealing with the complexity of real world samples. Clinical specimens often contain interfering substances or complex matrices, especially when underlying conditions are present, which can make extracting and analyzing lipids difficult particularly when working with limited material. Another challenge is translating lipidomic findings into practical tools that can be used reliably in clinical settings. By collaborating closely with clinicians, we aim to bridge this gap and ensure that our workflows are robust, reproducible, and scalable for real world use.

What technological or methodological developments do you believe are necessary to further advance lipidomics across different research areas?

Advancing lipidomics requires improvements in both analytical technology and data interpretation. High-resolution mass spectrometers with faster acquisition rates will help detect low-abundance lipid species more reliably. Standardized, automated extraction protocols are essential for reproducibility, especially when dealing with complex or limited samples. On the data side, more user-friendly bioinformatics tools for lipid identification and quantification are needed to make lipidomics accessible to broader research communities

How do you see lipidomics shaping your future research directions?

Lipidomics will remain at the core of my research as I continue exploring host-pathogen interactions. I plan to expand into comparative lipidomics across diverse bacterial species and infections to uncover unique lipid signatures that can inform diagnostics and treatment decisions. Moving forward, I plan to expand my work to include a broader range of pathogens and clinical conditions, while also exploring lipid-based biomarkers for early disease detection and treatment monitoring

MetaboReads

Environmental and Dietary Modulators of Cardiovascular and Metabolic Pathology

Collectively, these studies reveal diverse environmental and dietary cues that converge on lipid transport, mitochondrial integrity and immune tone to dictate cardiovascular or hepatic outcomes. Natural compounds such as nanocellulose, dehydrocostus lactone and epigallocatechin-3-gallate counter pathological lipid accrual, whereas amino-acid overload exacerbates it. By integrating microbiome, metabolite and signalling analyses, the authors

supply mechanistic blueprints that could guide nutritional or ecological interventions aimed at vascular and liver health

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Jute Nanocrystalline Cellulose Relieves Polystyrene Nanoplastic-Induced Acute Injuries by Modulating Gut Microbiota Gilliamella apicola

Deng and colleagues in ACS Nano showed that jute-derived nanocrystalline cellulose shields honey bees from polystyrene-nanoplastic injury by re-shaping the gut microbiota. Survival analysis, histopathology and transmission-electron microscopy demonstrated that nanoplastics provoke size-dependent autophagy and apoptosis in gut and tracheal tissues. Metabolomic profiling revealed that cellulose treatment restores glycerophospholipid metabolism and elevates regulators such as hexadecanamide and glycerophospho-N-palmitoyl-ethanolamine. Further experiments confirmed that enrichment of Gilliamella apicola is sufficient to blunt nanoplastic-induced cytotoxicity, underscoring a microbe-metabolite defence axis.

Dehydrocostus lactone attenuates atherogenesis by promoting cholesterol efflux and inhibiting inflammation via TLR2/PPAR-γ/NF-κB signaling pathway

Hong and colleagues in Molecular Medicine found that dehydrocostus lactone lowers circulating lipids, reduces aortic plaque burden and augments cholesterol efflux in ApoE-deficient mice. The compound up-regulates ABCA1, ABCG1 and PPAR-γ in macrophage-derived foam cells, thereby facilitating reverse-cholesterol transport. Parallel suppression of TLR2-MyD88-NF-κB signalling decreases IL-1β and TNF-α while favouring an anti-inflammatory M2 phenotype. These coordinated effects position dehydrocostus lactone as a dual modulator of lipid handling and innate immunity.

Multi-omics reveals EGCG's anti-calcification effects associated with gut microbiota and metabolite remodeling

Zhang and colleagues in Frontiers in Immunology demonstrated that epigallocatechin-3-gallate mitigates vitamin-D3-induced vascular calcification while restoring gut-microbiota diversity. Histological staining and alkaline-phosphatase assays confirmed attenuated calcification in treated rats. High-throughput sequencing revealed recovery of key bacterial taxa, and serum metabolomics showed normalisation of phosphatidylserine, phosphatidylcholine and lysophosphatidylcholine alongside activation of ubiquinone biosynthesis. The data link microbiota restoration and phospholipid remodelling to suppression of vascular-smooth-muscle osteogenic transformation.

L-Phenylalanine promotes liver steatosis by inhibiting BNIP3-mediated mitophagy

Sun and colleagues in Molecular Medicine showed that elevated plasma L-phenylalanine associates with metabolic dysfunction-associated steatotic liver disease and actively drives steatosis in rats. Proteomic and metabolomic analyses pinpointed repression of BNIP3-mediated mitophagy together with dampened PPAR-α signalling and fatty-acid β-oxidation. In hepatocyte culture, L-phenylalanine curtailed autophagic flux and promoted triglyceride deposition, effects reversed by rapamycin or BNIP3 over-expression. These findings connect amino-acid excess to impaired mitochondrial quality control and hepatic lipid

accumulation.

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Lipid Metabolism and Disease Mechanisms

The four studies establish lipid enzymes, intermediates and composite ratios as central determinants of disease onset, progression and therapeutic response. By combining omics profiling with functional validation, the authors connect molecular lipid alterations to concrete physiological and clinical endpoints. This integrative approach reinforces the promise of targeting specific lipid-processing nodes for both precision diagnostics and metabolic therapy.

SIRT5-modified human umbilical cord mesenchymal stem cells loaded with antioxidant polydopamine nanozyme enhance parpi resistance in ovarian cancer via fatty acid metabolism reprogramming

Zhang and colleagues in Journal of Nanobiotechnology showed that SIRT5-modified umbilical-cord mesenchymal stem cells, loaded with polydopamine nanozymes, desuccinylate enoyl-CoA hydratase, enhance fatty-acid β-oxidation and overcome PARP-inhibitor resistance in ovarian cancer. Transcriptomic, proteomic and metabolomic profiling traced resistance reversal to a rewired lipid-fuel programme driven by SIRT5 activity. In vitro assays and murine xenografts confirmed greater tumour suppression when engineered cells were combined with PARP inhibition. The study highlights metabolic desuccinylation as a leverage point against chemoresistance.

Deep sphingolipidomic and metabolomic analyses of ceramide synthase 2 null mice reveal complex pathway-specific effects

Oh and colleagues in Journal of Lipid Research found that ceramide-synthase-2 deletion perturbs 259 sphingolipid species across 18 mouse tissues, producing unexpected drops in brain ceramide-1-phosphate and rises in C26 ceramides in lung. Metabolomic surveys also uncovered alterations in six major non-lipid pathways, indicating extensive metabolic cross-talk. Tissue-specific patterns caution against attributing pathology to a single ceramide class. The resulting atlas offers a reference for future studies of sphingolipid-driven disease.

Unraveling the regulatory network of barley grain metabolism through the integrative analysis of multiomics and mQTL

Song and colleagues in Cell Metabolism reported that nicotinic-acid riboside accumulates in NMNAT1-deficient livers, circulates to the kidneys and is converted to NAD^+ through NRK1, thereby preserving systemic NAD^+ levels. Enzymology identified NT5C2 as the hepatic source of nicotinic-acid riboside, while isotopic tracing verified renal uptake and conversion. Ageing mice exhibited falling serum nicotinic-acid riboside; supplementation restored multi-organ NAD^+ and diminished kidney inflammation. This liver–kidney relay secures NAD^+ homeostasis during metabolic stress.

Lipid Ratios for Diagnosis and Prognosis of Pulmonary Hypertension.

Bordag and colleagues in American Journal of Respiratory and Critical Care Medicine showed that specific serum fatty-acid ratios diagnose pulmonary hypertension with high accuracy and predict mortality beyond established clinical scores. High-resolution mass spectrometry combined with machine learning identified lipid signatures that separated patients from controls in both training and validation cohorts. Pulmonary-artery tissue displayed lipid accumulation and dysregulated lipid-handling genes, while cultured vascular cells responded to fatty acids with hyper-proliferation and barrier dysfunction. Explainable lipid ratios thus serve as mechanistically anchored biomarkers.

Omics-Driven Diagnostic and Computational Advances

These studies advance metabolomics from data collection to actionable insight by pairing innovative computation with high-resolution measurement. Whether accelerating LC-MS workflows, sharpening biopsy diagnostics or visualising isotope flow, the authors demonstrate that rigorous benchmarking and multi-modal integration convert raw omics complexity into clinically and mechanistically useful knowledge.

Raman micro-spectroscopy reveals the metabolic alterations in primary prostate tumor tissues of patients with metastases

Shao and colleagues in Journal of Translational Medicine showed that Raman micro-spectroscopy, coupled with a convolutional neural network, distinguishes metastatic from localised prostate cancer with an accuracy of 81 percent. Spectral analysis of 42 tumours revealed higher unsaturated-fatty-acid peaks and lower amino-acid signals in metastatic lesions. Liquid-chromatography–mass-spectrometry metabolomics confirmed parallel shifts in prenol lipids and linolenic acid. The platform offers a rapid, label-free adjunct for biopsy evaluation.

Human Physiologic Responses to Insulin in Indigenous Americans Identify a Metabolic Susceptibility Profile Linked to Diabetes

Murthy and colleagues in Diabetes Care found that a 49-metabolite plasma signature derived from insulin-clamp measurements predicts incident diabetes over two decades, independent of body mass index and baseline glucose. Metabolites reflecting fatty-acid and branched-chain-amino-acid metabolism correlated with insulin sensitivity across multiple Indigenous American cohorts. The same signature forecast diabetes in the CARDIA study, and gene-metabolite mapping linked it to known diabetes loci. This work converts complex physiological traits into accessible risk scores.

MassCube improves accuracy for metabolomics data processing from raw files to phenotype classifiers

Yu and colleagues in Nature Communications introduced MassCube, an open-source Python

framework that detects all LC-MS peaks, annotates adducts and in-source fragments, and processes 105 GB of data in 64 minutes on a standard laptop. Benchmarking against MS-Dial, MZmine 3 and XCMS showed superior speed, isomer resolution and accuracy. Built-in quality controls and machine-learning modules correctly classified age, sex and regional differences in the mouse-brain ageing atlas despite batch effects. MassCube is freely available for integration into large-scale pipelines.

Spatial patterns of hepatocyte glucose flux revealed by stable isotope tracing and multi-scale microscopy

Habashy and colleagues in Nature Communications mapped glucose-derived ^{13}C atoms in mouse hepatocytes by combining multi-scale microscopy with machine-learning segmentation and spatial statistics. The approach revealed progressive expansion of mitochondria–endoplasmic-reticulum contacts following feeding, along with tight spatial coupling between nascent glycogen granules and lipid droplets. Quantitative flux analysis linked organellar architecture to metabolic routing. The methodology enables in situ isotope tracking at cellular and sub-cellular levels.

Exercise, Microbiome and Regenerative Metabolism

Across cell, animal and human studies, the papers in this theme connect mechanical or metabolic stress with adaptive proteomic, neurochemical and microbial shifts that underpin regeneration and systemic health. They underscore the importance of anatomical cell source, vascular signaling context and exercise modality in driving beneficial metabolic reprogramming. Future clinical translation will depend on harmonizing omics profiling with controlled interventions to personalize regenerative and lifestyle medicine.

Comparative cardiomyocyte differentiation potential of rat adipose-derived mesenchymal stem cells from two anatomical sites: metabolomic profiling and pathway analysis

Farag and colleagues in Frontiers in Cell and Developmental Biology showed that adipose-derived mesenchymal stem cells from peri-ovarian fat undergo broader metabolic reprogramming than peri-renal counterparts during cardiomyocyte differentiation. Gas-chromatography–mass-spectrometry profiling revealed enhanced engagement of glycolysis, glycerolipid metabolism and the tricarboxylic-acid cycle, indicating superior metabolic flexibility. Both cell sources expressed canonical markers and responded morphologically to 5-azacytidine, yet peri-ovarian cells displayed a richer metabolic palette. These traits may favour their use in cardiac repair.

Decreased non-neurogenic acetylcholine in bone marrow triggers age-related defective stem/progenitor cell homing

Morikawa and colleagues in Nature Communications found that ageing reduces non-neuronal acetylcholine in bone marrow, impairing Chrm5–eNOS signalling, lowering shear stress and

hampering homing of transplanted haematopoietic stem cells. Metabolomic analyses confirmed cholinergic decline, while lineage tracing demonstrated decreased Piezo1 activation in aged vessels. Pharmacological Piezo1 stimulation restored engraftment and survival. The work highlights vascular neurochemical modulation as a target for improving transplantation outcomes in older recipients.

Aerobic and resistance exercise-regulated phosphoproteome and acetylproteome modifications in human skeletal muscle

Pataky and colleagues in Nature Communications reported that twelve weeks of high-intensity interval training remodels the skeletal-muscle acetyl-proteome, especially within mitochondria, whereas resistance training chiefly modifies phosphoproteins in contractile and cytoskeletal machinery. Acute aerobic exercise elicited the most pronounced combined phosphoproteomic and metabolomic responses, including phosphorylation of membrane transporters and translation regulators. These post-translational patterns align with observed gains in endurance and strength. The study furnishes a molecular scaffold for tailoring exercise prescriptions.

Exercise, the Gut Microbiome and Gastrointestinal Diseases: Therapeutic Impact and Molecular Mechanisms.

Hawley and colleagues in Gastroenterology reviewed evidence that regular physical activity enhances gut-microbiota diversity, bolsters host immunity and reduces risk for gastrointestinal disease. The review discusses myokine–microbiota cross-talk, notes that extreme exertion can transiently increase intestinal permeability and calls for integrated meta-omics to define dose–response relationships. The authors propose that targeted exercise programmes could complement microbiome-based therapies. Key gaps include inter-individual variability and causal mechanisms.

Metabolic Regulation of Cell Fate and Tissue Development

Each study in this theme demonstrates that precise metabolic inputs, whether genetic variants, nutrient availability or enzyme activity, direct cellular differentiation in plants, animals and immune systems. By pairing multi-omics with functional interventions, the authors reveal actionable levers for improving milk production, crop quality, immune modulation and assisted reproduction. Metabolite-guided strategies therefore hold promise for diverse biotechnological and therapeutic applications.

Transcriptomic and metabolomic profiles reveal the functions of IGF-1 c.258 A > G synonymous mutation in milk fat content.

Fang and colleagues in Journal of Advanced Research showed that a synonymous IGF-1 c.258 A>G variant reduces milk-fat content in mice by altering hepatic and mammary lipid metabolism. Liver transcriptomics revealed ten-fold higher lipoprotein lipase and marked suppression of Acot3, Eci3, Fasn and Srebp1. Lipidomics confirmed lower triglycerides,

sphingolipids and specific acyl chains in lactating mammary tissue. The data indicate a trans-organ gene-diet interaction that shapes milk composition.

Unraveling the regulatory network of barley grain metabolism through the integrative analysis of multiomics and mQTL

Song and colleagues in Nature Communications integrated metabolomics, transcriptomics and metabolite-QTL mapping to chart 986 metabolites and 1 057 QTLs across six stages of barley-grain development. Co-expression analysis identified transcription factors HvC1-1 and HvMYC-1 as regulators of flavonoid pathways controlling grain colour. Stage-specific metabolite accumulation patterns were anchored to precise genomic loci. The resulting network offers a resource for breeding nutritionally enhanced barley.

Mitochondrial 1-Carbon Metabolism Drives CD34-Lineage Cells to Differentiate Into T Follicular Helper Cells to Form Tertiary Lymphoid Organs in Transplant Arteriosclerosis.

Sun and colleagues in Circulation found that mitochondrial one-carbon metabolism, driven by MTHFD2, propels CD34-lineage $CD4^+$ cells toward a T follicular-helper fate that supports tertiary lymphoid organ formation in transplant arteriosclerosis. Single-cell RNA-seq and metabolomics demonstrated up-regulated serine-driven one-carbon flux during differentiation. Pharmacological or genetic inhibition of MTHFD2 reduced Tfh numbers and vascular remodelling, whereas serine supplementation accelerated differentiation. The study links metabolic flux to immune-cell specification in vascular pathology.

Integrated ultrasensitive metabolomics and single-cell transcriptomics identify crucial regulators of sheep oocyte maturation and early embryo development in vitro

Pan and colleagues in Journal of Advanced Research used ultrasensitive metabolomics and single-cell RNA-seq to discover that betaine and L-carnitine are lacking in sheep oocyte and embryo culture media, limiting developmental competence. Supplementation raised blastocyst formation to 67 percent, promoted fatty-acid oxidation, reduced lipid peroxidation and improved spindle morphology. Creatine emerged as an additional candidate metabolite. These insights refine culture conditions for livestock and clinical embryology.

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The Metabolomist Podcast

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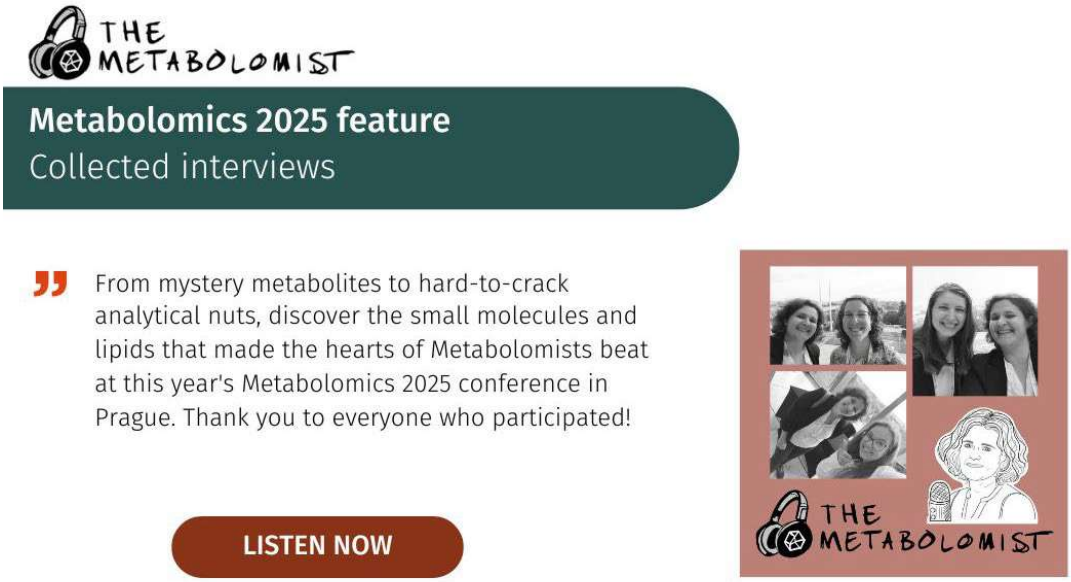

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Metabolomics Events

MANA SODAMeet

August 12, 2025

Venue: Online

The goal of SODA is to provide a community-driven resource of actively-maintained software, test datasets used for software benchmarking, and results produced by software. SODAMeets is a platform where data generators and computational scientists can share their use of software/data. During SODAMeets (every 2 months), two speakers will present on software or data they would like to share with the community, emphasizing how these software/data are used. Speakers will be requested to fill out a form on our SODA website so that we collect

relevant information on these software/data presented.

Join the web seminar

7th Annual Metabolomics Society of North America (MANA) Conference

September 2 - 5, 2025

Venue: Banff, Canada

Start planning for the 7th Annual Conference of the Metabolomics Association of North America (MANA), hosted by Dr. Ian Lewis, and featuring an engaging program developed by the organizers. This year's conference will be hosted in the heart of the Rocky Mountains. Visit the website for program information, speakers, events, registration, awards, and more.

Check for more details

Bits & Bites #5: Bayesian Statistics for Metabolomics

September 11, 2025

Venue: Online

The short course is taught by Dr. Christopher Brydges. This introductory-level session requires JASP (version will be announced before the course) and assumes only basic knowledge of statistics (for example, you know what a t-test and a correlation are); no coding experience is needed.

Short description of the course:
Bayesian statistics are a useful method for estimating effect sizes and testing the strength of evidence in favor of one hypothesis over another - things that p-values and traditional statistics can't do. However, they are under-utilized in metabolomics research. This short course will provide a brief refresher on traditional statistics, teach the basic principles behind Bayesian statistics, learn how to conduct basic Bayesian analysis in JASP, and learn how to report the results in the style of a journal article.

Check for more details

DG5th Annual Metabolomics Society of North America (MANA) Conference

October 1 - 2, 2025

Venue: Hanover, Germany

The DGMet Annual Meeting 2025 will take place at the Fraunhofer Institute for Toxicology and Experimental Medicine Fraunhofer ITEM in Hanover.

Key Topics:
Metabolomics and Nutrition
Exercise & Muscle Metabolism
Computational Metabolomics
Plant Metabolomics
Metabolomics and Lipidomics in Health and Disease

Visit the website for more details

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2025 World Critical Care and Anesthesiology Conference

October 10 - 11, 2025

Venue: Singapore/Hybrid Online

The 9th World Critical Care & Anesthesiology Congress (2025 WCAC) will take place in Singapore, offering both physical and virtual participation options. Speakers and delegates will have the chance to meet international faculty members, enjoy extensive networking sessions and explore the city's landmarks. The congress invites submission of speaker proposals as well as oral and poster presentations on the latest topics in critical care and emergency medicine, anesthesiology and pain medicine, trauma, pediatrics, neurocritical and cardiac critical care, COVID-19 and related subjects.

Check for more details

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Frontiers in Metabolomics & Metabolomic Imaging in Medicine: Challenges & Opportunities

October 16 - 18, 2025

Venue: Italy

This inaugural Metabolomics and Metabolomic Imaging (MMI) workshop is designed for scientists, clinicians, and trainees from academia, healthcare, and industry, who seek to learn and discuss the frontiers of metabolomics in medicine. The central focus of this workshop is medical metabolomics and metabolomic imaging, a burgeoning field with enormous potential for medical applications, particularly in the context of malignant and neurodegenerative diseases, which can present heterogenous systematic metabolic alterations that can only be collectively evaluated by metabolomics.

Learning Outcomes

- Identify technologies used in metabolomics and metabolomic imaging
- Understand the challenges and potential of metabolomics and metabolomic imaging for malignant and neurodegenerative disease studies
- Become familiar with advanced metabolomic data analysis using AI and machine learning
- Expand collaborative networks with metabolomic experts from multiple domains

Check for more details

Metabolomics Jobs

Metabolomics Jobs

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Job Title	Employer	Location	Source

Staff Scientist - Metabolomics	City of Hope	Duarte, CA, USA	City of Hope
Senior Research Scholar - Mass Spectrometry Metabolomics	North Carolina State University	Raleigh, NC, USA	North Carolina State University
Research Associate Principal	Berkeley Lab	Berkeley, CA, USA	Lawrence Berkeley National Laboratory
Metabolomics Associate Director	Botany and Plant Pathology Department at Purdue University	West Lafayette, IN, USA	Botany and Plant Pathology Department at Purdue University
Post Doctoral Fellow Research - American Elderberry Metabolomics (Dr. Lloyd Sumner's Lab)	University of Missouri-Columbia	Columbia, MO, USA	University of Missouri-Columbia
Assistant Professor, Cell Metabolism	University of Saskatchewan	Saskatoon, SK, Canada	University of Saskatchewan
Manager, Quantitative Metabolite Analysis Center	University of California, San Francisco	San Francisco, CA, USA	UC San Francisco

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