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MetaboNews

This month in metabolomics

October, 2025
Vol 15, Issue 10

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

METABOLOMICS SOCIETY

TMIC
The Metabolomics Innovation Centre

This Months Features:
MetaboInterview
Michael Atser

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,

In the UK it is starting to feel autumnal with shorter days, colder temperatures and the colour migration of leaves to glowing reds, oranges and yellows. Change is generally always good and it was great to welcome the new Directors to October's board meeting. Candice Ulmer-Holland was re-elected, and we welcome Anne Bendt (Singapore), Monica Cala (Colombia), Julia Kuligowski (Spain), Kyo Bin Kang (South Korea) and Masanori Arita (Japan). Being a Director is time consuming and I thank all current and new Directors for their commitment and drive.

As previously announced, Metabolomics 2026 will be hosted in late June in Buenos Aires. We wanted to share the *very likely* conference dates of June 21-24, 2026.

Natasa Giallourou completed five years as a Director in September. Natasa has kindly provided some thoughts below of her time as a Director and chair of the Conference committee.

I still vividly remember my first Metabolomics Society meeting in Seattle back in 2018. At the time, I was a new member, excited but unsure of where I fit into the community. That meeting set me on a path: first through the Early Career Members Network (EMN), then onto the Board of Directors, and eventually into the role of Conference Committee Chair. It feels both humbling and full circle to now be looking back on this chapter. When I took over as Chair in 2022, it was a particularly challenging moment. The world was just emerging from the disruptions of COVID-19, and the Valencia meeting was the first in-person conference after two years of virtual gatherings. It was a moment of uncertainty, but it turned into a big success and a reminder of how much this community values being together.

Behind the scenes, the work of the conference committee is wide-ranging: collaborating with scientific chairs and organizing committees to shape the program, working hand-in-hand with our professional organizers at SnapIT to navigate logistics and finances, and ensuring that the Board could focus on strategy rather than day-to-day details. I want to pause here to recognize how critical SnapIT, and especially Leslie LeClaire, have been in this process. Their professionalism, guidance, and dedication have been instrumental in making each meeting not only possible, but successful.

Looking ahead, there are important challenges we cannot ignore. Rising costs of conference organization demand a re-evaluation of our strategy. We must remain creative in finding ways to make meetings financially sustainable, while also ensuring accessibility and inclusivity. Strengthening industry engagement, exploring innovative formats, and continuing to support the next generation of metabolomics scientists will be essential.

As I step away from my role as Conference Committee Chair and from the Board of Directors, I do so with immense gratitude for the colleagues I've worked alongside, the countless volunteers who make the meetings possible, our sponsors whose support has been indispensable, and the community that continues to inspire me. I look forward to joining you all in Argentina in 2026, this time as an attendee without the stress of organizing, and with renewed excitement for what's ahead. Thank you for the trust and support over these past years. It has been an honor.

Finally, mQACC is currently performing a survey on the reporting of concentration data in metabolomics. Please complete the survey below which mQACC assembled to gather data on the processes scientists are currently using to generate and report concentration data. This survey is open for full quantitation and other types of quantitation and so please do complete.

https://www.surveymonkey.com/r/KP8QZH6
YOU TOO CAN BE A PART OF DEFINING THE FUTURE!

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

Early-career Members Network (EMN)

The EMN 2025-2026 committee kicked into action this month, welcoming back returning members as well as new committee members from across the globe. EMN is happy to announce Thomas Dussarrat has been elected as the new treasurer of EMN, while Jayden Lee Roberts has been elected as the new secretary. Breanna Dixon has commenced as the EMN chair. The EMN committee would also like to congratulate our new committee members again, Renata Garbellini Duft, Maria Llambrich, Shauni Loopmans, Luciana Ribeiro da Silva Lima, Dakshat Trivedi, and Carolina Thomaz dos Santos D'Almeida!

Task Groups Corner

Sakda Khoomrung
Mahidol University, Thailand

Mónica Cala
Universidad de los Andes, Columbia

Dear colleagues,

It is a great honor for us to serve as the new **Chair and Co-Chair of the International Affiliations Task Group (IATG)** of the Metabolomics Society. We are deeply grateful to **Dr. Matej Orešič** and **Dr. María Eugenia Monge** for their outstanding leadership and dedication in strengthening our global metabolomics community. Building on their achievements, we are excited to continue advancing meaningful collaborations among national and regional networks worldwide. As many of you know, the affiliations program plays a vital role in connecting the Society with metabolomics communities around the globe—sharing knowledge, coordinating training, and promoting inclusivity across diverse regions.

Over the coming year, our task group will focus on:
- ***Expanding engagement*** with existing affiliate networks and assisting new groups in joining the Society.
- ***Facilitating joint workshops, exchange programs, and regional events*** to enhance visibility and impact.
- ***Establishing structured communication channels*** between affiliates and the Society's leadership to ensure mutual support and shared growth.
- ***Network training*** – fostering knowledge sharing and skill-building among members through collaborative sessions.
- ***Information exchange*** – promoting communication of ongoing projects, opportunities, and updates within the metabolomics community.

With representation spanning every continent, we have an exceptional opportunity to make metabolomics a truly global and collaborative science. We look forward to working closely with affiliate leaders, the Society's Board, and our broader community to build bridges that foster discovery, capacity building, and equitable access to metabolomics resources.

We warmly welcome your ideas and participation—together, let us strengthen the global metabolomics network and ensure that our field continues to thrive through connection, inclusivity, and innovation.

With warm regards,

Dr. Sakda Khoomrung, Chair
Dr. Mónica Cala Molina, Co-Chair
International Affiliations Task Group
Metabolomics Society

October 25, 2025

International Affiliates' Corner

Australian & New Zealand Metabolomics Society
Visit https://anzmetabolomics.org/what-we-do

ANZ Metabolomics Society
Australian and New Zealand Metabolomics Society Inc.

We are pleased to invite you to the **2025 Annual General Meeting of the Australian and New Zealand Metabolomics Society** which will be held **online via Teams**. This AGM is an excellent opportunity for members to reflect on the society's activities over the past year, engage in open discussion and provide feedback on future directions. Please ensure you are subscribed to our mailing list to receive the Teams link closer to the date.

Meeting Details:

- **Date:** 26 November 2025
- **Time:** 11:00 AM AWST / 1:00 PM AEST / 2:00 PM AEDT / 2:30 PM ACDT / 4:00 PM NZDT

This year's AGM will also include **elections** for the following positions:

- President
- Vice President
- Secretary
- Treasurer
- EMCR Representative Lead
- Regional Representatives

All members are welcome to submit nominations for any of these positions via our email: **ANZ_metabolomics_society@outlook.com**.

Réseau Français de Métabolomique et Fluxomique (RFMF)

Visit http://www.rfmf.fr/

RFMF
Réseau Francophone de Métabolomique et Fluxomique

Fifth Edition of the Young Autumn School – French-Speaking Network of Metabolomics and Fluxomics Junior

The **RFMF Junior** is organizing a new edition of its **Young Autumn School**, open to RFMF members under 33 years old. The event will take place **from November 17 to 20, 2025**, at the **Espace Beaulieu, Bordeaux, France**.
This year's program will address key stages of the metabolomics workflow, including:

- Mass spectrometry in metabolomics
- Data pre-processing and processing
- Introduction to ChemFlow statistics
- Metabolomics in the private sector
- MetaNetX annotations
- Modelling and molecular networks

Confirmed speakers include **Pierre Pétriacq, Josep Valls-Fonayet, Alexandre Pons, Benoit Jaillais, Florence Mehl, Marion Brandolini-Bunlon**, and **Sylvain Prigent**.

This edition is organized with the support of our sponsors Thermo Fisher Scientific, Agilent, LECO, Waters, UMR 1332 BFP, and the MetaboHUB-Bordeaux Metabolome Facility.

Please note that the entire school will be conducted in French.

Places are limited – don't miss this opportunity and join us here (deadline is Oct 31st, 2025).

20th Edition of the BBBS Webinar Series – Plant Metabolism and Biochemistry

The **20th BBBS Webinar Series**, organised by **RFMF and RFMF Junior**, will be held on **December 18th, 2025 (3:00-4:30 pm, GMT+2)**.
This edition will focus on **Plant Metabolism and Biochemistry**, chaired by **Téo Hebra** (*Prague, CZ*) and **Pierre Pétriacq (*Bordeaux, FR*),** and will feature a **keynote lecture by Henriette Uthe** (*Leibniz Institute of Plant Biochemistry, Halle, Germany*).

Free access - No registration required - Full program available on the flyer below
Join here: https://meet.goto.com/406078373

Join the 20th RFMF webinar!

18th December 2025, 3-4:30pm (GMT+2)

Plant metabolism and biochemistry

Chaired by Téo Hebra et Pierre Pétriacq

To join the webinar: https://meet.goto.com/406078373

03.00 pm

KEYNOTE Speaker

"Ecometabolomics-Challenges and Visions"

Henriette Uthe
Group Leader Metabolomics Facilities and Chemical Analytics (MetaCom) at Leibniz Institute of Plant Biochemistry (Halle, Germany)

3.45 pm

"Predictive metabolomics to unravel phenotypic traits in pearl millet grains from a Brazilian germplasm panel"

Mariana Pimentel
UMR 1332 Fruit Biology and Pathology, INRAE, Bordeaux University (France)

4.00 pm

"Explore different methods to improve the reproducibility of results and field sampling in metabolomics"

Mazzarine Laboureau
Institute of Biology, Laboratory of Functional Ecology, Neuchatel University (Neuchatel, Switzerland)

4.15 pm

"Deciphering the vanadium-dependent haloperoxidase roles in brown algal model using knock-out mutants and metabolomic analysis"

Eurydice Peti-Jean
Sorbonne Université, CNRS, LBI2M (Roscoff, France)
MNHN, CNRS, MCAM (Paris, France)

4.30 pm

Latin American Metabolic Profiling Society (LAMPS)

Visit https://jwist.github.io/lamps/

Decentralizing Knowledge: The Second School of Integrated Metabolomics, Fortaleza, CE, 2025

In the vibrant city of Fortaleza, Ceará, during the Annual Meeting of the Brazilian Proteomic Society (BrProt), the academic community convened for the Second School of Integrated Metabolomics (SSIM). Held at the Universidade de Fortaleza (UNIFOR) from September 29 to October 3, the event sought to decentralize metabolomics expertise, traditionally concentrated in Brazil's Southeast, and to broaden training opportunities across the North and Northeast regions.

Building on the success of its 2023 debut, the school gathered distinguished instructors such as Professors Marina Amaral (UFRJ), Gisele Canuto (UFBA), Ricardo Silva (FCFRP-USP), Alan Cesar Pilon (IQ-UNESP), and Ian Castro-Gamboa (IQ-UNESP, and LAMPS founding member), for lectures and hands-on sessions fostering dialogue, learning, and technical skill-building. Invited experts Dr. Mariana Fioramonte (Waters) and Dr. Luiz Santos (Thermo Fisher) further enriched the program.

Across two days, participants explored topics from metabolomics in natural products and human health to bioinformatics, data quality, and emerging challenges in Brazilian science. Engaging local researchers and students strengthened institutional ties and promoted a fairer distribution of expertise nationwide.

The event welcomed 75 attendees—students, researchers, and professionals—from across Brazil, Uruguay, and Pakistan, underscoring its global reach. Supported by LAMPS, the School highlighted the value of building sustainable scientific communities beyond borders.

As a special finale, Prof. Peter Dorrestein (UC San Diego), joined the closing session to present new GNPS tools, inspiring participants with a glimpse into the future of community-driven metabolomics.

With the success of this second edition, organizers and participants now look forward to 2027, continuing to advance metabolomics research and collaboration across Brazil.

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MetaboInterview

This MetaboInterview series highlights up-and-comers in the field of Canadian metabolomics, and award winners at the 2025 Canadian Metabolomics Conference

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Mikkey Atser

Mikky is a PhD candidate in Dr. Jim Johnson lab's lab at UBC. He completed his BSc at the University of Saskatchewan, Saskatoon with double honors in Biochemistry and Anatomy & Cell Biology. His undergraduate thesis was completed in the laboratory of Dr. Scot Stone, where he characterized the effect of different fatty acids on DGAT2 co-localization with lipid droplet. His current research focuses on understanding the role of PDK1 in the regulation of glucose and fatty acid metabolism in cardiomyocytes using untargeted tracer metabolomics/lipidomics techniques. In his free time, Mikky enjoys photography, creative writing and debates on why Steph Curry is the greatest basketball player of all time.

1. Could you share your journey into metabolomics and what initially sparked your interest in this field?

Our advent into the field of metabolomics began with a simple question focused on the role of pyruvate dehydrogenase kinase 1(PDK1) in cardiomyocyte metabolism. Our preliminary data showed some novel impact on fat metabolism in hearts. Particularly, fat breakdown was reduced leading to accumulation of fats in mice and cell lines studies following the loss of PDK1. The natural next step for us was to delineate, as much as we could, the mechanism behind this and we guessed that metabolites were responsible for the conductance of this effect. Our interest in metabolomics was sparked by its potential to profile associated metabolites to better understand the mechanism behind this metabolic phenotype.

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

In collaboration with our amazing collaborators, we are currently experimenting with stable isotope-resolved metabolomic approaches to better understand metabolic flux in the context of cardiomyocyte and diabetes research. We are increasingly appreciating that mere metabolite abundances do not paint the entire picture of metabolic pathways.

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3. What excites you most about the potential of metabolomics in your research?

I am most excited by the potential of discovering new mechanisms behind cardiomyocyte substrate preference, thereby increasing our collective understanding of the regulation behind the phenomenon. Particularly, in context of glucose and fatty acids. I am also excited to discover the ramifications of disturbances on metabolism and ultimately, cardiac function.

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4. How is metabolomics research progressing in your country, especially in the context of cardiovascular metabolism and related areas?

I think Canada already has a solid national infrastructure for metabolomics and keeps investing to make it even stronger. The field here is becoming more connected, clinically focused, and technologically advanced. Many universities have state-of-the-art instruments, and we’re increasingly using hybrid targeted and untargeted approaches to find both known and new cardiometabolic biomarkers. There’s also a big push toward lipidomics, mitochondrial and cardiac energetics, and integrating different ‘omics’ layers.

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5. In your experience, what are the primary strengths of metabolomics for uncovering metabolic pathways in complex systems such as cardiomyocytes?

Cardiomyocyte metabolism can be challenging due to the integrative contributions of diverse pathways to maintaining its essential function. The reason this poses a challenge is that a particular metabolic phenotype may be driven by complex interactions between metabolic pathways that would be challenging to decipher with traditional analysis methods, which attempts to isolate a single or relatively pathways for investigation. The primary strength of metabolomics is that its comprehensive nature enables assessment of a wider range of pathways which can be instrumental in exposing novel pathway interactions or improving our appreciation of the downstream impact of certain metabolic perturbations.

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6. What challenges or barriers have you encountered applying metabolomics and proteomics techniques to you research?

I think a challenge I experienced early on was the need for programming languages to analyse the huge datasets. I had never used R previously and I was all of a sudden faced with a complex dataset and was initially unsure of how to begin. I was, however, fortunate to have senior lab members that could lend their expertise and provide guidance on getting started. Another challenge I have experienced is being able to glean confident biological insights from the results. At its core, we are left with a question that asks, “what does this all mean?”. New advancements with different computational tools are helping in this regard but there remain knowledge gaps that need to be addressed.

7. How important is interdisciplinary collaboration in metabolomics research?

Interdisciplinarity lies at the core of metabolomics. From the physicists and engineers that construct the mass spectrometry instruments that we use to the analytical chemists that perform detailed analyte analysis to the computational biologists that develop platforms that aid biological interpretation. Without interdisciplinary collaboration, the entire enterprise of metabolomics falls flat. Our group is constantly collaborating with experts in diverse fields, leveraging their expertise to better understand our biological questions.

8. What technological or methodological advancements do you believe are necessary to further enhance metabolomics studies?

I think there are two key areas of technological advancements. The first would be increasing the confidence and coverage of metabolite annotations from public repositories. The gold standard for metabolite annotation involves the use of known standards for validation which comes at great cost to a lot of researchers, particularly when hundreds of metabolites are in need of validation. Another consequence of improving confident annotation is that we are able to annotate more metabolites from a single mass-spectrometry run, which is meaningful in providing a more comprehensive outlook into biology. The second would be improving integration algorithms with different omics modalities. With the rise of omics approaches, biologists increasingly perform more than one modality but often wander in the wilderness trying to get a comprehensive view of biology. Another room for advancements is in the better understanding of the biological systems being studied. Take urine or plasma, for example, it is incredibly challenging to interpret results from such complex matrices due to the interconnectedness of metabolic pathways across different tissues. A metabolite identified in either urine or plasma can be difficult to determine its tissue of origin, severely limiting our biological interpretations. Advancements of our biological understanding can significantly expand the utility of these kinds of results in therapeutic design.

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Microbiome and metabolome pathways in sleep, neurodevelopment, and infection control

The papers in this section converge on a central idea: the gut ecosystem and its metabolic output are not mere correlates but active participants in host physiology across the lifespan. Experimental and cohort data link microbial composition and core energy pathways, particularly pyruvate metabolism, to complex outcomes such as sleep quality, frailty, and neurodevelopmental behavior. Interventional work underscores that viable microbes carry causal weight in preventing infection recurrence, while targeted probiotics during pregnancy can reshape maternal immunity and offspring neurodevelopmental trajectories. Together, these studies argue for mechanistic specificity over generic "microbiome health," pointing to discriminating taxa, metabolites, and immune mediators that mediate benefit. The translational path now requires rigorous dose–response testing, durable phenotyping, and attention to which benefits require live consortia versus defined microbial products.

Pediococcus acidilactici CCFM1344 intervention during pregnancy prevents maternal high-fat diet-induced autism-like behaviors in early-life offspring mice.

Sun and colleagues in Food Bioscience found that maternal supplementation with Pediococcus acidilactici CCFM1344 (approximately 1×10^9 CFU/day) during a high-fat diet reshaped the maternal gut microbiota, lowering the Firmicutes-to-Bacteroidetes ratio and enriching Alloprevotella and Rikenellaceae RC9. They reported amelioration of hyperactivity and social deficits in juvenile offspring, with partial normalization into adulthood. Maternal fecal metabolomics and cytokines indicated modulation of taurine, L-histidine, TNF-α, IFN-γ, and IL-10. Neonatal brain transcriptomics showed reversal of neuroinflammatory and myelination-related gene dysregulation, including Gfap, Mmp9, Il1b, and Mobp. The findings position pregnancy-specific probiotic intervention as a leverage point for neurodevelopmental health via immunometabolic reprogramming.

Gut metagenome and plasma metabolome profiles in older adults suggest pyruvate metabolism as a link between sleep quality and frailty.

Pu and colleagues in Cell Reports found that poor sleep quality in 1,225 adults aged 62–96 was associated with reduced abundances of potential probiotics such as Faecalibacterium prausnitzii and increased pathobionts. They developed a gut microbiome sleep quality index that inversely associated with frailty and related traits. Multi-omic integration implicated pyruvate metabolism as a key pathway connecting microbial balance to sleep and frailty, alongside microbial pyridoxal 5′-phosphate biosynthesis. Specific microbial features, including F. prausnitzii, tracked with plasma metabolites along this axis. The study provides a data-rich framework for prospective testing of microbiome-metabolome interventions to mitigate frailty.

Effects of lyophilised faecal filtrate compared with lyophilised donor stool on Clostridioides difficile recurrence: a multicentre, randomised, double-blinded, non-inferiority trial.

Kao and colleagues in The Lancet Gastroenterology & Hepatology showed that a sterile, lyophilised faecal filtrate lacking live bacteria did not meet non-inferiority to lyophilised donor stool for preventing recurrence at 8 weeks. In per-protocol analysis, 65% of filtrate recipients and 88% of donor-stool recipients avoided recurrence, a −23% difference that crossed the pre-specified margin. Safety profiles were acceptable, with expected gastrointestinal adverse events. The trial was stopped at interim analysis for failure to show non-inferiority. These data reinforce that live microbes are pivotal to the clinical efficacy of faecal microbiota transplantation in recurrent C. difficile infection.

Natural products and traditional medicines tracked by metabolomics

These studies exemplify how modern metabolomics, allied to network pharmacology and classical pathology, can deconstruct multi-component therapeutics. Despite distinct indications, including sepsis-associated intestinal injury, pulmonary ground-glass nodules, skin homeostasis, and migraine, the mechanistic motifs repeat: attenuation of inflammatory signalling, correction of glycolytic and mitochondrial metabolism, and modulation of barrier function and neurotransmission. Methodologically, the field is maturing from descriptive metabolite shifts to pathway-level validation with targeted protein and gene assays, and, critically, to randomized trials. The imperative now is standardization of botanical composition and dose, resolution of batch-to-batch chemistry, and quantitative linking of exposure to clinical effect sizes. Such discipline will help separate pharmacologically active signatures from background nutraceutical noise.

Metabolomics-guided analysis combined with network pharmacology and molecular simulations reveals the mechanism of JHT in treating septic intestinal dysfunction.

Deng and colleagues in Journal of Ethnopharmacology showed that Jinhong Tang mitigated sepsis-induced intestinal dysfunction through modulation of the AMPK/SIRT1/NF-κB axis. Untargeted metabolomics demonstrated reversal of glycolysis and TCA-cycle disruptions and normalization of tryptophan metabolism. In a murine cecal ligation and puncture model, JHT reduced serum TNF-α, IL-6, and IL-1β, while histology showed preserved mucosal architecture. Western blots confirmed increased AMPK and SIRT1 and reduced phosphorylated NF-κB, with downregulation of glycolytic enzymes PFKFB3 and LDHA. The integrated approach supports a multi-target, energy-metabolism–centric mechanism in sepsis-associated intestinal injury.

Effects of herbal medicine on clinical characteristics and biological markers in pulmonary pure ground-glass nodules: study protocol for a multicenter randomized triple-blind controlled trial.

Tan and colleagues in Frontiers in Medicine designed a randomized, triple-blind, placebo-controlled multicenter trial to test whether Chuanjie Granules can reduce the size or risk profile of stable pulmonary pure ground-glass nodules. The trial plans to enroll 172 radiologically diagnosed patients, randomizing to active therapy or placebo for three months with one year of follow-up. The primary endpoint is change in maximal nodule diameter, with secondary endpoints including density, malignancy risk, and patient-reported outcomes. Mechanistic profiling will integrate oral and gut microbiota 16S rRNA sequencing with GC–MS-based metabolomics. The study is positioned to provide first high-quality efficacy and mechanism data for early intervention in pGGNs.

Integrative analysis by targeted metabolomics revealed the regulatory function of donkey oil on skin metabolites.

Li and colleagues in Frontiers in Medicine found that 28 days of topical donkey oil altered organic acids, amino acids and derivatives, and free fatty acids in both healthy and inflammatory skin. Shared shifts included 4-hydroxyphenylacetic acid, 5-hydroxytryptamine, tryptophan, and 5-aminovaleric acid, alongside medium-chain and long-chain fatty acids. Pathway annotation implicated aromatic amino acid metabolism and fatty acid biosynthesis as key routes supporting skin homeostasis. Distinct metabolite patterns were observed between healthy and inflamed skin, with several overlapping nodes suggesting common regulatory targets. The results support donkey oil as a candidate multifunctional ingredient for maintaining epidermal metabolic balance.

Multi-omics analysis reveals Angelica dahurica radix extract alleviates migraine in rats via gut microbiota–metabolome–gut–brain axis regulation.

Lian and colleagues in Frontiers in Pharmacology showed that Baizhi extract reduced nitroglycerin-induced migraine behaviors and normalized neurotransmitter and inflammatory markers in plasma and brain. The intervention restored intestinal barrier proteins Occludin and ZO-1 and reduced colonic inflammation. 16S rRNA sequencing revealed enrichment of Firmicutes and beneficial genera such as Lactobacillus, with decreases in Bacteroidetes. Serum metabolomics highlighted tryptophan metabolism and mitochondrial arginine–proline pathways that regulate serotonin and nitric oxide. The data support a microbiota-modulating, barrier-stabilizing mechanism that intersects neurovascular mediators, including CGRP1 signalling.

Cancer metabolism and metabolomic diagnostics

This set pairs molecular drivers with metabolic phenotypes to illuminate both mechanism and translation. Targeted perturbation of KISS1 signalling in triple-negative breast cancer and identification of MFSD12 as a PLAGL2-regulated oncogene in bladder cancer reveal tractable axes that remodel apoptosis, epithelial–mesenchymal programs, and metabolic states. On the diagnostic front, matrix-engineered LDI–MS of urine delivers fast, noninvasive, multiclass discrimination across urologic cancers, moving metabolic fingerprinting toward clinical utility. Foundational steroidogenic maps across human and mouse cell models provide the necessary context to select appropriate in vitro systems and interpret endocrine metabolites that often confound tumor readouts. The common thread is disciplined cross-validation across transcriptomics, proteomics, and metabolomics to separate signal from artefact.

Exogenous kisspeptin-10 treatment shows pleiotropy via induction of KISS1 expression, metastasis suppression, and promotes apoptosis in triple-negative breast cancer.

Shah and colleagues in Scientific Reports found that Kisspeptin-10 reduced viability and migration in MDA-MB-231 and MDA-MB-468 cells while upregulating KISS1, indicating a positive feedback loop. They observed EMT reversal with increased E-cadherin and β-catenin and decreased N-cadherin, CD44, and vimentin. Pro-apoptotic genes (CASP3, CASP8, CASP9, and BAX) were induced and BCL2 was suppressed, consistent with activation of apoptotic pathways. Metabolomics revealed pathway shifts linked to apoptosis, anti-angiogenesis, and redox homeostasis. In silico analyses showed lower KISS1 in metastatic TNBC and associated higher GATA2/CASP9 expression with improved survival, supporting therapeutic potential.

MFSD12, transcriptionally regulated by PLAGL2, promotes bladder cancer progression.

He and colleagues in Communications Biology showed that MFSD12 acts as an oncogene in bladder cancer, with elevated expression in patient datasets and cell lines. Knockdown inhibited proliferation, migration, and invasion and induced G1 cell-cycle arrest. In vivo, silencing MFSD12 reduced lung metastases and xenograft growth. Omics profiling of MFSD12-overexpressing cells delineated downstream pathways, while reporter and ChIP–PCR assays demonstrated direct transcriptional activation by PLAGL2. The PLAGL2–MFSD12 axis emerges as a candidate target for therapeutics and biomarker development.

Hollow Dodecahedral Nanocages for Reliable Multi-Level Differentiation of Urological Cancers through Non-Invasive Metabolic Fingerprinting.

Zhang and colleagues in Analytical Chemistry found that trimetallic oxide nanocages function as a high-performance LDI–MS matrix to profile urine metabolites within seconds. The approach enabled multiclass discrimination of bladder, prostate, and renal cancers, achieving AUCs near 0.94 in training and testing. A nine-feature panel (UC-D9) retained high classification performance with simplified implementation. The nanocage matrix reduced background and improved ionization stability, supporting throughput and reproducibility. Pathway analysis linked selected features to cancer-relevant metabolic mechanisms, suggesting translational potential for noninvasive triage.

Characterization of Steroid Metabolic Pathways in Established Human and Mouse Cell Models.

du Toit and colleagues in the International Journal of Molecular Sciences found distinct steroidogenic outputs across adrenal, placental, and gonadal cell lines under varied conditions. They reported differences in mineralocorticoid and glucocorticoid production between human adrenal models and between species, and identified unconventional hydroxylated progesterone metabolites most abundant in MA-10 cells. 11-oxy androgens were prominent in H295R/H295A and MA-10, while placental models showed high pregnenolone and progesterone with limited hydroxylated progesterones. Classical androgen levels were comparable in H295R and MA-10, highlighting model choice implications. Detailed protocols and comprehensive profiles provide a practical guide for in vitro steroidogenesis studies relevant to cancer endocrinology.

Fermentation, flavor, and functional nutrition metabolomics

Food systems metabolomics is moving beyond catalogues to actionable levers that shape flavor, quality, shelf life, and host resilience. Across dairy and fruit fermentations, time-resolved microbial succession aligns with amino acid and branched-chain pathways that define sensory inflection points. High-coverage volatilome databases for staple crops enable cultivar differentiation and standardized flavor benchmarking. Functional nutrition is not an abstraction: dietary taurine supplementation increases survival in pathogen challenge while reshaping microbial ecology and tempering host inflammation. The next step is to link metabolite shifts to blinded sensory panels and field-scale outcomes to support process control and regulatory acceptance.

Microbial dynamics and metabolic changes during Qula fermentation from skimmed yak milk.

Liang and colleagues in Food Bioscience found that raw yak milk had the highest bacterial diversity, while the 8-hour fermentation stage showed the lowest bacterial relative abundance and marked metabolic reprogramming. They identified 65 differential metabolites across five stages, including organic acids and lipid-like molecules, with branched-chain amino acid biosynthesis tightly linked to the 8-hour stage that shapes quality. Fungal diversity peaked in dried Qula, and integrated analyses highlighted five core genera, including Streptococcus and Lactobacillus. Microbe–metabolite correlations delineated functional consortia that track key flavor trajectories. The work delivers the first comprehensive view of fungal dynamics in Qula and actionable markers for flavor control.

Dual-Ionization SPME-GC-HRMS Metabolomic Profiling of Broccoli Volatiles for the Construction of a Broccoli Metabolic Database.

Song and colleagues in Molecules showed that a pooled-sample, dual-ionization GC–HRMS workflow captured 206 volatile compounds across nine classes from 191 cultivars. Thirty-seven compounds were confirmed via synchronized chemical ionization, and 187 were observed in at least one of seven validation cultivars. Thirty-eight VOCs formed a conserved core volatilome across all cultivars. Principal component analysis separated cultivars by VOC profiles, and freeze-dried tissue proved suitable for reproducible large-scale work. The resulting database is a resource for Brassica flavor research, cultivar selection, and environmental response studies.

Two lactic acid bacteria strains isolated from naturally fermented foods improves physicochemical quality, antioxidant capacity, shelf life stability and metabolic profiles of Dangshan pear (Pyrus spp.) juice.

Jiang and colleagues in Food Research International found that Lactiplantibacillus plantarum and Lacticaseibacillus paracasei adapted to pear juice, converting sugars to organic acids and lowering pH from 5.37 to 3.59. Fermentation reduced stone cell mass and particle size, improved antioxidant capacity, and extended shelf stability. Untargeted metabolomics mapped 343 differential metabolites enriched in metabolism and amino acid biosynthesis. Metabolites such as D-phenyllactic acid, N-lactoyl-phenylalanine, and indole-3-lactic acid were implicated in stability and functional attributes. Both single and mixed cultures provided quality gains with distinct metabolic footprints.

Identification of taurine as a resistance-associated metabolite against Aeromonas salmonicida and its protective, immune-regulatory, and microbiota-shaping effects in turbot (Scophthalmus maximus).

Pereiro and colleagues in Aquaculture found taurine-linked metabolites enriched in resistant fish families and identified 5-L-glutamyl-taurine as protective in zebrafish larval screens. Due to cost, taurine and L-glutamic acid were tested and improved survival against Aeromonas infection. In turbot, dietary taurine at 1.5% increased survival by 34% despite higher early bacterial loads. Taurine reshaped intestinal microbiota, reducing alpha diversity with expansion of Vibrionaceae and Marinobacteraceae, and dampened early inflammatory responses on RNA-Seq. The results support taurine supplementation as a practical, environmentally compatible strategy for aquaculture disease resilience.

Systems and clinical metabolomics in aging, ischemia, risk prediction, and pre-analytics

The studies here span bench to bedside, mapping how metabolic networks shift with aging, ischemia–reperfusion, and environmental exposures, and how these signals can be measured rigorously and used clinically. An organ-spanning atlas reveals conserved age effects in nucleotide and redox metabolism, while porcine transplantation work pinpoints the timing and pathways of graft injury. Cardiovascular risk prediction gains a modest but real improvement from an objective plasma fatty-acid ratio, a reminder that diet-quality biomarkers can augment algorithms. Pre-analytical work shows that low-cost microsampling is fit for purpose for most analytes, reducing barriers to decentralized studies. A cellular model study of radiofrequency exposure adds a complementary note, highlighting cell type–specific susceptibilities and candidate energy-currency readouts.

Differential metabolic responses of mouse Leydig and spermatogonia cells to radiofrequency electromagnetic field exposure.

Miao and colleagues in Frontiers in Public Health showed that continuous RF-EMF exposure had a stronger metabolic impact on Leydig TM3 cells than intermittent exposure, altering amino acid metabolism, the TCA cycle, ABC transporters, bile secretion, and glutathione pathways. Intermittent exposure predominantly affected fatty acyls and purine nucleosides, with enrichment in purine and unsaturated fatty-acid metabolism. GC-1 spermatogonia cells were less sensitive overall. Both exposure modes perturbed purine metabolism and lysine degradation in TM3 cells, implicating ADP level changes as a candidate exposure signature. ELISA assays supported glutathione perturbations, consistent with redox stress.

The polyunsaturated-to-monounsaturated fatty acid ratio and cardiovascular risk prediction: a prospective cohort study of 183,237 adults.

Sun and colleagues in Lipids in Health and Disease found that adding the plasma PUFA/MUFA ratio to the SCORE2 algorithm produced a statistically significant improvement in predicting 10-year major adverse cardiovascular events. In an independent validation set, the C-index increased from 0.740 to 0.744, with significant net reclassification improvement and integrated discrimination improvement. Higher PUFA/MUFA ratios associated with lower event risk. Calibration remained strong for both models. The work positions PUFA/MUFA as an objective dietary fat–quality biomarker to complement risk tools, pending cost-effectiveness analyses.

Quantitative comparison of whole blood, plasma and serum metabolomes across different blood collection methods.

Zubkowski and colleagues in Metabolomics showed that fresh whole blood has a distinct metabolite profile from plasma and serum, regardless of collection method. When comparing identical biofluids, capillary fingerstick, microblade, and venous draws produced nearly identical profiles across 142 quantified metabolites. Plasma and serum differed in only two metabolites, sarcosine and pyruvate. Body location and peripheral source had minimal impact on metabolite composition. The study supports adoption of inexpensive microsampling devices for quantitative metabolomics, enabling broader clinical and field applications.

Metabolic changes during cold ischemic preservation and reperfusion in porcine lung transplants.

Liang and colleagues in the American Journal of Transplantation found time-dependent metabolic alterations during cold storage and marked shifts upon reperfusion. Lungs subjected to 30 hours of cold ischemia showed significant changes in carbohydrate and amino acid pathways, consumption of energy substrates, and reductions in antioxidants during reperfusion. Donor lungs after brain death with 24 hours of cold storage exhibited some similar trends but distinct reductions in lysophospholipids after reperfusion. An ex vivo perfusion platform followed by transplantation and short reperfusion enabled precise temporal mapping of injury metabolism. The results highlight targets for improving preservation strategies and early post-transplant care.

Ten mouse organs proteome and metabolome atlas from adult to aging.

Wang and colleagues in Genome Medicine found conserved and organ-specific molecular trajectories across brain, heart, intestine, kidney, liver, lung, muscle, skin, spleen, and stomach from 4 to 20 months of age. They quantified 14,763 protein groups and 3,779 metabolites, identifying 18 proteins with consistent age-related changes and enrichment of humoral immune response as a dominant driver. Key metabolites, including NAD+, inosine, xanthine, and hypoxanthine, shifted across multiple organs. Pathway analyses pointed to coordinated alterations in purine, pyrimidine, riboflavin, and nicotinate/nicotinamide metabolism. The atlas furnishes a foundational resource for early-warning biomarkers and targeted interventions in aging biology.

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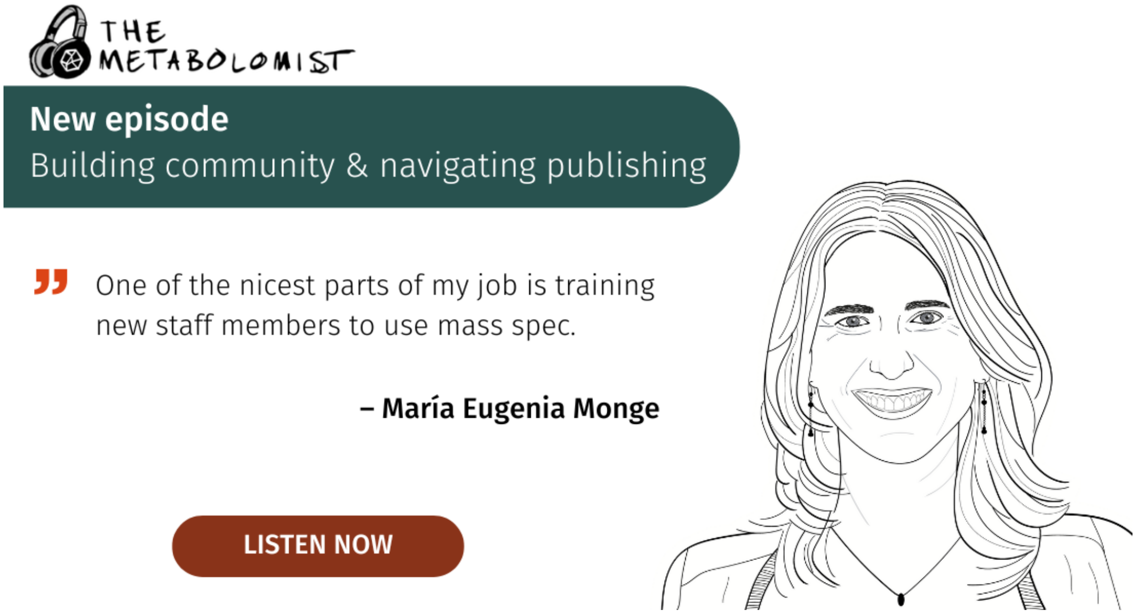
The Metabolomist Podcast



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Metabolomics Events

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Introduction to Applying LC-MS in Untargeted Metabolomics Course

November 3 - 5, 2025

Venue: Online

The course introduces attendees to the metabolomics workflow and applying LC-MS in metabolomics. It is designed to develop knowledge, skills and experience in small group session with hands-on experience in sample preparation, LC-MS data acquisition (MS and MS/MS), data analysis and metabolite annotation and identification. The course is aimed at individuals with minimal knowledge of LC-MS based metabolomics and only a small number of attendees are accepted on each course to maximise opportunities for laboratory experience and interaction with instructors.

Check for more details

Bits & Bites #8: What is your Metabolomics Data Telling You? Data Interpretation for Biomedical Scientists and Clinicians

November 6, 2025

Venue: Online

The short course is taught by Dr. Oliver Fiehn, UC Davis and requires no prior programming experience. Participants will learn how to interpret metabolomics data, generate hypotheses, and integrate biological and metabolomics datasets using freely available online resources. The course also offers hands-on tips on curation, data mapping, and visualization.

Check for more details

Imperial College London Metabolomics training

course: Hands-on Data Analysis for Metabolic Profiling

December 1 - 5, 2025

Venue: Online

This 5 day course provides a comprehensive overview of data analysis for metabolic profiling studies focusing on data from NMR spectroscopy and Liquid Chromatography-Mass Spectrometry. It combines lectures and tutorial sessions using open source software to ensure a thorough understanding of the theory and practical applications.

Visit the website for more details

EBRAINS Summit 2025

December 8 - 11, 2025

Venue: Brussels

The EBRAINS Summit 2025 will feature scientific talks with leading experts, a public day, a science slam, poster sessions, and a science market exhibition - all focused on advancing digital neuroscience. This year's programme includes a special joint day with the International Neuroinformatics Coordinating Facility (INCF).

Exhibitors will have the opportunity to showcase their work and engage with Europe's neuroscience and brain tech community.

Visit the website for more details

MANA SODAMeet

December 9, 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

Metabolomics in Life Science 2026

January 27 - 28, 2026

Venue: Vävenscenen, Umeå, Sweden

Umeå University invites participants to explore the latest NMR- and MS-based metabolomics research from Sweden, the Nordics, and beyond. The conference will cover topics such as clinical and precision medicine, plant metabolomics, spatial and single-cell metabolomics, multi-omics, and computational/AI applications.

The program features six keynote speakers from leading institutions and an industry exhibition showcasing cutting-edge technologies and services in metabolomics research.

Early bird registration deadline: **December 8, 2025**
Abstract submission deadline for poster presentations: **December 8, 2025**

Learn more and register here

World Critical Care & Anesthesiology Conference 2026 (WCAC26)

March 6 - 7, 2026

Venue: Bangkok, Thailand

The 10th WCAC brings together professionals from around the globe to advance knowledge and expertise in Critical Care Medicine and Anesthesiology. Hosted in partnership with leading societies, this hybrid event offers an essential platform for multidisciplinary exchange, case discussions, and research in critical care and perioperative medicine. The conference’s theme, “Advancing Patient Care in a Rapidly Evolving Field,” reflects its commitment to sharing impactful insights and innovative solutions to complex clinical challenges. The event rotates worldwide and fosters collaboration among surgical and medical teams dedicated to improving patient outcomes.

Visit the website for more details

2026 Prague Metabolism and Signaling Symposium

June 24 - 27, 2026

Venue: Prague, Czech Republic

Discover the latest breakthroughs at the intersection of metabolism and signal transduction research. This international meeting in Prague features sessions on energy and metabolite sensing, organellar signaling, autophagy, aging, cancer, immune and stem cell metabolism, and host-pathogen interactions. Expect a diverse lineup of about 30 speakers, including two keynote addresses, covering topics from human studies to structural biology. The event also offers networking opportunities and the chance to experience beautiful Prague.

Check for more details

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Job Title	Employer	Location	Source
Research Scientist 4	G-27 Division of Environmental Health Sciences	Albany, New York, USA	Metabolomics Society
Postdoctoral Fellow – Metabolomics, Proteomics, Exposomics,	Metabolomics & Systems Biology Laboratory (Huan Lab), Department of	Vancouver, BC, Canada	University of British Columbia

and Biology	Chemistry, University of British Columbia		
Post-Doctoral Research Fellow	MITACS and Nova Medical Testing Inc	Edmonton, AB, Canada	[University of Alberta]()
Principal Scientist, Metabolomics	Novartis	Cambridge, MA, USA	[Novartis]()
Research Associate II - Metabolomics	Broad Institute of MIT and Harvard	Cambridge, MA, USA	[Broad Institute]()
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]()
Post Doctoral Fellow Research - American Elderberry Metabolomics (Dr. Lloyd Sumner's Lab)	University of Missouri-Columbia	Columbia, MO, USA	[University of Missouri-Columbia]()
Manager, Quantitative Metabolite Analysis Center	University of California, San Francisco	San Francisco, CA, USA	[UC San Francisco]()

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