MetaboNews

This month in metabolomics

May, 2026
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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

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METABOLOMICS SOCIETY

METABOLOMICS SOCIETY
EARLY- CAREER MEMBERS NETWORK

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

Conference Corner

See you in Argentina!
A few important updates for Metabolomics 2026, as we are busy planning the annual conference of the Metabolomics Society.

June 21 – 24, 2026
www.metabolomics2026.org

Register Today!
Take advantage of the early registration rates – complete your registration online by May 20. You can view the **registration fees** and important dates on the website.

Additional discounts apply if you sign up for Society membership first, then register at the discounted Member conference rate.

Agenda Available
The agenda has been updated with sessions and workshops. **Take a look!**

Last Call for Posters – Extended!
Abstract submission is still open – plan to submit your work soon. The deadline for poster abstracts has been extended to May 24!

If you submitted an abstract in the Oral or Poster category, you should have received your acceptance status. Contact us if you have questions. info@metabolomicssociety.org

Workshops
We're hosting an assortment of workshop on Sunday, June 21. The complete listing is available online. Keep in mind that several workshops are dedicated to hands-on training, they will have limited capacity.

Workshop sign-up will open this week, spots are available on a first-come, first serve basis. You can also sign-up to attend a sponsor presentation over lunch.

Plan Your Trip to Buenos Aires
Buenos Aires is an exciting destination, full of culture, character, and spice! Make the most of your time in this vibrant city – consider planning a walking tour or visiting some of the sites. Visit the **Local Information** page online for suggestions. There is a very helpful "Buenos Aires Highlights" pdf document at the top of the page.

Visa Information
Now is the time to apply for an Argentine tourist visa if required for your country. You may need to submit an official Invitation Letter for visa purposes, which is managed through an electronic TAD system. **Review complete details and fees here.**

Members Corner

Board of Directors

Dear Metabolomics Society Members and metabolomics friends,

The continued efforts to organise the annual conference in Buenos Aires in late June are reaping rewards. The Scientific Organising Committee has worked hard with all the high-quality abstracts to develop a scientific programme which will interest all. The full programme will be available soon. As President, it is great to see the high diversity in speakers in relation to geography, gender and career which is something we are working very hard to achieve. For those unsuccessful in being awarded an oral presentation, do not be disheartened and ensure you present your work as a poster at the conference. One of my favourite things to do at the annual conferences is to walk around and read them when they are not so busy.

Do support the conference and Metabolomics Society by attending - all information on the conference is available at https://www.metabolomics2026.org/

I spoke last month about the Metabolomics Society representing and supporting the metabolomics community globally and to ensure there is a society for all in the years and decades to come. The Directors have been discussing routes to ensure financial sustainability in the future while continuing to ensure the membership are supported. A number of options are being assessed and we of course need your support through your membership. Please do renew memberships every year, membership will be required to access some resources in the future for example. We are also working to ensure conferences are cost-neutral at a minimum and some of these will be observed in Argentina.

All the very best,

Warwick (Rick) Dunn, University of Liverpool, UK
President, Metabolomics Society

Early-career Members Network (EMN)

EMN Webinars

May EMN Webinar — Register Now!
The EMN committee welcomes **Dr. Fidele Tugizimana** for the May webinar entitled “Beyond the Spray: Decoding Biostimulant Modes of Action with Computational Metabolomics”. The webinar is taking place on Friday May 29th 15:00 (SAST)/ 13:00 UTC.

Register here: https://zoom.us/webinar/register/WN_WNsDW8gZRAaM56-2Thi1RA

EMN Virtual Networking Event
The EMN committee extends its gratitude to speakers **Prof. Elaine Holmes, Dr. Anne Bendt, Assoc. Prof. Kyo Bin Kang and Asst. Prof. Won Dong Lee** for their contribution to the 2026 Virtual Networking Event. The event recording is available on the MetSoc website:
https://metabolomicssociety.org/resources/multimedia/emn-webinars-2026

International Affiliates Corner

Korea Metabolomics Society (KoMetS)

Visit http://komets.or.kr/english05.html

KoMetS 2026 Annual Meeting Successfully Concluded

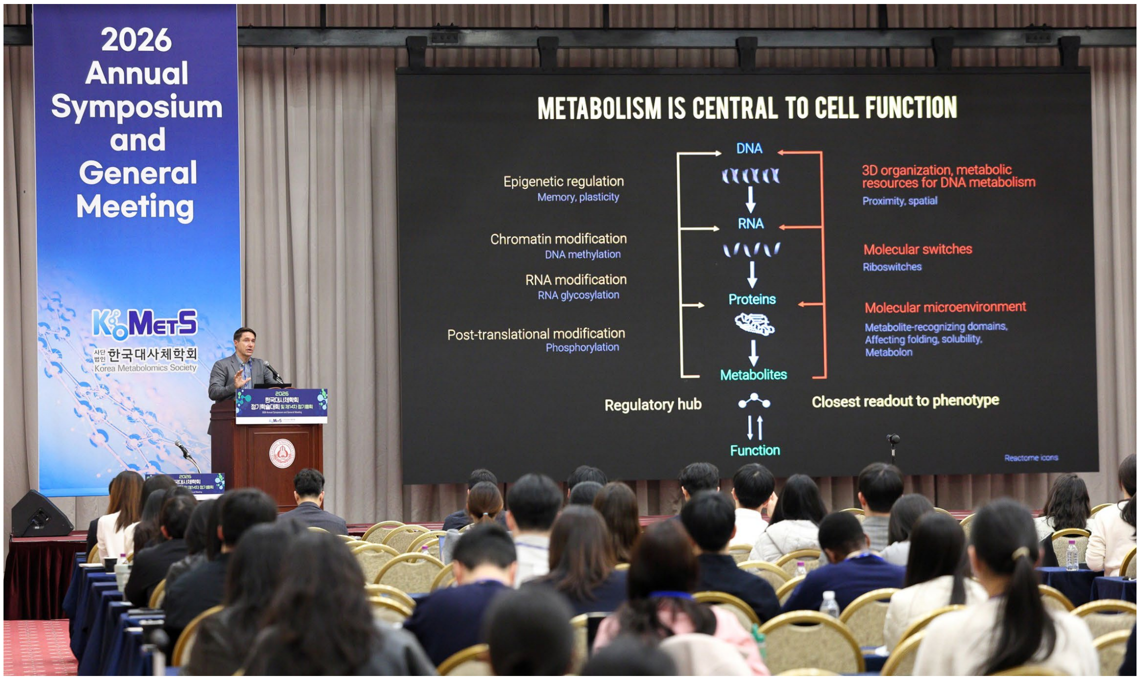
The 2026 Annual Symposium of the Korea Metabolomics Society (KoMetS) and the 14th General Meeting, held **from April 1 to 3, 2026**, at the Sejong University Convention Center in Seoul, was successfully concluded.

Approximately **600 participants** attended this year's meeting, creating a vibrant platform to share the latest advances and innovations in metabolomics**. A total of 40 distinguished speakers contributed to the scientific program.** In particular, the plenary lectures by **Prof. Ron M.A. Heeren** (Maastricht University, the Netherlands) **and Prof. Theodore Alexandrov** (University of California San Diego, USA) provided insightful perspectives on mass spectrometry–based imaging and advanced data interpretation.

On the first day, the **MZmine workshop**, organized in collaboration with **the Tomáš Pluskal group** from IOCB Prague, the Czech Republic, was held with great enthusiasm. The workshop offered valuable hands-on experience in data analysis and fostered deeper interaction among participants. In addition, **136 poster presentations** showcased a wide range of research achievements. Expanded sessions for early-career researchers and students highlighted innovative ideas and emerging talents, offering a glimpse into the future of metabolomics.

This meeting provided an important opportunity to explore emerging research directions at the intersection of metabolomics, artificial intelligence, and multidisciplinary approaches across clinical, pharmaceutical, food, plant, microbial and environmental sciences.

We sincerely thank all organizing committee members, speakers, session chairs, sponsors, and participants for their invaluable contributions. We look forward to your continued support and engagement with the Korea Metabolomics Society.



Latin American Metabolic Profiling Society (LAMPS)

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

LAMPS grants Seven Travel Awards to Support the Next Generation of Metabolomics researchers in Latin America

The Latin American Metabolic Profiling Society (LAMPS) is pleased to announce the awarding of **seven early career LAMPS members residing and studying/working in Latin American countries.**

The Travel Grant aims at supporting emerging talent and strengthening the future of a growing metabolomics community across the region. Proof of this growth, and certainly enthusiasm, was the number of applications received.

This initiative reflects LAMPS' continued commitment to fostering scientific excellence, promoting inclusion, and expanding opportunities for students and early-career researchers in Latin America. More than financial support, this effort represents a clear commitment to people, ideas, and regional development. Each scholarship is an invitation to grow, to exchange knowledge across borders, and to contribute to the advancement of metabolomics in ways that are both scientifically rigorous and socially meaningful.
LAMPS warmly congratulates the selected awardees and celebrates this important step toward building a stronger and more integrated Latin American metabolomics network. Supporting young scientists today means shaping the scientific community we want to see tomorrow: diverse, engaged, and prepared to address complex challenges through cooperation and excellence.

Congratulations to:

- Nicolás Zabalegui Argentina
- Ana Júlia Silva Moreira Brazil
- Hanna Carvalho de Sá Brazil
- Maximiliano José Ramm Montiel Chile
- Juan David Dereix Restrepo Colombia
- Vanessa Jessenia Mayorga Martino Perú
- Ignacio Migues Borghini Uruguay

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METABOLOMICS
ASSOCIATION OF
NORTH AMERICA

MANA 2026

UC DAVIS, CALIFORNIA
SEPTEMBER 8-11

SHARE IDEAS, SPARK COLLABORATIONS,
ADVANCE SCIENCE, BUILD NETWORKS

MetaboInterview

Dr. Benjamin Bourrie

Dr. Bourrie is a microbial ecologist with a particular interest in food fermentation. His research investigates the role of microbial interactions in shaping traditional fermented foods and their qualities. To answer these questions, Dr. Bourrie utilizes a combination of genomics, metabolomics, and synthetic microbial communities in his research. Current research projects include improving the cholesterol-lowering properties of kefir through the use of novel starter cultures and fermentation techniques as well as examining how microbial community dynamics influence flavour profiles in spontaneous beer fermentations.

How did your background in microbial ecology lead you to incorporate metabolomics into your research on fermented foods?

Metabolites are what makes food smell and taste the way it does. In fermented foods, metabolites represent the end products of all the complex interactions and community dynamics that occur during fermentation. By incorporating metabolomics into this work, we can gain a more complete understanding of the end result of these interactions. Metabolomics also allows us to learn more about how differences in microbial communities or fermentation parameters impacts important flavour compounds, leading to informed and targeted strategies for improving food quality and flavour. Since incorporating metabolomics into my work, we have been able to generate some really exciting results and ask much more targeted questions.

Reflecting on your career, what is the most valuable piece of advice you would give to a new researcher looking to combine metabolomics with microbial ecology or food science?

Collaborate! I am not a metabolomics expert by any means, but I am lucky to have fantastic collaborators that I can work with to make sure that we are using the best techniques and analyses possible to answer the questions we have. I collaborate extensively in my work and believe that this allows me to answer questions that neither group would be able to on their own.

How has cross-disciplinary collaboration — across microbiology, food science, sensory science, and genomics — shaped how you approach your research questions?

I think that collaboration is a key component of science. Working with experts in other fields allows us to more effectively integrate these fields into our research and better answer the questions that we are interested in. I work with a number of collaborators across metabolomics, sensory science, and genomics and I know that these collaborations have improved the quality of research that I conduct and have allowed me to pursue avenues of research that would not have been possible for me otherwise.

What role do you see for artificial intelligence and machine learning in metabolomics, particularly in linking microbial community dynamics to metabolite profiles and sensory outcomes?

I think that with the decrease in sequencing and metabolomics costs we are going to continue to see increases in the size of datasets generated. This, along with the advent of improved metabolic modelling software presents some interesting possibilities for the use of AI and machine learning to utilize mult-omics data sets to improve metabolic predictions based on specific microbial populations and fermentation conditions. These types of tools can prove incredibly valuable in the development of novel starter culture mixtures, particularly when trying to replicate complex spontaneous fermentations or design for desired metabolic outcomes. This could lead to the creation of entirely new fermented foods, while improving existing foods as well.

Your work on spontaneous beer fermentation uses metabolomics to understand how sporadic yeast species like *Pichia fermentans* influence community metabolism and aroma. How did metabolomics help reveal what genomics or microbial enumeration alone couldn't?

Tools like genomics, transcriptomics, and classical microbiological techniques are valuable for understanding what is going on with the microbial populations present in the food but they don’t tell us much about potential differences in the aroma or flavour profile of the food itself. While gene expression can give us hints, there is not always a direct 1:1 correlation between the expression of a gene and the production of a specific metabolite associated with that gene. By using untargeted metabolomics alongside genomic and other microbiological analyses, we were able to identify specific yeasts that were associated with increases in important compounds associated with floral aromas in beer. This allowed us to follow up with quantitative methods to confirm that there were differences in the levels of these compounds, as well as sensory analysis which showed that these differences actually translated into consumer perception of the product.

Your research spans both beer fermentation and kefir's cholesterol-lowering properties. How does your metabolomics approach differ between those two applications, and are there common threads?

At its core, the approach for both of these questions is the same: “what happens to the metabolites present in this food when we change the microbes present in the fermentation?” however, the specific way we go about answering this question is different. With beer, we are largely interested in the flavour and sensory characteristics of the product, which leads us to look at the volatile compounds present often using GCxGC-TOFMS and untargeted approaches. For health benefits associated with fermented foods, many of these are associated with bioactive peptides that are formed during fermentation. This necessitates the use of methods such as LC-MS and fully quantitative analysis so we can determine concentrations and potential dosage necessary for the observed benefits. This makes it easier for us to test the compounds themselves as we have a clear idea of the doses we need to test.

Sensory analysis played a role in your beer fermentation work alongside volatile metabolite profiling. How do you see the relationship between metabolomics and sensory science evolving in food research?

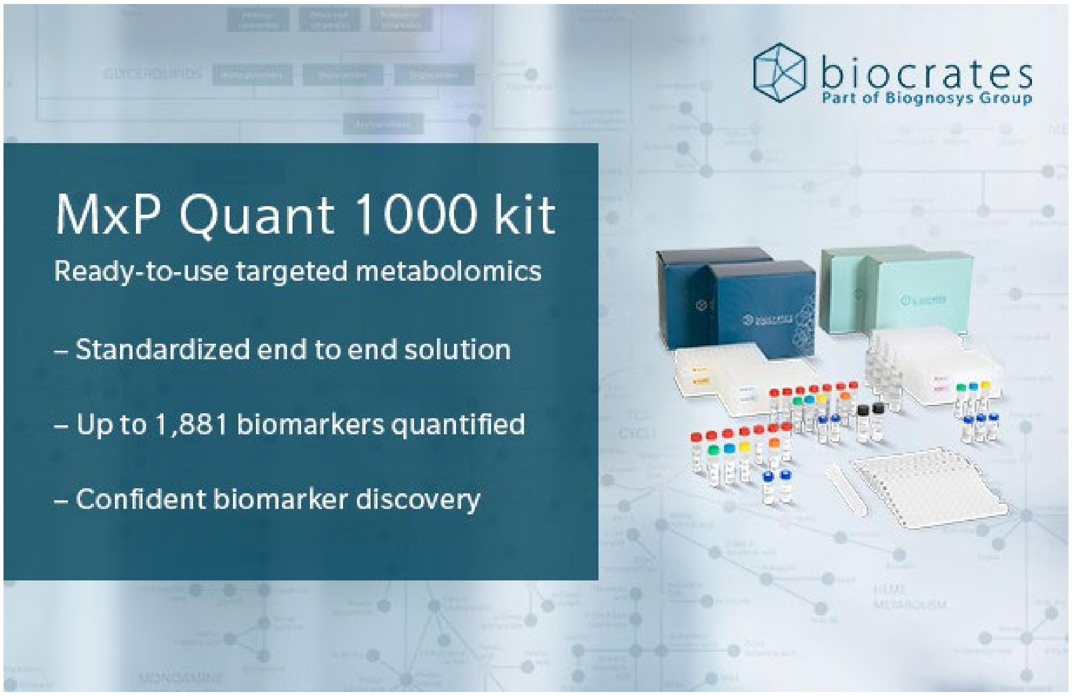
Metabolomics play complementary roles in my type of food research. Metabolomics specifically represents a powerful tool for us to identify differences in microbial community metabolism in the fermentations that I study. This can be in the context of health benefits, or flavour and aroma attributes which is where sensory science comes in. While many of the metabolites we are interested in are associated with specific aromas or flavours, the detection of a difference in concentration is not enough to be sure there will be a discernible difference in the food itself. Human sensory experiences are shaped by complex interactions between many different compounds present in these foods and we still can’t accurately make predictions based on metabolite concentrations alone. By pairing metabolomics with sensory we can identify the specific fermentation alterations that show the most promise and further explore these samples using sensory analyses to confirm these differences are meaningful for the consumer. This is key to connecting microbial activity and interactions during fermentation with the final outcomes associated with consuming the food whether they be health benefits or just enjoying tastier food.

What areas or sectors do you foresee as being most impactful for metabolomics in the coming years — do you see food and fermentation moving more into the spotlight?

I believe that food and fermentation will continue to move into the spotlight as we have been seeing recently. While already used for this, I think the advent of increased data set size, machine learning, and improved identification of compounds will improve our ability to detect fraud in the food industry which currently costs Canada ~$2 billion a year. Identifying reliable marker compounds for confirming the purity, quality, or other characteristics of foods can help to detect fraudulent products before they make it to market. I also believe that metabolic modeling will continue to improve using these metabolomics data sets, allowing for better identification and prediction of microbial interactions in food fermentations.

How do you envision your current research on novel starter cultures translating into practical applications for the food and beverage industry?

I hope to be able to continue to contribute to the development of healthier, more delicious foods through this work. There has been increasing interest in fermented foods in recent years, largely due to the perceived health benefits associated with them, however I believe that there is still a lot of room for improvement in the foods that are offered commercially. By continuing to investigate how starter culture composition influences fermentation outcomes, I think we can improve these aspects of our food supply and achieve an overall healthier population. I'm also very excited about the potential for developing novel starters to generate new flavour profiles in foods. By utilizing non-conventional yeasts and bacteria we can push flavours in directions that haven't been explored before which is always fun!



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Conference Spotlight

Thank you for Joining Us at the 7th Annual Canadian Metabolomics Conference

CanMetCon
Canadian Metabolomics Conference

Metabolomics of Health and Disease

The 7th Annual Canadian Metabolomics Conference hosted at the Second Student Centre (York University), bought together the Canadian Metabolomics Community including senior and early career researchers, and industry experts. Organized by The Metabolomics Innovation Centre (TMIC), the conference highlighted key advanced in Metabolomics, Proteomics, and Lipidomics.

Program Highlights

Themed “Metabolomics in Health and Disease” the two day conference featured Speakers in a variety of sessions including:

- Decoding the Metabolome
  - Dr. Tao Huan
  - Dr. David Goodlett
- Improving the Toolbox: Metabolomics Assay Development
  - Dr. Dajana Vuckovic
  - Dr. Evgeniy Petrotchenko
  - Dr. James Harynuk
- Metabolomics in Medicine
  - Dr. Philip Britz-Mckibbin
  - Dr. Jeff Xia
  - Dr. Jason Acker
- The Big Picture: Where is Metabolomics Headed?
  - Dr. Liang Li
  - Dr. David Wishart
- Clinical Frontiers

    - Dr. Daina Avizonis
    - Dr. Mohit Kapoor
- Oncometabolomics
    - Dr. Thmoas Velenosi
    - Dr. Rafa Montenegro Burke
    - Dr. Hartland Jackson
- Metabolomics of the Microbial Universe
    - Dr. Rachel Gregor
    - Dr. Courtney Toth
    - Dr. Derek Wilson

Additionally, each day featured a plenary speaker including Dr. Oliver Fiehn (UC David), presenting “Fast, Quantitative, Open & Confident: Merging Targeted and Nontargeted Methods for Biomedical Research” and Dr. Sebastian Böcker (Friedrich-Schiller-Universität Jena) presenting “SIRIUS 6: New developments, and adding retention time prediction to the mix”.

CanMetCon Awards

The 7th Annual Canadian Metabolomics Conference (CanMetCon) 2026 brought together emerging researchers from across Canada and beyond to showcase advances in metabolomics and multi-omics research. This year’s award recipients were recognized for exceptional oral and poster presentations spanning diverse applications in health, computational biology, environmental science, and translational research. Their work reflects the interdisciplinary spirit of the metabolomics community and highlights the next generation of scientists driving discovery and innovation in the field.

Best Oral Presentation:

Simona Indzhova (McMaster University) for “Plasma Metabolomic Profiling to Predict Mortality in the Canadian Longitudinal Study on Aging”

First Place Poster Presentation:

Alyss McPherson (McMaster University) for “Comparing the Nontargeted Chemical Profiles of Firefighters, Office Workers, and Paramedics”

Second Place Poster Presentation:

Constanca Silva (University of Toronto) for “Characterization of a Metabolomic Signature of Almonds in Trials of the Portfolio Diet”

Third Place Poster Presentation:

Zachary Kroezen (McMaster University) for “Fructose-linked plasma metabolomic signatures reveals early biomarkers of metabolic syndrome in obese Mexican children”

Congratulations to all of the winners!

The 8th Annual Canadian Metabolomics Conference

The CanMetCon organizing committee is excited to announce that #CanMetCon2027 will be taking place in Alberta.

For Save the Dates and additional details about CanMetCon 2027 follow TMIC on our Social Media Platforms. Follow us here: https://linktr.ee/tmic_canada

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MetaboReads

Twenty papers crossed the desk this month, and the through-line is hard to miss: the field is moving past catalogues of differential metabolites toward causal mechanism and clinical decision-making. Microbial metabolites are being tested as interventions rather than described as correlates, diagnostic workflows are being held to genuine analytical rigour, and plant and environmental studies are using metabolomic space itself as an evolutionary and ecological readout. What follows is grouped into five themes that capture where the intellectual energy is concentrated right now.

Microbiota-Derived Metabolites as Therapeutic Levers

A longstanding challenge in microbiome metabolomics has been the primarily correlational nature of the findings. This is beginning to shift to a more mechanistic view, which is, of course, important for developing meaningful and impactful interventions. Across inflammatory bowel disease, diabetic kidney injury, colitis, alcohol-related organ stress, and prostate cancer, the common theme in this month’s papers is to isolate a specific microbial metabolite or community function and then perturb it directly, whether through transplantation, supplementation, a defined probiotic strain, or a herbal formula with a traceable metabolic footprint. Read together, they suggest that the therapeutic unit of interest is no longer the microbiome as a whole but identifiable metabolite-pathway pairs that can be measured, restored, and dosed. That reframing matters because it brings microbiome science into contact with the standards of pharmacology, and several of these studies pair their multi-omics with the readouts a clinician would actually want. The breadth of disease contexts here is the real signal: the same logic is being stress-tested in immunology, nephrology, hepatology, and oncology at once.

Additive effects of fecal microbiota transplantation and infliximab on gut microbiome and metabolome in refractory inflammatory bowel disease patients

Wang and colleagues in *mSystems* reported that fecal microbiota transplantation from a single donor induced clinical response by week four in a cohort of 37 patients refractory to conventional therapy, with responders sustaining remission and most reaching endoscopic remission by week 14. Integrated multi-omics showed that FMT restored microbial diversity and reorganised host-microbiota-metabolite networks rather than simply shifting a few taxa. In nine refractory Crohn's disease patients, combining FMT with infliximab produced more complete microbial and metabolic normalisation than either therapy alone and rescued remission where monotherapy had failed. The work frames ecosystem-level network rewiring as the operative mechanism and makes a concrete case for microbiome-directed adjunctive strategies in severe disease.

Gut microbiota-derived eicosapentaenoic acid alleviates kidney fibrosis in diabetic nephropathy following acute kidney injury

Peng and colleagues in *European Journal of Pharmacology* demonstrated that gut dysbiosis acts as a pathological amplifier of fibrosis when acute kidney injury is superimposed on diabetic nephropathy. In a folic acid injury model, metabolomic profiling pinpointed a sharp decline in microbiota-derived eicosapentaenoic acid across serum and feces, tracking with macrophage to myofibroblast transition in the injured kidney. Fecal microbiota transplantation and direct EPA supplementation each blunted that transition and reduced collagen deposition, while macrophage depletion confirmed the cellular route. The study isolates a single microbial lipid as a tractable target in a setting where fibrotic progression is otherwise difficult to interrupt.

Gegen Qinlian decoction alleviates DSS-induced colitis in mice through coordinated modulation of gut microbiota, serum metabolome, and colonic γδT cell responses

Shao and colleagues in *Frontiers in Immunology* found that the traditional formula Gegen Qinlian decoction eased DSS-induced colitis through a coordinated microbiota-metabolome-immune effect rather than a single active mechanism. Serum metabolomics and 16S sequencing tied the response to shifts in succinic acid, glyoxylate, and xanthine, implicating amino acid and purine metabolism, alongside reshaped microbial composition. Immunohistochemistry showed enhanced γδ T cell infiltration with lower TNF-α, IFN-γ, and IL-17. By holding a multi-component herbal preparation to a defined metabolic and immunological readout, the work offers a usable template for mechanistic study of traditional formulas.

Weizmannia coagulans BC99 alleviates alcohol-induced oxidative stress and gut barrier dysfunction via modulation of butyrate metabolism: A randomized, double-blind, placebo-controlled trial

Wang and colleagues in *Free Radical Biology and Medicine* showed that a defined probiotic strain can shift alcohol-related physiology in humans, not just in models. In a 60-day placebo-controlled trial of 60 chronic alcohol consumers, Weizmannia coagulans BC99 raised alcohol and aldehyde dehydrogenase activity, improved lipid profiles, lowered oxidative stress markers, and reduced circulating lipopolysaccharide, consistent with better barrier integrity. Fecal short-chain fatty acids, butyrate in particular, rose substantially, and untargeted serum metabolomics tied butyrate-pathway metabolites inversely to LPS and oxidative stress. The correlation structure points to enhanced SCFA metabolism as a plausible mechanistic bridge and makes a credible case for BC99 as a therapeutic probiotic.

Indole-3-propionic acid suppresses prostate cancer by inducing cell cycle arrest and apoptosis associated with p53 activation

Huang and colleagues in *Frontiers in Oncology* described that the microbial tryptophan metabolite indole-3-propionic acid as a direct antitumor agent in prostate cancer. Untargeted metabolomics of patient serum showed markedly lower IPA levels in prostate cancer than in benign prostatic hyperplasia, with the lowest values in high-grade disease. In vitro and xenograft work showed IPA curbed proliferation, migration, and invasion while driving cell cycle arrest and apoptosis, and transcriptomics localised the effect to the p53-p21-RB axis. The result positions IPA as both a candidate prognostic marker and a starting point for microbiota-based metabolic intervention in a disease where castration-resistant progression remains the central problem.

Metabolic Signatures of Neurological and Psychiatric Disease

Psychiatric and neurological diagnosis still leans almost entirely on clinical observation, and that dependence is the shared starting point for this group of papers. Bipolar disorder, the anxiety subtypes, Parkinson's disease with REM sleep behavior disorder, and central post-stroke pain are all conditions where overlapping presentations or opaque pathophysiology blunt clinical certainty, and each study treats the metabolome as a route to objective stratification or mechanism. Collectively they show the field working at two levels at once: building discriminative fingerprints rigorous enough to complement clinical assessment, and using causal or integrative designs to ask why those fingerprints exist. A recurring thread is the gut, with microbial amino acid catabolites surfacing as a driver in the Parkinson's work and metabolite ratios carrying causal weight in the anxiety analysis. The activity here reflects a discipline under pressure to produce biomarkers that survive contact with confounders, comorbidity, and medication effects.

A rigorous UHPLC-HRMS untargeted workflow for bipolar disorder metabolic fingerprinting

Tanilli and colleagues in *Microchemical Journal* demonstrated that a urinary metabolic fingerprint can separate bipolar disorder patients from healthy controls with accuracy above 90 percent. Working with 20 patients and 20 controls analysed in both ionisation modes, the authors built an untargeted UHPLC-HRMS workflow with blanks, internal standards, and pooled quality controls, then applied a structured filtering pipeline aimed squarely at high-dimensional data and treatment-related confounding. PLS-DA delivered the classification performance, and the retained features held up as discriminators. The contribution is less a single biomarker than a validated analytical and chemometric template for psychiatric metabolomics, which is where the bottleneck has been.

Distinct metabolomic and proteomic signatures in Parkinson's disease patients with REM sleep behavior disorder

Shao and colleagues in *Signal Transduction and Targeted Therapy* found that Parkinson's disease patients with REM sleep behavior disorder carry a molecular signature distinct from other subtypes. Multiplatform plasma metabolomics and proteomics showed broad metabolic reprogramming in Parkinson's, a shift from the TCA cycle toward glycolysis, a dysregulated urea cycle, lipid remodelling, and wide inflammatory pathway activation. The RBD subgroup was set apart by an accumulation of gut microbiota-derived toxic aromatic amino acid catabolites, a pattern also present in idiopathic RBD at the prodromal stage. Metagenomics tied this to a microbial functional shift away from fiber fermentation and toward degradation of protein, aromatic amino acids, and mucin glycans, implicating gut dysbiosis in the aggressive RBD-linked course.

Integrative multi-omics identifies lyn-mediated microglial activation as a key driver of central post-stroke pain

Zhao and colleagues in *Behavioural Brain Research* reported that the kinase Lyn links systemic metabolic disturbance to microglial activation in central post-stroke pain. Using a thalamic collagenase injection model, the authors confirmed elevated inflammatory cytokines and microglial activation, then combined nontargeted metabolomics with transcriptomics to surface Lyn as the differentially expressed gene tying these changes together. Lyn colocalised with activated microglia and pushed them toward a pro-inflammatory phenotype, and pharmacological inhibition with bafetinib eased pain hypersensitivity while suppressing microglial proliferation and cytokine release. The integrative design moves central post-stroke pain from a poorly understood sequela toward a defined therapeutic target.

Anxiety Disorder Types From a Metabolomics Perspective: A Mendelian Randomization Analysis Based on 1400 Plasma Metabolites

Xiao and colleagues in *Brain and Behavior* reported that a Mendelian randomization analysis of 1,400 plasma metabolites can resolve shared from distinct causal signals across generalized anxiety disorder, social anxiety disorder, and panic disorder. After instrument-variable evaluation and sensitivity testing for heterogeneity and pleiotropy, the analysis identified subtype-specific risk markers, including 3-hydroxy-2-ethylpropionate and a glutarate-to-salicylate ratio for generalized anxiety disorder and several ratios implicating panic disorder. Protective signals, such as a salicylate-to-citrate ratio, were also resolved. By grounding the associations in genetic instruments, the work proposes biomarker candidates with a causal claim attached rather than correlation alone.

Biomarker Discovery for Diagnosis and Risk Stratification

Some conditions are defined by a single measurement or by invasive confirmation, and the desire to develop less invasive and more robust diagnostic tools underlies the papers in that theme this month. Ovarian endometriosis still lacks a reliable non-invasive test, gestational diabetes is pinned to glucose alone, and even calcium oxalate urolithiasis in a predisposed dog breed is understood mostly through stone composition rather than systemic metabolism. Each study uses metabolomic profiling to expose heterogeneity that the standard diagnostic criterion hides, and in two cases the metabolic signature carries clinically actionable prognostic weight that, for example, glucose or imaging does not. The shared goal of biomarker identification is risk stratification fine enough to change management, not just a longer list of associated metabolites. That this is happening across human reproductive medicine, obstetrics, and veterinary nephrology shows how multidisciplinary a toolset metabolomics has become, and the canine study is a reminder that naturally occurring animal disease can be a genuine model rather than an afterthought.

Serum metabolic fingerprinting for diagnosis and therapeutic applications of ovarian endometriosis

Dai and colleagues in *iScience* reported that serum metabolomics can support both diagnosis and treatment leads for ovarian endometriosis, a condition still without a reliable non-invasive test. Untargeted profiling across discovery and validation cohorts identified 56 differential metabolites, which weighted gene co-expression network analysis and targeted profiling narrowed to a smaller validated panel. Five machine learning algorithms confirmed the panel's diagnostic stability, and a LASSO-logit model combining six metabolites with two clinicopathological features reached high accuracy. Three of the differential metabolites showed therapeutic potential in vivo, extending the work from a diagnostic claim to a candidate intervention.

Metabolic Signature of Gestational Diabetes Mellitus and Risk of Adverse Birth Outcomes: A Prospective Birth Cohort Study

Wang and colleagues in *Diabetes* found that a 30-metabolite signature stratifies gestational diabetes risk in a way blood glucose alone cannot. Nontargeted profiling of 2,050 women in midpregnancy defined the signature, and participants were split into four groups by glycemic and metabolic profile. Strikingly, normoglycemic women carrying the metabolic signature had roughly twice the risk of preterm birth and large-for-gestational-age infants, while hyperglycemic women without the signature showed no elevated risk. Adverse outcomes rose stepwise across the four categories, and the hyperglycemic signature-positive group carried the heaviest burden, making a direct case for integrating metabolomics into maternal risk assessment.

Serum and urine metabolomic profiling in Miniature Schnauzer dogs with and without calcium oxalate urolithiasis

Coffey and colleagues in *Metabolomics* found that no lipidomic differences distinguish Miniature Schnauzers with calcium oxalate urolithiasis from stone-free controls, despite the breed's well-known hyperlipidemia. UHPLC-MS/MS of serum from 15 cases and 27 controls turned up only three differential serum metabolites, all lower in cases, while urine told a richer story with 202 differentially abundant metabolites including elevated acetylcarnitine and carnitine. Cluster analysis of prespecified high-priority metabolites flagged a subset of stone formers with a distinct profile of lower citrate and higher phosphate, glycine, and hippurate. Reduced N-delta-acetylornithine echoes findings in human stone formers and may reflect dietary acid load, pointing to metabolically distinct subgroups within the breed.

Analytical Platforms and Machine Learning for Cancer Detection

Cancer diagnostics has long wanted tools that are sensitive, non-invasive, and interpretable, and these two papers pursue this from different directions. One demonstrates a real-time breath analysis platform that has resisted clinical translation for four decades; the other builds an interpretable machine learning pipeline that compresses immunometabolic data to a minimal, mechanistically meaningful feature set. What links them is a refusal to treat the classifier as a black box: both insist on tracing predictive performance back to identifiable metabolites and biology. That emphasis on interpretability is the timely part, because the field has enough accurate-but-opaque models and not enough that a clinician or biologist can reason about. Taken together they sketch what credible metabolomic cancer diagnostics might look like, where the platform is practical and the model is legible.

Real-time breath metabolomics as catalyst for personalized lung cancer diagnostics: prospective matched case-control trial (LUCAbreath)

Schmidt and colleagues in *Translational Lung Cancer Research* showed that real-time secondary electrospray ionization high-resolution mass spectrometry can separate treatment-naive lung cancer patients from matched controls on breath profiles alone. The prospective study analysed 178 patients matched on age, sex, and smoking status, and the platform captured 3,750 exhaled breath features, 18 of which held up after correction. Classification reached an accuracy of 0.75 with sensitivity of 0.80, and functional enrichment separated histological types, linking de novo fatty acid metabolism to adenocarcinoma and glucose metabolism to squamous cell carcinoma. After decades of stalled translation, the trial gives breath analysis a credible foothold as a complement to imaging and genomic profiling.

Systemic immunometabolic profiling classifies cisplatin sensitivity states using interpretable machine learning

Kim and colleagues in *iScience* introduced that IMPACT, an interpretable machine learning pipeline that classifies cisplatin sensitivity from systemic immunometabolic state. In a syngeneic orthotopic lung adenocarcinoma model, the authors quantified 25 serum amino acids and 16 immune cell populations across bone marrow, spleen, lung, and lymph nodes, then used recursive feature elimination to reduce the model to a minimal, mechanistically informative set. The pipeline separated cisplatin-sensitive from resistant tumors at an AUC of 0.950, driven mainly by bone marrow MDSCs and serum glutamine, and distinguished cancer from controls with comparable accuracy. The value lies in coupling strong classification to a feature set a biologist can actually interrogate.

Plant, Food, and Environmental Metabolomics

Outside the clinic, metabolomics is increasingly used as a lens on adaptation, quality, and ecological risk, and this group of papers shows how wide that application has grown. The work spans the evolution of plant chemical defense, the regulatory layers behind floral scent, cultivar-level quality traits in fruit, tissue-specific metabolism in a medicinal tree, and the toxicity of consumer sunscreen on coral. What ties them is a treatment of the metabolome as a functional phenotype, whether the question is how a structural innovation restores toxicity against a coevolved herbivore, how DNA methylation tunes terpenoid aroma, or how a product's formulation governs what actually leaches into seawater. Two of these studies also push method, integrating GC-MS with high-resolution LC-MS or combining metabolomics with docking and phylogenetics to read deeper biology. The breadth signals a field comfortable moving between agriculture, evolutionary ecology, and environmental toxicology with the same analytical toolkit.

Structural innovation in the evolution of plant chemical defense

Rubiano-Buitrago and colleagues in *Proceedings of the National Academy of Sciences* demonstrated that structural innovation, not just toxin abundance, defines a distinct evolutionary axis in plant chemical defense. Combining molecular complexity metrics, metabolomics, docking, and phylogenetics on milkweed cardenolides, the authors identify a nitrogen-sulfur heterocycle in highly substituted cardenolides as a major innovation that restores toxicity against the coevolved monarch butterfly. The added ring appears to rigidify the scaffold and create nonelectrostatic contacts in the Na+/K+-ATPase pocket, raising binding affinity despite target-site resistance. Two such cardenolides show divergent macroevolutionary histories across Asclepiadoideae, with N,S-cardenolide producers carrying greater cardenolide richness, metabolomic space, and toxicity, evidence that innovation builds on existing scaffolds under herbivore pressure.

Epigenetic regulation of aroma formation in single-petal jasmine 'Bijian' (Jasminum sambac): The role of DNA methylation

Zhang and colleagues in *Industrial Crops and Products* found that DNA methylation helps govern terpenoid aroma biosynthesis in single-petal jasmine. Integrating metabolomic, transcriptomic, and methylomic data across floral development, the authors tracked a progressive buildup of volatile terpenoids and pinned the characteristic scent to fifteen compounds including alpha-farnesene, germacrene D, and geraniol. Overall 5mC methylation density rose during flowering, and CHH-type methylation in gene-body regions increased in parallel with specific terpene synthase expression, a pattern confirmed by bisulfite sequencing. The study adds an epigenetic layer to floral scent biosynthesis that breeding and cultivation work has not previously had to account for.

Red but not the same: Biochemical, metabolomic and flavoromic analyses reveal signature variations in red-fleshed kiwifruit cultivars

Bovio-Zenteno and colleagues in *Food Chemistry-X* showed that three red-fleshed kiwifruit cultivars marketed under a similar appearance carry sharply different biochemical signatures. UPLC-MS/MS and GC-MS profiling found 'RubyRed' enriched in flavonoids, particularly anthocyanins, with a volatile profile of esters, aldehydes, and ketones behind its fruity and floral notes, while 'Donghong' and 'Hongyang' were defined by pyrazines and monoterpenes respectively. Pathway analysis tied 'RubyRed' to activated flavonoid and volatile metabolism, and 'Hongyang' stood out for higher essential amino acid content. The cultivar-resolved map gives breeders concrete pathway targets for pigmentation, aroma, and nutritional value.

Integrated GC-MS and UPLC-Q-Orbitrap MS untargeted metabolomics for the comprehensive identification of metabolites and characterization of metabolic pathways in key tissues of Cinnamomum cassia

Yao and colleagues in *Food Chemistry-X* reported that bark, fruit, and leaf of Cinnamomum cassia hold distinct metabolic profiles that point to inter-tissue coordination. Integrating GC-MS with UPLC-Q-Orbitrap MS, the authors catalogued 71 volatile and 2,882 non-volatile metabolites, with terpenoids dominating and bark carrying the highest volatile oil content, led by trans-cinnamaldehyde. Tissue-specific biomarkers emerged, with fruit accumulating fatty acids, terpenoids, and alkaloids and bark enriched in carbohydrates and phenylpropanoids. The authors propose an acetyl-CoA-centered exchange network linking leaf-derived photosynthate to bark and fruit, a framework for quality evaluation and fuller use of the plant's tissues.

Acute toxicity assessment of sunscreen products in corals using single-polyp metabolomics

Suga and colleagues in *Marine Pollution Bulletin* showed that testing whole sunscreen products, rather than isolated UV filters, changes the conclusions about coral toxicity. Using single-polyp metabolomics that works with or without zooxanthellae, the authors found that solvent-prepared ZnO induced changes consistent with glutathione-related oxidative stress and glycolytic activation in aposymbiotic polyps, yet ZnO-containing products produced no such response. The difference tracks with limited zinc ion leaching from the product matrix into seawater, indicating that formulation itself can suppress the bioavailable toxic species. The result is a direct argument for toxicity testing that preserves realistic environmental exposure rather than idealised single-compound mixtures.

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Metabolomics Events

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MANA SODAMeet

June 9, 2026

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

Untargeted Metabolomics LC/MS Data Processing and Statistical Analysis Course

June 15 - 17, 2026

Venue: Elm House, University of Birmingham

Birmingham Metabolomics Training Centre’s upcoming course will focus on:

- Introduction to metabolomics datasets and data processing in R
- Raw data processing and generating peak tables using XCMS
- Importing untargeted metabolomics datasets into R

- Hands-on experience using PCB R packages for data processing and statistics including:
    - Data QA/QC, cleaning and filtering
    - Peak Matrix Processing (normalisation, imputation, scaling etc)
    - Univariate statistical analysis (t-statistics, ANOVA)
    - Multivariate analysis (PCA, PLS)
- Annotation and annotation processing for untargeted metabolomics
- An introduction to pathway analysis

Registration is **open.**

Check for more details

Conference of the Metabolomics Society - Metabolomics 2026

June 21 - 24, 2026

Venue: Buenos Aires, Argentina

22nd International Conference of the Metabolomics Society, Metabolomics 2026 will be held in South America for the first time. Buenos Aires, Argentina is excited to welcome you. The conference will cover in four full days the major scientific themes of Technological Advances; Computational Metabolomics, Statistics, and Bioinformatics; Metabolomics in Health and Disease; and Metabolomics of Food, Plants, Environment, and Microbes. A special focus will highlight metabolomics for sustainable development, underscoring our collective commitment to addressing global challenges related to health, biodiversity, and environmental stewardship.

The scientific program will feature plenary and keynote lectures, parallel sessions, interactive poster presentations, and industry forums, alongside introductory and advanced workshops designed to foster learning and exchange. Complementing these academic activities, participants will be immersed in the warmth and hospitality of Latin American culture through a welcome social event, early-career gatherings, and a conference party that will celebrate the region’s music, flavors, and spirit of community.

Poster submission deadline extended to **May 24, 2026.**
Early Bird registration is until **May 20, 2026.**

Check 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.

Secure your spot at the 2026 Prague Metabolism and Signaling Symposium.

Check for more details

MANA 2026

8th Annual Conference

September 8 - 11, 2026

Venue: UC Davis, California, USA

The Metabolomics Association of North America (MANA) is a non-profit organization that brings together a community of dedicated scientists and professionals in the field of metabolomics. With members from Canada, Mexico, and the USA, MANA is committed to fostering cooperation, coordination, and the advancement of metabolomics research in North America.

The 8th Annual MANA Conference will be hosted at the University of California. Check out the website for program information, speakers, events, registration, awards, and more.

Abstract submissions for oral presentations are open until **June 8, 2026.**
Abstract submissions for poster presentations are open until **June 15, 2026.**
Early-bird registration is available until **July 15, 2026.**

Check for more details

Benelux Metabolomics Days 2026

September 22 - 23, 2026

Venue: Antwerpen, Belgium

The Benelux Metabolomics Days is the annual conference of the Benelux Metabolomics Centre (BMC), bringing together the metabolomics community from the Netherlands, Belgium, and Luxembourg. It will take place at Stadscampus – Hof van Liere, University of Antwerp (Belgium). Hosted by Professor Wout Bittremieux and Professor Adrian Covaci, the conference will feature keynote lectures and sessions highlighting emerging and topical areas in metabolomics. Oral and poster presentations by early-career researchers will be selected through the abstract submission process.

Abstract submission for oral presentations is **open.**
Registration is **open**.

Visit the website for more details

5th Nordic Metabolomics Conference 2026

September 28 - 30, 2026

Venue: Uppsala, Sweden

The 5th Nordic Metabolomics Conference is the official annual conference of the Nordic Metabolomics Society and will be organized at Uppsala Konsert & Kongress (UKK) in Uppsala, Sweden. The city hosts Uppsala University, who has a longstanding tradition in Analytical Chemistry and Mass Spectrometry. The conference will host the entire depth of the metabolomics community in the Nordic Countries, high profile (inter)national speakers, will include an Early Career Event, and a dinner at Uppsala Castle.

Abstract submission deadline extended - **May 20, 2026**
Travel awards deadline - **May 20, 2026**
Early bird registration deadline - **June 30, 2026**

Check for more details

Metabolomics Jobs

Metabolomics Jobs

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Job Title	Employer	Location	Source
Senior Research Scientist (R3) – Biotransformation & Metabolite Identification	MERCK	West Point, PA, USA	MERCK
Postdoctoral Associate – Metabolomics and Exposomics	Li Lab The Jackson Laboratory for Genomic Medicine	Farmington, CT, USA	Metabolomics Society
Staff Associate – LCMS	Columbia University	New York, NY, USA	Metabolomics Society

Metabolomics & Exposomics			
Senior Metabolomics Bioinformatician	Syngenta Jealott's Hill International Research Centre	Bracknell, United Kingdom	Metabolomics Society
Research Associate – Environmental Analytical Chemistry	Algoma University	Sault Ste. Marie, ON, Canada	Metabolomics Society

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