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MetaboNews

This month in metabolomics

March, 2026
Vol 16, Issue 3

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

In This Issue

This Months Features:

Conference Spotlight
7th Annual
Canadian Metabolomics Conference

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

Conference Corner

Join us in Buenos Aires!
Plan to attend Metabolomics 2026, the 22nd Annual Conference of the Metabolomics Society. This is the first time the conference will be held in South America.

June 21 – 24, 2026
www.metabolomics2026.org

Call for Poster Abstracts
Abstract submission is open – plan to submit your work soon. We welcome poster abstracts through May 14. Take a moment to review the webpage for abstract guidelines, themes, sub-topics and scoring rubric.

If you need early approval on your poster abstract for internal travel approval or funding, contact info@metabolomicssociety.org and we can assist.

Registration is Open
Visit the website to review the registration fees and important dates, noting the early registration discount is available through April 8.

Save more money by becoming a member of the Society first, then completing your conference registration!

Workshops
Workshops will be posted online in the next couple of weeks. Shortly after they are posted, we will announce the date you can sign-up to reserve your seat in a workshop.
Remember: workshops have limited capacity and are available on a first-come, first-served basis.

See you in Argentina!

Members Corner

Board of Directors

Message from Warwick (Rick) Dunn, President

Dear Metabolomics Society Members and metabolomics friends,

The devasting events in the Middle East during the last few weeks are difficult to watch and I hope all of our members (and their families) who live in the Middle East are safe. As President of the Metabolomics Society, it is not my place to define rights and wrongs and we all have our own opinions; I believe LC-MS is the best analytical platform for metabolomics but I am sure many NMR spectroscopists will disagree (: . The events have made me reflect on what a President is (whether of a Society or country). From my point of view, the President of the Metabolomics Society is there to represent and support the metabolomics community globally and to ensure there is a society for all in the years and decades to come. As President I am lucky to work with our Officers, Board of Directors, Early Members Network, committees and task groups and my workload is small compared to all the others who contribute. All of us work for the Society and you and many thanks to all who positively contribute to the Society and the metabolomics community.

Organization of the annual conference in Buenos Aires in late June is progressing with high speed. The oral abstract submission deadline has passed and a large number of members are now scoring these abstracts. I scored my selection yesterday and enjoyed viewing the great diversity of impactful research, I am already looking forward to the presentations and posters. For others reviewing abstracts, you will notice a change from previous years – our membership and conference software have been aligned by Leslie LeClaire and I hope all of you will agree that this has made it easier to renew your membership but also review abstracts easily, thank you Leslie from us all. More information on the conference is available at https://www.metabolomics2026.org/

Our annual awards have been finalised this week for Honorary Fellows, Society Medal and President's Medal. The Board of Directors score on multiple criteria and we always have many excellent applications, too many to award to all. I had the pleasure yesterday in notifying the successful applications and also the not so great job of notifying the unsuccessful applications. Thanks to Roy and Leslie for this important process. We will announce these in the coming weeks.

On a separate note. I wrote in MetaboNews last month about beautiful downtown Bramall Lane where Sheffield United play their home football games. It appears not everyone agrees with me looking at the volumes of friendly and constructive emails on this topic. We all have our won opinions.

All the very best,

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

Early-career Members Network (EMN)

Virtual Networking Event
The EMN-MetSoc, in collaboration with the Korea Metabolomics Society, invites you to its annual virtual networking event focused on "Developing a scientific identity as an ECR in metabolomics (and beyond)" for Early Career Researchers (ECRs) working in metabolomics. Join us for an insightful discussion featuring **Assoc. Prof. Kyo Bin Kang** (Sookmyung Women's University, Korea), **Prof. Elaine Holmes** (Murdoch University, Australia), **Asst. Prof. Won Dong Lee** (Yonsei University, Korea), and **Dr. Anne K Bendt** (National University of Singapore, Singapore). When: MARCH 31 | 9:30 to 11 AM CEST.

Register here to secure your spot:

https://zoom.us/meeting/register/R8Kx57gqSmagdfUSbyncog

EMN Webinars

April EMN Webinar — Register Now!
The EMN committee welcomes **Prof. Rob Keyzers** and **Prof. Andrew Munkacsi** (Victoria University of Wellington, New Zealand) for the April webinar entitled "Metabolomics and biological activities of steam extracts of the NZ endemic plant, kānuka (*Kunzea robusta*)". The webinar is taking place on Thursday April 28 20:00 UTC/Friday April 29 at 08:00 NZST.

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

March Webinar
The EMN committee extends its gratitude to speaker **Dr. Diego Armando Badillo Sanchez** (Universidad Militar Nueva Granada) for the March webinar entitled *"Archaeometabolomics: A New Way to Delve into the Past"*. The webinar recording is available on the MetSoc website: https://metabolomicssociety.org/resources/multimedia/emn-webinars-2026

International Affiliates Corner

Australia & New Zealand Metabolomics Society (ANZMetSoc)
Visit https://anzmetabolomics.org/what-we-do

The ANZMetSoc is offering two (2) travel grants for the upcoming Metabolomics 2026 conference. Students and Early Career Researchers (ECR) can apply to support their attendance at **Metabolomics 2026** in Buenos Aires, Argentina. Two (2) grants of up to **$1,000 AUD** will be awarded.
To be eligible, applicants must:

- Be a current **paid member** of ANZ Metabolomics Society **before applying** (Sign up here: https://tinyurl.com/5pskem6e)
- Have your abstract (poster or oral) accepted for the Metabolomics 2026 and **attend in-person** (*For the purposes of this application, please assume your abstract has been accepted as long as you have submitted one*)
- Be currently enrolled in full or part-time education (**student**) OR within 5 years of obtaining highest degree (**ECR**)

Application form: ANZMetSoc Travel Bursary

For the full terms and conditions with evaluation criteria, please follow this link: Terms and Conditions

Any questions, please submit your enquiry to: ANZ_metabolomics_society@outlook.com

Deadline: **21 April 2026, 11:59 PM AEDT**

Benelux Metabolomics Centre (BMC)
Visit www.metabolomicscentre.nl/

Three days of Metabolomics at the University of Antwerp!

On **Monday 21 September 2026**, the YBMC will host the **YoungBMC Symposium 2026** at the **Hof van Liere (Stadscampus, University of Antwerp, Belgium)**. This annual symposium provides a dynamic platform for PhD candidates, postdocs, early-career scientists, and metabolomics enthusiasts from across the Benelux region to connect and share their research. Ahead of the main conference, the YoungBMC warmly invites early-career researchers to join this inspiring and interactive event. More information [soon] on the website: https://www.aanmelder.nl/beneluxmetabolomicsdays2026/ybmc-symposium-2026

The **Benelux Metabolomics Days 2026** will take place on 22–23 September 2026 at the University of Antwerp (Stadscampus – Hof van Liere, Belgium).
Find here the **BMD-2026 flyer**:
https://metabolomicscentre.nl/wp-content/uploads/2025/09/2600323-BMC_Flyer.pdf

The **Call for Abstracts** is now open, and we warmly invite PhD candidates, postdoctoral researchers, and senior scientists to submit abstracts for oral or poster presentations. Topics span untargeted and targeted metabolomics, lipidomics, fluxomics and stable-isotope tracing, single-cell and spatial metabolomics, and multi-omics integration. Contributions in computational metabolomics and AI, clinical and translational research,

exposomics and environmental health, plant and ecological metabolomics, as well as food, nutrition and microbial applications, and standardisation and open science are also welcome.

The deadline for oral presentations is 30 April 2026.

Don’t miss this opportunity to present your work, engage with peers, and contribute to shaping the future of metabolomics. We very much look forward to your contribution! Have a look at the list of awesome keynotes: Erin Baker, Emma Schymanski, Arthur David, Melanie Bailey, Kyo Bin Kang, Joleen Masschelein, Maria Fedorova, and Gabi Kastenmüller!

Early Bird Registration is open until April 30!
Link to registration page:
https://www.aanmelder.nl/beneluxmetabolomicsdays2026/subscribe
We look forward to meeting and discussing with you in Antwerp!
On behalf of the programme committee: Wout Bittremieux, Adrian Covaci, Mariadelmar Delgado, Julia Gauglitz, Bart Ghesquière, Geert Goeminne, Nathalie Legrave, Ahmed Ali, Sofia Moco, Michel van Weeghel, Meike Bünger

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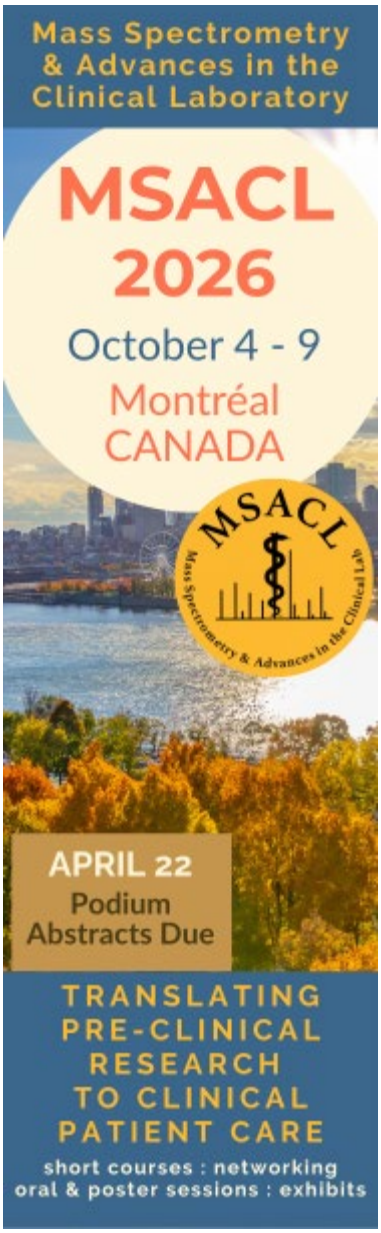

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Conference Spotlight

Final Call: Join Us at the 7th Annual Canadian Metabolomics Conference

CanMetCon
Canadian Metabolomics Conference

Metabolomics of Health and Disease

The 7th Annual Canadian Metabolomics Conference (CanMetCon 2026), is taking place **April 30–May 1, 2026**, at the **York University Cornerstone Centre** in Toronto, Ontario.

CanMetCon is a platform for in-depth discussion and networking among researchers, industry experts, and trainees, focused on the latest trends, technologies, and innovations in metabolomics. Attendees will have the opportunity to engage with thought leaders, build collaborations, and exchange insights that advance this rapidly evolving field.

This year's theme, **"Metabolomics of Health and Disease,"** will be explored through plenary lectures from internationally recognized leaders, including **Oliver Fiehn** and **Sebastian Böcker**, alongside a strong lineup of invited speakers such as **Rafa Montenegro-Burke**, **David Wishart**, **Derek Wilson**, **Jason Acker**, and many more featured on this year's program.

Beyond talks, CanMetCon offers valuable opportunities to connect with industry partners who are actively supporting and advancing the field. Attendees can engage with sponsors, explore emerging technologies, and learn about new tools shaping metabolomics research. The conference also features **15-minute oral presentations**, **5-minute lightning talks**, and **poster sessions**, showcasing new research across diverse areas of metabolomics and providing a platform for researchers at all stages to share their work.

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CanMetCon Canadian Metabolomics Conference

7TH ANNUAL CANADIAN METABOLOMICS CONFERENCE

TMIC The Metabolomics Innovation Centre

Plenary Speakers

Sebastian Böcker (Friedrich Schiller University Jena)

SIRIUS 6: New developments, and adding retention time prediction to the mix

Oliver Fiehn (University of California, Davis)

Fast, Quantitative, Open & Confident: Merging Targeted and Nontargeted Methods for Biomedical Research

Invited Speakers

Jason Acker (University of Alberta)

Metabolomic Engineering of Red Cells to Enhance Transfusion Outcomes

Daina Avionis (McGill University)

The Impact of Extracellular Adenosine: Revealing a Hidden Metabolic Checkpoint in Immuno-oncology

Hartland Jackson (University of Toronto)

A Lipidomics Based Approach to Screen Urinary Tract Pathogens in the General Population

Rachel Gregor (University of Toronto)

A sea of signals: chemical interactions in the ocean microbiome

Mohit Kapoor (University of Toronto)

Endophenotyping Osteoarthritis: utility of Metabolomics

Rafa Montenegro Burke (University of Toronto)

Uncovering the Heterogeneity of the Human Metabolome

Courtney Toth (University of Toronto, NAIT)

Anaerobic Benzene Bioremediation: Insights from Meta-Omics and Field Studies

Thomas Velenosi (University of British Columiba)

Spatially resolved proteomics identifies localized intra-tumour metabolic heterogeneity

Derek J. Wilson (York University)

Yes, there is an intersection between dynamic structural biology and metabolomics... and interesting things happen there!

Location: Second Student Centre
Cedarstone Events Centre
15 Library Ln, North York, ON

Date: April 30th - May 1st, 2026

TMIC Node Leaders

Christoph Borchers (McGill University)

No derivatization single-run RP-UPLC targeted assay for 370 metabolites in plasma samples.

Philip Britz-McKibbin (McMaster University)

Validation of Urinary Biomarkers of Coffee Intake: Deciphering its Putative Health Benefits and Harms

David Goodlett (University of Victoria)

Characterizing the Tumor Microenvironment

James Harynuk (University of Alberta)

Comparing Metabolomic Tools for Species-Level Identification of Wood

Tao Huan (University of British Columbia)

Bioinformatic development for confident compound annotation from tandem mass spectrometry

Liang Li (University of Alberta)

Deep Metabolomics: Analytical Innovations for Comprehensive Small-Molecule Profiling

Dajana Vuckovic (Concordia University)

Advances in Microsampling and Microextraction Techniques for Oxylipin Analysis

David Wishart (University of Alberta)

Precision Health or Precision Medicine? Finding the Right Place for Metabolomics

Jianguo (Jeff) Xia (McGill University)

Integrating metabolomics and GEMs to understand host-microbiome interactions

Sponsors

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Agilent LECO LGC trc LINEARIS MetabolomiX Multiplatform Metabolomics Kits

BRUKER biocrates Part of Biognosys Group Waters ZefSci MS ACL Ontario Genomics

Register Here

www.canmetcon.com

Program Preview: A Sneak Peek at CanMetCon 2026

This year's program highlights advances in analytical technologies, clinical research, and multi-omics integration. From cancer and precision health to microbiome interactions and environmental applications, CanMetCon 2026 showcases the real-world impact and expanding reach of metabolomics.

Below is a preview of select talks from this year's speakers.

Dr. David Wishart presenting:

Precision Health or Precision Medicine? Finding the Right Place for Metabolomics

Precision medicine and precision health represent distinct yet complementary paradigms in modern healthcare, each offering unique opportunities for metabolomics applications. Precision medicine epitomizes reactive healthcare, centered on delivering the right drug to the right patient at the right time—a paradigm fundamentally about treating illness. Conversely, precision health embodies proactive care, emphasizing prevention through individualized risk identification and personalized diet and lifestyle interventions to maintain wellness in healthy individuals. While metabolomics can support precision medicine applications, its true potential lies in precision health and precision nutrition. In this presentation I will demonstrate how metabolomic profiling uniquely captures the dynamic interplay between genetics, environment, diet, and lifestyle, making it ideally suited for identifying personalized health trajectories before disease manifests. The pathway to implementation differs dramatically between precision medicine and precision health. Conventional precision medicine approaches—pursuing formal biomarker approvals and pharmaceutical development—typically require decades of validation and billions in investment. In contrast, precision health strategies leveraging metabolomics for public health applications, curiosity-driven testing, and dietary interventions can be deployed rapidly and cost-effectively. Canadian companies like Molecular You and NutroWell, working closely with TMIC, exemplify this accelerated path, successfully translating metabolomic insights into actionable health recommendations without the regulatory burdens of precision medicine. These organizations demonstrate that metabolomics-guided interventions can reach consumers within months rather than decades, at accessible price points rather than prohibitive costs. My hope is that this presentation will illustrate how metabolomics is transforming precision health from aspiration to reality, offering personalized preventive strategies that keep healthy individuals healthy—a fundamentally different, yet arguably more impactful, mission than treating established

disease.

Dr. Derek J Wilson presenting:

Yes, there is an intersection between dynamic structural biology and metabolomics... and interesting things happen there!

If you think about it (really hard) you may be able to imagine how dynamic structural biology - the characterization of protein structure and conformational dynamics - might intersect with metabolomics. After all, proteins bind and transform metabolites all the time, and metabolic pathways can fail if one protein or another is structurally damaged... But what about the link between protein structure and metabol*omics*, that is, can protein structure and dynamics be linked not just to one metabolic pathway, but to cellular metabolism as a system. Of course, I'm going to say the answer is yes, and the reason is that, at the molecular level, protein specificity in ligand or substrate binding is often determined by subtle differences in structure or dynamics. The GST family of proteins, for instance, have highly similar structures, but engage structurally dissimilar metabolites with a range of specificities that is determined by their expression of particular dynamic modes. The same can be said of the apoptosis associated Bcl family of proteins whose members exhibit a complex web of overlapping binding specificities that either drives or abrogates apoptosis in response to a set of signals. This talk will explore conformational dynamics and it's role in ligand/substrate specificity in 'promiscuous' proteins and protein families.

Dr. Thomas Velenosi presenting:

Leveraging patient-derived xenograft models to characterize cancer lipid metabolism and treatment response

Lipid metabolism drives cancer progression but is difficult to model using conventional methods. Cell lines often fail to recapitulate in vivo cancer metabolism due in part to the limited availability of lipids in culture media and the absence of heterogeneity found in tumours. Triple-negative breast cancer (TNBC) is the most aggressive breast cancer subtype. TNBC tumours obtain lipids through de novo synthesis and uptake from their environment to support growth and proliferation. In addition, TNBC tumours are highly heterogenous with marked metabolic differences between the tumour core and the leading-edge. TNBC patient-derived xenograft (PDX) models contain similar tumour heterogeneity, vascular network and metabolic phenotypes when compared to patient tumours.

In this study, we evaluate the utility of ex vivo tumour slices and the chick chorioallantoic membrane (CAM)-PDX as ex vivo models for studying TNBC lipid metabolism over time. In addition, we characterize the in vivo spatial lipidome of TNBC tumours engrafted into mice then treated with and without the chemotherapy, doxorubicin, using dissected concentric tumour layers. Our lipidomics analysis indicate that lipid differences were driven by inherent primary and metastatic tumours, then by ex vivo model. Hierarchical clustering of total saponified fatty acids revealed ex vivo model dependent differences, suggesting that the lipids available in the tumour environment may influence fatty acyl composition, but not the distribution of esterified lipids. In lipidomics analysis of TNBC-PDX tumours from mice, differences in lipid metabolism were mainly driven by the tumour layer location, then by drug treatment, with nearly 50% of lipid features progressively increasing or decreasing from the tumour core to the leading-edge.

Our findings define the time-dependent lipid subclass accumulation in CAM-PDX and ex vivo tumour slice models and highlight their utility in the study of TNBC lipid metabolism. In addition, we reveal the importance of evaluating spatial heterogeneity in TNBC tumour lipid metabolism and demonstrate that doxorubicin exerts spatially distinct effects within the tumour lipidome.

Dr. Mohit Kapoor presenting:

Endophenotyping Osteoarthritis: utility of Metabolomics

Knee osteoarthritis (KOA) is a complex disease. Patients have a variety of clinical characteristics that influence time of diagnosis, disease progression, and perceived severity of symptoms, including pain. More recently, studies have sought to identify molecular signatures underlying subsets of KOA patients; however, distinct patient subsets based on molecular profiles have been poorly defined. To overcome this gap, we have developed a novel machine-learning approach to integrate complex molecular data obtained by multi-omic profiling of three distinct biofluids (urine, synovial fluid and blood). In this talk, we will discuss the utility of integrating a variety of omic approaches (such as metabolomics, transcriptomics, miRNomics etc) to understand OA endophenotypes.

Dr. Jason Acker presenting:

Metabolomic Engineering of Red Cells to Enhance Transfusion Outcomes

Red blood cell (RBC) transfusion is a life-saving intervention, yet the quality of stored blood is challenged by the storage lesion—a suite of biochemical and structural changes occurring ex vivo. While standard quality controls monitor hemolysis and other physical parameters, metabolomics offers a deeper understanding of the molecular shifts that govern blood product efficacy and patient safety. Metabolomic analysis reveals that refrigeration at 1-6°C triggers a rapid decline in essential metabolites, specifically ATP, 2,3-DPG and various REDOX regulators. These losses impair cellular deformability and the ability of hemoglobin to release oxygen effectively. Furthermore, metabolomics identifies the accumulation of oxidative biomarkers and bioactive lipids tha an provoke inflammatory responses in recipients. Studying these pathways is vital for developing innovative approaches to enhance the stability and function of stored red blood cells. Developing targeted treatments and storage solutions to augment the capacity of red blood cells to deliver oxygen and perform novel in vivo effects is an area of active investigation. Ultimately, metabolomics transitions transfusion medicine from a "one-size-fits-all" approach toward a precision model for therapeutic interventions that can improve transfusion outcomes and enhance patient care.

Dr. James Harynuk presenting:

Comparing Metabolomic Tools for Species-Level Identification of Wood

Wood is a valuable commodity, and Illegal logging poses a significant threat to ecosystems and undermines legal timber markets. Even within legal timber markets, verifying the identity of produced lumber to certify the identify of the wood is important. In the context of the Canadian forest products industry, the valuable Spruce-Pine-Fir (SPF) lumber group accounts for 80% of softwood lumber production. To ensure that only approved species are included and sold within the SPF grouping, reliable analytical tools are needed. Two tools have emerged which can be used to classify lumber species based on metabolite profiles in the wood. Direct Analysis in Real Time Time-of-Flight Mass Spectrometry (DART-TOFMS) and Comprehensive Two-Dimensional Gas Chromatography Time-of-Flight Mass Spectrometry (GC×GC-TOFMS) offer unique strengths for wood identification. DART-TOFMS enables rapid chemical analysis with minimal sample preparation, but does not distinguish isomeric species, whereas GC×GC-TOFMS is slower, but provides detailed chemical profiles of samples including separations of isomeric compounds. In this presentation, a direct comparison of DART-TOFMS and GC×GC- TOFMS is performed on a series of hardwood and softwood species. Then, results into a large data set comprising samples from five species in the SPF lumber group analyzed by GC×GC-TOFMS will be presented. This will show how these two techniques can potentially work together to provide a robust system for wood certification.

For additional sneak peeks into the program follow The Metabolomics Innovation Centre (TMIC) on LinkedIn for more updates or visit the official conference website

Final Opportunity: Submit Your Abstract

Researchers are invited to contribute to the scientific program through:

- Poster Presentations
- 5-Minute Lightning Talks
- 15-Minute Oral Presentations

Abstracts are being accepted in the following areas:

- Cancer Metabolomics
- Microbiomes and Meta-Omics
- Clinical Applications

Submission deadline: April 3rd, 2026
Submission Form: https://forms.gle/BP2vyLn2LFrBZunZ7

This is the final opportunity to share your work, gain visibility, and connect with the Canadian and international metabolomics community.

Visit the official conference website for full details, registration, and the complete speaker list.

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MetaboReads

Plant Abiotic Stress and Physiological Disorder

Salinity, heavy metal contamination, and oxidative imbalance remain pervasive threats to crop productivity, and metabolomics continues to sharpen our view of how plants navigate these challenges at the molecular level. The papers assembled here address salt, alkali, cadmium, and endogenous oxidative stress across four distinct species, yet they converge on a shared set of metabolic strategies: amino acid remodeling, antioxidant mobilization, and reconfiguration of lipid and energy pathways. What stands out in this month's selection is the growing emphasis on root-level metabolite profiling and exudate analysis, reflecting a recognition that belowground chemistry is as consequential as foliar responses. Several studies also underscore the value of pairing metabolomics with physiological and ultrastructural data to ground biochemical observations in organismal outcomes. The practical orientation of this work, directed toward breeding targets, remediation agents, and post-harvest quality, signals the maturation of plant stress metabolomics beyond descriptive cataloguing.

Metabolomics and physiological regulation processes unveil differential mechanisms underlying salt and alkali tolerance in roots of canola (Brassica napus L.) seedlings

Sun and colleagues in Industrial Crops and Products showed that canola seedlings deploy fundamentally distinct metabolic strategies when confronting salt versus alkali stress. Under salt stress, the root metabolome shifted toward elevated fatty acid metabolism and reactive oxygen species scavenging, with increased secretion of 2-hydroxyisovaleric acid, 3-hydroxyisovaleric acid, kynurenic acid, and glutaric acid. Alkali stress instead triggered accumulation of glutamic acid derivatives, organic acids, and amino acids, consistent with intracellular pH buffering, while roots secreted adipic acid and taurine. The study's attention to root exudate composition, analyzed alongside TCA cycle enzyme activities and KEGG pathway enrichment, adds a dimension often absent from abiotic stress metabolomics and points toward secretion-based markers for stress-type discrimination.

Zinc Sulfate-Mediated Modulation of Growth, Physiology, Yield, and Metabolome in Capsicum annuum L. Under Salinity Stress

Singh and Choudhary in Physiologia Plantarum demonstrated that exogenous zinc sulfate application at 0.1% concentration substantially mitigated salinity damage in Capsicum annuum, while a fivefold higher dose proved phytotoxic. UHPLC-HRMS-based untargeted metabolomics revealed that the protective dose upregulated phenylpropanoids, amino acids, and fatty acid amides, all metabolite classes linked to antioxidant defense and stress signaling, whereas the toxic concentration disrupted cellular homeostasis and intensified ROS accumulation. The integration of metabolomic, ultrastructural, and yield data under natural pot conditions strengthens the translational relevance of these findings for zinc-based salinity management in horticultural crops.

Unraveling the mechanism of cadmium stress alleviation in Forsythia suspensa by SeNPs-enriched Rhodopseudomonas palustris via root metabolomics

Fan and colleagues in Journal of Hazardous Materials reported that inoculation of Forsythia suspensa with selenium nanoparticle-enriched Rhodopseudomonas palustris reduced shoot cadmium content by up to 54% while increasing selenium content 58-fold. Root metabolomic profiling under the most effective treatment revealed significant upregulation of L-glutamate, L-aspartate, L-arginine, and scopoletin, with differentially expressed metabolites mapping to amino acid metabolism, unsaturated fatty acid metabolism, ABC transporter biosynthesis, and glutathione metabolism. The combined enhancement of antioxidant enzyme activity, metallothionein expression, and phytochelatin synthase levels provides a mechanistic framework for plant-microbe co-remediation of cadmium-contaminated soils, with particular relevance for medicinal plant cultivation.

An Untargeted Metabolomic Approach to Characterize the Emerging Kernel Disorder Orange Spot in Walnut (Juglans regia L.) cv. Chandler

Hernández and colleagues in Metabolites found that orange spot, an emerging kernel quality defect in Chilean walnuts, is a non-infectious physiological disorder linked to premature oxidative stress. PCR screening for bacterial DNA yielded no amplicons, ruling out microbial etiology under the conditions tested. Untargeted metabolomic comparison of affected and unaffected kernels across two harvest seasons revealed disruptions in glyoxylate and dicarboxylate metabolism, glutamate-related pathways, and glycerophospholipid metabolism, with affected tissue showing depleted L-glutamic acid and antioxidant-associated metabolites alongside elevated gluconic, citric, and quinic acids. FAME analysis additionally showed higher total fatty acid content in orange-spotted kernels, consistent with intensified lipid turnover under oxidative conditions.

Plant Defense and Secondary Metabolite Biosynthesis

The biosynthesis and accumulation of specialized metabolites sit at the intersection of plant ecology, crop improvement, and natural product chemistry. This month, three studies pair metabolomics with transcriptomics to connect metabolite abundance patterns to the genes that regulate them, an approach that is becoming standard practice for pathway elucidation in non-model species. The systems studied range from grapevine woody tissue responding to trunk disease pathogens, to ornamental cherry blossoms varying in floral pigmentation, to the pericarp chemistry distinguishing red and green Sichuan pepper. Across all three, the integration of multi-omics data enables the identification of candidate biosynthetic genes with a precision that neither platform achieves alone. The resulting gene lists are not merely descriptive; they represent actionable targets for breeding and metabolic engineering.

Multiplexed LC-MS analysis reveals novel insights into grapevine defense mechanisms by expanding metabolome coverage

Vásquez-Ocmín and colleagues in Metabolomics introduced a multiplexed LC-MS workflow combining reverse-phase, HILIC, and lipidomics-focused chromatography to expand metabolome coverage in grapevine wood by 83% over previous studies, annotating 1,425 unique features.

Applied to Vitis vinifera cv. Cabernet-Sauvignon inoculated with esca-associated pathogens and the biocontrol fungus Trichoderma atroviride, the approach revealed distinct metabolomic and lipidomic signatures for infection and biocontrol treatments. The lipidomic dimension proved especially informative: oxidized fatty acids, specifically hydroxy-eicosatetraenoic acids (13-HETE, 16(R)-HETE, 11(R)-HETE), emerged as candidate defense signaling molecules, a finding that reinforces the case for routine lipidomic inclusion in plant-pathogen interaction studies.

Integrated Analysis of Metabolomics and Transcriptomics of the Differences in Flower Colors of Hybrid Cherry Blossoms

Yun and colleagues in Plants described the molecular basis of flower color variation between Prunus campanulata (red), P. dielsiana (white), and two open-pollinated hybrid varieties spanning deep pink to pinkish white. Targeted metabolomics identified 84 flavonoid-related metabolites, including 31 anthocyanin pathway compounds representing cyanidin, delphinidin, and malvidin classes. Joint analysis with transcriptomic data pinpointed nine key enzyme genes whose expression patterns, particularly PAL, 4CL, CHI, DFR, and CYP75B, tracked closely with anthocyanin accumulation across the parent-offspring color gradient. The work establishes a molecular foundation for directed breeding of ornamental cherry blossom color.

Integrated Metabolomic and Transcriptomic Analyses Reveal the Coumarin Biosynthesis Pathway and Key Regulatory Genes in the Pericarp of Zanthoxylum

Chen and colleagues in Plants reported that coumarins, which contribute to the characteristic numbing-aromatic profile of Sichuan pepper, accumulate at markedly higher levels in green Zanthoxylum planispinum var. dingtanensis than in red Z. bungeanum. Widely targeted UPLC-ESI-MS/MS metabolomics detected 583 metabolites across both materials, with 24 coumarins identified and most enriched in the green variety. Integration with transcriptome data yielded 56 candidate genes correlated with scopoletin and scopolin levels, and transient overexpression of CCoAOMT, COMT, and F6'H in Nicotiana benthamiana confirmed their involvement in coumarin biosynthesis. These validated gene targets offer clear entry points for quality improvement and metabolic engineering in Sichuan pepper.

Food Quality, Flavor Chemistry, and Authentication

Metabolomics is now deeply embedded in food science, where it serves purposes ranging from flavor characterization and process optimization to geographic traceability and shelf-life extension. The five papers collected here span fermented dairy, baked goods, wine, aquatic food resources, and a conceptual framework for spatial flavor mapping, yet all share an interest in linking metabolite profiles to sensory or quality outcomes. A notable thread running through this group is the push to move food metabolomics beyond broad profiling toward functional interpretation: identifying the specific compounds that drive consumer-relevant attributes like taste, aroma, and textural quality. The inclusion of machine learning for origin authentication and the proposal of spatial metabolomics as a distinct analytical paradigm both reflect a field that is expanding its methodological vocabulary at pace.

[Spatial flavor metabolomics: probing food flavor distribution with MALDI-MSI technology]

Wang and colleagues in Food Chemistry introduced the concept of Food Spatial Flavor Metabolomics (FSFM) as an operational framework for investigating the spatial heterogeneity of flavor formation. The review synthesizes evidence from MALDI-MSI studies across multiple food systems, identifying recurring spatial patterns: interfacial enrichment, gradient migration, functional co-localization, and processing-induced remodeling. The authors argue that conventional homogenization-based extraction obscures tissue-level spatial information critical to mechanistic understanding. Practical decision rules are proposed for when spatial imaging should be prioritized over, or coupled with, bulk analytical methods, though the review acknowledges persistent bottlenecks in volatile loss, matrix effects, and quantitative reproducibility.

[Sugar stress attenuates fruity aroma in sweet wine by suppressing ethyl ester biosynthesis: Insights from integrated sensory, metabolome, and transcriptomic analyses]

Li and colleagues in Food Chemistry-X demonstrated that increasing initial sugar concentration in grape must progressively suppresses ethyl ester accumulation, accounting for the diminished fruity aroma characteristic of sweet wines. Sensory evaluation and metabolomic profiling of wines fermented from musts at 204, 260, and 316 g/L sugar confirmed the dose-dependent decline. Transcriptomic analysis identified differentially expressed genes in ethyl ester metabolism, and weighted gene co-expression network analysis (WGCNA) revealed 14 candidate hub genes potentially governing ethyl ester production in Saccharomyces cerevisiae under sugar stress. The work provides a molecular basis for strategies to retain fruity character in high-sugar fermentations.

[Synergistic effects of Lactiplantibacillus plantarum P-8 and Lacticaseibacillus paracasei ProSci-92 in cofermented milk: Metabolomic and physicochemical evaluation]

Liu and colleagues in Journal of Dairy Science found that co-culturing Lactiplantibacillus plantarum P-8 and Lacticaseibacillus paracasei ProSci-92 at a 1,000:1 ratio produced synergistic improvements in viable counts, acid production, water-holding capacity, and texture of fermented milk. Untargeted metabolomics revealed that co-fermentation enhanced accumulation of flavor-active compounds including acetoin, acetaldehyde, butyric acid, and propionic acid, alongside functionally relevant amino acids such as lysine, ornithine, and phenylalanine. Glutathione was identified as a candidate metabolic biomarker of strain synergy. The combined physicochemical and metabolomic characterization offers a template for rational probiotic strain pairing in next-generation dairy products.

[Metabolomics characteristics of γ-aminobutyric acid-enriched steamed bread made by wild jujube powder and mixed lactic acid bacteria strains with good antimicrobial ability]

Hou and colleagues in LWT-Food Science and Technology showed that combining GABA-producing lactic acid bacteria with wild jujube powder at 4% incorporation achieved an eight-fold increase in steamed bread GABA content (to 8.25 mg/g) while extending shelf life from two to four days. Metabolomic profiling of the sourdough identified upregulated phenylalanine metabolism and serotonergic synapse pathways, suggesting enhanced biosynthesis of health-promoting

compounds including free GABA, vitamin P, and indolelactic acid. Rising jujube powder concentration also increased DPPH and ABTS radical scavenging capacity, though it reduced lightness and increased hardness. The 4% formulation emerged as an optimum balancing functional enrichment, antioxidant activity, and textural acceptability.

Metabolomic profiling and machine learning reveal geographic origin markers and quality trade-offs in Sulcospira hainanensis

Li and colleagues in Food Research International presented the first comprehensive metabolomic characterization of five Sulcospira hainanensis populations in southern China, combining large-scale targeted metabolomics (504 metabolites) with morphometrics and machine learning. PLS-DA clearly separated populations, and free amino acid profiling uncovered a yield-versus-palatability trade-off: high-yield Yunfu populations had maximal bitter amino acid content, while wild Huizhou specimens showed 12-fold glycine enrichment potentially linked to osmotic adaptation. Multi-algorithm feature selection identified 14 molecular biomarkers achieving 96% classification accuracy with an ROC-AUC of 0.998, with quinic acid as the strongest geographic discriminator. The framework is directly applicable to authentication and quality certification in emerging aquatic food resources.

Bioactive Compounds and Metabolic Disease Intervention

Metabolomics has become indispensable for dissecting the mechanisms by which dietary compounds, gut-derived metabolites, and traditional medicines exert their therapeutic effects. The five studies in this section tackle distinct disease models (obesity, alcoholic liver disease, acute pancreatitis, nephropathy, and high-fat-diet-induced testicular injury) yet each uses metabolomic profiling to trace the pathway from compound exposure to phenotypic rescue. A recurring finding is the centrality of lipid metabolism and redox homeostasis as convergent therapeutic targets, regardless of the specific tissue or intervention. The integration of network pharmacology, serum pharmacochemistry, and multi-tissue metabolomics in several of these studies reflects an increasing expectation that mechanistic claims be supported by more than pathway enrichment alone.

Taurine attenuates lipid accumulation via the eCB-CB1 axis: evidence from adipose metabolomics in HFD-fed mice and 3D adipocyte spheroids

Wu and colleagues in Frontiers in Nutrition demonstrated that oral taurine supplementation reversed high-fat-diet-induced adipocyte hypertrophy and epididymal fat accumulation in mice, with UPLC-MS metabolomics of epididymal white adipose tissue revealing correction of 15 of 35 HFD-altered metabolites. Three anandamide precursors were among the reversed features, implicating reduced endocannabinoid biosynthetic substrate availability as a mechanism. Taurine suppressed CB1 receptor signaling, downregulating lipogenic genes (Srebf1, Acaca, Cd36, Pparg) and upregulating lipolytic genes (Pnpla2, Lipe, Ppargc1a), effects confirmed in 3T3-L1 adipocyte spheroids using CB1 agonist and antagonist co-treatments. The identification of the

endocannabinoid-CB1 axis as a taurine target adds a specific mechanistic layer to its known anti-obesity properties.

Integrated Proteomics and Metabolomics Reveal the Direct Hepatic Protection of Propionate Against Alcoholic Liver Disease via the RGN-PPARα Pathway

Wang and colleagues in Nutrients found that the gut microbiota-derived short-chain fatty acid propionate directly protects the liver against alcoholic injury, independent of gut barrier effects. Using an acute ALD mouse model designed to minimize gut-liver axis confounding, and validated in ethanol/oleic acid-exposed AML-12 hepatocytes, the authors showed that propionate attenuated hepatic steatosis and oxidative stress. Integrated proteomic and metabolomic analyses converged on regucalcin (RGN) upregulation as the mechanistic driver, activating downstream PPARα signaling via phospho-AMPK, ACOX1, and CPT1A to promote lipolysis and fatty acid oxidation. The dissection of liver-centric versus gut-mediated effects addresses a gap that has complicated interpretation of prior propionate supplementation studies.

Revealing the temporal metabolic trajectory and potential pharmacodynamic substances of Da-Cheng-Qi Decoction in treating patients with acute pancreatitis: A serum metabolomics-based study

Wang and colleagues in Journal of Ethnopharmacology described the dynamic metabolic effects of Da-Cheng-Qi Decoction (DCQD) in acute pancreatitis patients using serial serum metabolomics at four time points from admission to discharge. Both conventional therapy and DCQD-adjuvant treatment reversed disease-associated disruptions in energy, amino acid, and lipid metabolism, but DCQD accelerated early-stage inflammation resolution and energy homeostasis restoration while producing more comprehensive lipid metabolic improvements at later stages. Serum pharmacochemistry identified 48 blood-migrated DCQD components in patients, and correlation analysis with AP biomarkers yielded eight candidate pharmacodynamic substances validated in an L-arginine-induced severe AP mouse model. The temporal resolution of this study is a notable design strength, capturing treatment-phase-specific metabolic effects that single-timepoint designs would miss.

Exploring the kidney-protective potential of traditional Zhuang medicine ‘Yingbupu’: Insights from serum metabolomics, network pharmacology, and experimental validation

Su and colleagues in Journal of Ethnopharmacology showed that Yingbupu (YBP), a traditional Zhuang ethnic medicine with folk applications in proteinuria reduction, protects against adriamycin-induced renal injury in rats. UPLC-Q-Orbitrap HRMS analysis identified 24 absorbed constituents, and network pharmacology screening yielded 136 key targets converging on the Wnt/β-catenin signaling pathway. Animal experiments confirmed that YBP reduced urinary protein levels, inhibited β-catenin nuclear translocation, and downregulated Cyclin D1 and Axin-2 expression. The study exemplifies the now-standard tripartite approach of serum pharmacochemistry, network pharmacology, and in vivo validation for mechanistic characterization of complex herbal medicines.

Resveratrol attenuates high-fat diet-induced testicular injury via the NRF2/GPX4 pathway: an

integrated metabolomics and network pharmacology study

Lai and colleagues in Food & Function demonstrated that resveratrol ameliorated high-fat-diet-induced testicular damage in mice, restoring sperm quality and blood-testis barrier integrity. Combined network pharmacology and metabolomic enrichment analysis converged on oxidative stress inhibition, lipid metabolism regulation, and glutathione metabolism modulation as primary protective mechanisms. Resveratrol upregulated both NRF2 and GPX4 protein expression, positioning the NRF2/GPX4 axis as the signaling pathway mediating these effects. The work adds testicular protection to the growing inventory of tissue-specific resveratrol actions characterized through metabolomics-guided pathway analysis.

Animal Physiology, Reproduction, and Developmental Metabolomics

Metabolomic profiling of animal tissues and biofluids is yielding new insight into physiological transitions: from reproductive aging in humans, to diapause preparation in insects, to the periparturient metabolic crisis in dairy cattle. These three studies share an interest in how organisms reconfigure their metabolomes in anticipation of, or in response to, energetically demanding life stages. The analytical platforms differ (LC-MS/MS, GC-MS, untargeted LC-MS), as do the organisms, but each exploits the capacity of metabolomics to capture system-wide biochemical states that conventional targeted assays would miss. The practical endpoints also vary: biomarker identification for age-related fertility decline, nest-level diagnostics for managed pollinator populations, and nutritional strategies for transition dairy cows.

Age-Associated Metabolomic Changes in Human Spermatozoa

Beg and colleagues in International Journal of Molecular Sciences found that the sperm metabolome of healthy fertile men undergoes substantial remodeling with advancing age, identifying 164 significantly altered metabolites out of 380 detected by LC-MS/MS across three age groups (21–30, 31–40, 41–51 years). PLS-DA and sparse PLS-DA both confirmed clear separation between the youngest and oldest cohorts. L-homocysteine was undetectable in advanced-age spermatozoa while methyloctadecanoyl-CoA was uniquely abundant, and biomarker analysis identified 137 candidate aging markers (AUC = 1) spanning motility, energy metabolism, membrane remodeling, and oxidative stress regulation. The authors frame these findings around the concept of disrupted “metabolostasis,” positioning the identified biomarkers as potential intervention targets for preserving sperm function with age.

Metabolome of diapause-destined Megachile rotundata prepupae differs from those undergoing direct development

Mondal and colleagues in Journal of Insect Physiology reported that diapause-destined and directly developing prepupae of the alfalfa leafcutting bee Megachile rotundata possess distinct metabolomic signatures detectable before the developmental switch occurs. GC-MS-based

untargeted profiling identified 57 discriminating metabolites: 17 (predominantly carbohydrates, at 60%) were elevated in diapause-destined prepupae, while 40 (30% amino acids) were more abundant in non-diapausing individuals, consistent with differential energy storage versus active biosynthetic investment. Several of the enriched metabolites, including polyols and TCA cycle intermediates, have been implicated in diapause physiology in other insect taxa. The authors highlight putrescine as a candidate field-deployable biomarker for nest-level diapause status, which would benefit both bee growers and pollination-dependent agriculture.

Liver and Skeletal Muscle Metabolome Characterization in Peripartal Dairy Cows Fed Rumen-Protected Methionine or Rumen-Protected Choline

Palombo and colleagues in Animals characterized the hepatic and skeletal muscle metabolomes of periparturient Holstein cows receiving rumen-protected methionine (RPM) or choline (RPC) across a time course spanning late gestation through early lactation. Untargeted LC-MS detected 2,288 hepatic and 1,454 muscle molecular features, with time exerting the dominant effect (552 temporally regulated liver metabolites versus 105 affected by diet). Network analysis identified nine hepatic co-expression modules linked to supplementation, with hub metabolites including glucose-6-phosphate, mannose-6-phosphate, and sphingomyelins pointing to modulated carbohydrate and lipid metabolism. Muscle responses were comparatively modest, reinforcing the liver as the primary site of methyl donor action during the transition period.

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Metabolomics Events

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X-omics Festival 2026

April 13, 2026

Venue: Nijmegen, the Netherlands

The X-omics festival, a yearly symposium organized by X-omics, will bring together a community of researchers and technology experts who share a common interest in advancing brain research through multi-omics approaches.

Organized by X-omics and Institute for Chemical Neuroscience, this year's festival highlights how integrated omics approaches – combining genomics, proteomics, metabolomics and advanced data integration – are enabling us to study the central nervous system with increasing depth and precision. This multi-omics approach helps researchers uncover brain disease mechanisms and identify new directions for diagnostics and therapy.

Building on the success of previous editions, this 8th edition will offer a focused yet diverse program, including:

- Two keynote lectures by leading experts
- Talks from X-omics and iCNS investigators
- Sponsored user pitches
- Scientific posters and poster pitches
- Extended networking time

Join the X-omics festival 2026

MANA SODAMeet

April 14, 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

7th Annual Canadian Metabolomics Conference (CanMetCon)

April 30 - May 1, 2026

Venue: Toronto, Ontario, Canada

Join the 7th Annual Canadian Metabolomics Conference 2026 in Toronto, Canada - a conference bringing together researchers, professionals, and students in the field of metabolomics. This conference offers a platform to explore the latest advancements, share innovative research, and foster collaborations through plenary and keynote presentations, poster sessions, and networking opportunities.

CanMetCon is actively working on integration with various other omics disciplines to cultivate a more expansive and nuanced perspective for research in the realm of multi-omics. Recognizing the interconnected nature of genomics, transcriptomics, proteomics, and other omics domains, the conference aims to forge synergies that transcend traditional disciplinary boundaries. This year conference is themed **"Metabolomics of Health and Disease"** and will feature plenary talks from leading Canadian and international metabolomics experts.

Abstract submission deadline is extended until **April 3rd, 2026.**

Check for more details

Imperial College London Metabolomics training course: Hands-on Data Analysis for Metabolomics

June 15 - 19, 2026

Venue: In person, London Hammersmith

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.

Early Bird registration is until **May 15, 2026.**
Three bursaries are available for this course which cover the early bird fee.

Register now

Untargeted Metabolomics LC/MS Data Processing and Statistical Analysis

June 15 - 17, 2026

Venue: University of Birmingham – Edgbaston, UK

This 3-day course is designed to specifically address challenges associated with untargeted metabolomics data processing, and is recommended for either (i) individuals who have already completed an introductory-level BMTC course, or (ii) delegates with existing intermediate experience operating LC-MS metabolomics, and will provide trainees with furthered skills in metabolomics data processing and analytics.

Delegates will be provided with real LC-MS datasets for hands-on analysis, and over the course of several sessions will be guided through various tools for metabolomic data processing and statistical analysis, including XCMS, univariate statistics, multivariate analysis, and annotation processing.

This course is led and delivered by three experts in the field of metabolomics data processing and statistical analysis and includes lectures to provide a detailed overview of the tools available to process and analyse metabolomics data, and computer workshops to give delegates hands-on experience using workflows and R-packages developed by Phenome Centre Birmingham.

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.

Abstract submission and registration are open now.

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.

Check for more details

The 1st Congress of Instrumental Analysis (CAI2026)

July 21 - 24, 2026

Venue: Salamanca, Spain

The 1st Congress of Instrumental Analysis (CAI2026) is the result of a collaboration between Spanish scientific societies to create a forum for discussion on the fundamental and applied aspects of chemical analysis.

This first meeting will integrate cutting-edge methodologies in spectroscopy, mass spectrometry, chromatography, and other related separation techniques, as well as electrochemistry. The congress aims to present both the latest advances in instrumentation and their applications in metabolomics, biomedicine, the environment, food science, and other areas of interest.

The congress aims to create a multidisciplinary forum designed to stimulate scientific exchange, foster synergies between communities, and promote the transfer of knowledge towards new analytical challenges.

Early Bird registration is until **June 5, 2026**

Visit the website 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.

Workshop and Interactive Forum submissions will start in March and close on **May 4, 2026**
Abstract submissions will open mid-April and close for oral presentations on **June 8, 2026**, for poster presentations will close on **June 15, 2026.**
Early bird registration will open mid-July.

Check for more details

International Summer School on MS-Based Metabolomic Data Processing (ISS-MetMS26)

September 14 - 18, 2026

Venue: Granada, Spain

The International Summer School on MS-Based Metabolomic Data Processing (ISS-MetMS26) is designed for early-stage researchers and aims to provide both theoretical knowledge and practical training in the processing of MS-based metabolomics data. With a multidisciplinary approach and around 50 international participants, the programme combines lectures and hands-on workshops covering the full metabolomics data workflow, from quality control and data preprocessing to statistical analysis, metabolite annotation, biological interpretation, and multi-omics integration, while fostering collaboration and professional networking.

Pre-registration deadline - **March 20, 2026**

Visit the website 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.

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 for oral and poster presentations deadline - **May 11, 2026**
Travel awards deadline - **May 11, 2026**
Early bird registration deadline - **June 30, 2026**

Check for more details

Metabolomics Jobs

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Job Title	Employer	Location	Source
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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, Ontario, Canada	Metabolomics Society
Research Scientist 4	G-27 Division of Environmental Health Sciences	Albany, New York, USA	Metabolomics Society
Post-Doctoral Research Fellow	MITACS and Nova Medical Testing Inc	Edmonton, AB, Canada	University of Alberta

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