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# MetaboNews

## This month in metabolomics

January, 2026
Vol 16, Issue 1

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:**

Spotlight Article

Bruker LCMS
( A Bruker & Amsterdam UMC Collaboration )

## 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.

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METABOLOMICS SOCIETY

METABOLOMICS SOCIETY
EARLY- CAREER MEMBERS NETWORK

General Enquiries

info@metabolomicssociety.org

## Conference Corner


**See you in Buenos Aires!**

Plan to join us in Buenos Aires this June for the 22nd Annual Conference of the Metabolomics Society. Buenos Aires, Argentina is excited to welcome you! This is the first time the conference will be held in South America.

**June 21 – 24, 2026**
www.metabolomics2026.org

All conference activities will take place at the **Centro de Convenciones Buenos Aires (CEC)**. Don't miss the agenda-packed 4-day conference!

Buenos Aires is known for its vibrant cultural scene with rich food experiences, urban art displays, and lively dance performances. BA is the largest city in and capital city of Argentina, ready to welcome the metabolomics community to engage in science and technology.

Come for the educational content, stay to dance tango!
Follow along on **LinkedIn** for updates about the Society and the conference.

**Call for Workshop Proposals – Deadline January 30**

The conference workshops provide a terrific venue to discuss a wide range of important topics and practical aspects of metabolomics and may include hands-on learning opportunities.

You can submit your workshop application online, click below for more information.
The deadline to submit a workshop proposal is **January 30.**

**Plenary Speakers**

We're pleased to announce the following presenters for the (5) plenary sessions. Don't miss these highly attended talks from leaders in the field, including the two recipients of the 2025 Metabolomics Society Honorary Fellowships!

- **Marta Cascante**, University of Barcelona-Institute of Biomedicine (Spain)
- **Jessica Lasky-Su**, Brigham and Women's Hospital, Harvard Medical School (United States)
- **Mariana Simões Larraz Ferreira**, UNIRIO, IMasS (Brazil)
- **Huiru Tang,** Fudan University (China)
- **Fidele Tugizimana,** University of Johannesburg (South Africa)

Learn more about the conference speakers here.

**Calling all Sponsors!**

The **Sponsorship Brochure** is available for Metabolomics 2026.

We look forward to partnering with your organization to continue the success of bringing together all the major international organizations involved in human, plant, microbial, animal, and environmental metabolomics.

**Do not miss out on this sponsorship opportunity!**

We have a variety of packages available, including a few new opportunities to position your brand and product at the forefront of the scientific community. Spots are limited and available on a first-come first-served basis, do not delay!

Sponsor registration is open, register early to get first choice of booth location and presentation timing!

**Coming Soon: Abstracts and Registration**

Abstract submission will open in early February. Review the themes and sub-themes, along with submission deadlines, on the website.

Registration will be available in February, save money with early-bird registration rates offered through April 1.

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## Members Corner

**Board of Directors**

Dear Metabolomics Society Members and metabolomics friends,

It is probably too late to say the following, but hey – Happy New Year and I hope 2026 is a successful and peaceful year.

Preparations for our annual conference, Metabolomics 2026, are in full swing. The conference dates are finalised for June 21st to June 24th and the conference website which contain a range of information is available at the link below.

https://www.metabolomics2026.org/

The conference is one day shorter this year but is still packed with as much science, network-building and fun. The decision to have a four-day and not a five-day conference revolved around costs; we are all seeing high inflation rates and this is also being seen in the costs associated with operating a conference. We decided to reduce the conference costs so that we do not have to significantly increase registration or sponsorship costs (though these have had to be increased a bit).

There is a ***call for workshop proposals*** currently open, the deadline is January 30th. We do recommend submitting your workshop proposals. Workshops will discuss a wide range of important topics and practical aspects of metabolomics and can include hands-on learning opportunities. ***Abstract submissions for oral and poster presentations*** will open in early February with the deadline for oral presentations on March 5th. Do consider submitting a workshop proposal and an abstract to present your exciting science.

At any of our conferences you always see a calm and professional exterior. The planning and operation of the conference typically starts 18 months in advance; we have already received and are reviewing proposals for the Metabolomics 2027 conference. Metabolomics 2026 has been in full operational mode from October 2025. My thanks for the 2026 conference go to María Eugenia Monge, Mónica Cala and Ian Castro-Gamboa who are acting as conference co-chairs, Aurelia Williams as the Society's Conference committee chair, to Leslie LeClaire and her team at Snap Conference Solutions and to all of the global scientists on the Scientific Organising Committee who among other tasks, score all of the abstracts submitted for oral or poster presentations.

Personally, I am very excited that Metabolomics 2026 is in South America. During my role as President, I wanted to ensure a greater geographical reach for the Society, and this included ensuring our Board of Directors is geographically diverse and holding the 2026 conference in South America. I am also excited about visiting Argentina for the first time and Maria has already sent me a long list of locations to visit, which would take about two months! I will definitely think about visiting the Iguazu Falls which look spectacular and a trip to Mendosa to acquire a taste of the Andes and internationally renowned wine.

See you all hopefully in Buenos Aires.

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

**Early-career Members Network (EMN)**

**Upcoming EMN Webinar**
January 30 at 07:00 EST | 12:00 UTC | 13:00 CET | 21:00 JST
**Advancing Data Sharing, Prediction, and Reuse in Metabolomics**

**Speakers:**

- Masanori Arita, National Institute of Genetics
- Shohei Nakamukai, RIKEN Center for Sustainable Resource Science
- Eisuke Hayakawa, Kyushu Institute of Technology

**Masanori Arita** obtained his Ph.D. in Information Science in 1999. He was a developer of the original MassBank database, and also a supervisor of the MS-DIAL software platform. His talk is titled '**From Sharing to Reusing Metabolomics Data'**. When the metabolomics society was established in 2005, there were no open repositories for mass spectra. MassBank first started as a database for standard MS spectra. Now, after 20 years, there are multiple repositories and databases, and efforts should focus on standardizing metadata description and nomenclature to optimize the use of already existing data

**Shohei Nakamukai** obtained his Ph.D. in Agricultural Science in 2022. He is interested in marine metabolomics and works on the identification and synthesis of bioactive peptides. He will present on '**Retention order prediction of peptides containing non-proteinogenic amino acids'.** Identification of marine natural products is still challenging, due to the limited amount of information. In this talk, prediction of retention order is sought, using machine learning on different types of small metabolites. The newly developed prediction model is introduced and evaluated for its applicability to marine natural products.

**Eisuke Hayakawa** obtained his Ph. D. in General Science in 2006. Using expertise in metabolomics, he develops a platform to reanalyze and compare public metabolomic data. His talk is titled **'Toward Repository-Level Reuse of Metabolomics Data Through Metabolic Changes'.** Mass spectrometry–based metabolomics data are inherently difficult to compare across studies because measurements depend strongly on analytical platforms and workflows. This webinar provides an overview of integMET, an ongoing project that enables repository-level, cross-study reuse of metabolomics data by transforming study-specific measurements into comparable representations based on metabolic changes. integMET integrates metabolic changes with study background information and supports network-based visualization, enabling large-scale cross-study exploration and knowledge discovery at the level of metabolic change.

Click here to learn more about this latest webinar.

Please register for, "Advancing Data Sharing, Prediction, and Reuse in Metabolomics," to be held on January 30 at 07:00 EST, 12:00 UTC, 13:00 CET, 21:00 JST at: https://zoom.us/webinar/register/WN_gXh5iCXeSpulHRrrIUyUrQ

After registering, you will receive a confirmation email with information about joining the webinar.

Brought to you by the EMN of the Metabolomics Society.

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## International Affiliates Corner

**Réseau Francophone de Métabolomique et Fluxomique (RFMF)**
Visit http://www.rfmf.fr/

**RFMF Travel Awards: Supporting Attendance at MetSoc Meetings**

RFMF offers travel grants through their website, up to 1,000 Euros each. To be eligible, applicants need to submit an abstract and present either a poster or orally.

You must complete the application form on the RFMF site. For complete terms and the application form visit: https://www.rfmf.fr/bourse-de-voyage/.

You also need to submit your abstract through the Metabolomics 2026 conference website.

Deadline to apply for a RFMF travel grant used for Metabolomics 2026 is **April 21**.

**W4E training**

Analyse your data with Galaxy and the Workflow4metabolomics infrastructure!

The next Workflow4Experimenters session (W4E2026) will take place in April 2026 (on-line week of 30th of March – on-site week of 20th of April). During this course (entirely in English), you will learn how to use the W4M infrastructure and analyse your own LC-MS, GC-MS, or NMR data.

Pre-registration has been extended and is available at: https://sondages.inrae.fr/index.php/576765?lang=fr up to 6th of February 2026.

You will find more information at: https://workflow4metabolomics.github.io/website/W4E/w4e2026.html

**MetaboHUB TRAINING "Hands-On Metabolomics: From Bench to Data"**

**Why this training?**

Want to integrate metabolomics into your research or analytical projects, but don't know where to start?

Whether your focus is on agrosciences, nutrition, human health, environmental science, biotechnology, or animal health,

This training designed by MetaboHUB is for you!

**Information:**

- **When?** From March 16 to 20, 2026
- **Where?** Toulouse, France on the INSA Campus
- **Target audience?** Researchers, engineers, technicians, doctoral and postdoctoral students, academics or industrials, biologists or analysts

**What you will learn:**

Expert scientists from the MetaboHUB infrastructure will introduce you to the fundamental principles and cutting-edge techniques of metabolomics through a dynamic blend of theoretical and hands-on sessions!"

**Extra:**

- **Interactive format**: Practical workshops, discussions, case studies, keynote and workshop
- **Certification**: Training certificate issued

**Registration & Contact: Hurry, limited space available! All the information is in the flyer below.**

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MARCH
16-20
2026

INSA
Toulouse

METABOHUB

FRANCE 2030

# Hands-On Metabolomics: From Bench to Data

Want to integrate metabolomics into your research or analytical projects, but don't know where to start?
Whether your focus is on **agrosciences, nutrition, human health, environmental science, biotechnology, or animal health**, this training designed by **MetaboHUB** is for you!

## Program

| MON | TUE | WED | THU | FRI |
|---|---|---|---|---|
| Basics in Metabolomics | Acquisitions and processing in MS | Acquisitions and processing in NMR | Statistics, chemometrics | Workshops |
| Practical session | Practical session + Keynote: Open Science, MetExplore3, MSi... | Practical session + Keynote: Open Science, MetExplore3, MSi... | Practical session | |

**Duration : 4.5 days - 31 hours**

### Target audience

10 to 20 participants

- Academics or industrials
- Researchers, engineers, technicians, PhDs and post-docs
- Biologists, analysts

### Fees

**2050 €** for academics
**2900 €** for industrials

Teaching materials and lunches included

### Contacts

Scientific coordinators
Marie Tremblay-Franco, IR INRAE
Pierre Pétriacq, DR, INRAE

Informations and registrations
05.61.55.92.53 - fcq@insa-toulouse.fr

INSA TOULOUSE

**The knowledge acquired during the training will be assessed throughout the session by means of practical exercises or round-table discussions.
A certificate of attendance will be issued at the end of the training course.**

## 18th Scientific Days of RFMF in Lille

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**Join us in Lille, 19–22 May 2026, for the 18th Scientific Days of the RFMF!**

We are thrilled to welcome a lineup of distinguished speakers who will share their cutting-edge research and insights:

**Confirmed speakers:**

- **Prof. Cédric Bertrand** – University of Perpignan
- **Prof. Lynn Vanhaecke** – Ghent University
- **Prof. Nicole van Dam** – Friedrich Schiller University Jena
- **Prof. Tim Ebbels** – Imperial College London
- **Prof. Manuel Liebeke** – Kiel University

Set in the vibrant city of Lille, this event promises to be a hub for scientific exchange, collaboration, and inspiration. Don't miss this opportunity to engage with leading experts in metabolomics and fluxomics!
More details and registration here: https://18-js-rfmf-2026.sciencesconf.org/

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## Other News

**Call for Society Award Nominations**

**Honorary Fellows and Career Medals**
**Deadline: February 25, 2026**

**2026 Honorary Fellows of the Metabolomics Society**
An Honorary Fellowship is a significant lifetime award granted by the Metabolomics Society to exceptional members of our community. Commissioned in 2012, and with up to two awards each year, the Board of Directors welcomes nominations from Members for these Fellowships, with a closing date of February 25, 2026.

See http://metabolomicssociety.org/awards/honorary-fellowships for further details. The Board will consider only complete nomination packages, and these consist of the four items mentioned on the web page.

**Metabolomics Society Career Medals**
We are excited to continue the Society awards which seek to recognize the outstanding contributions of individuals to the field of metabolomics through the presentation of up to two Metabolomics Society Medals. These awards are open to all Society members who meet the eligibility criteria. While research contributions are of primary importance, other contributions, including the teaching of metabolomics and/or service to the field or the society will also be strongly considered. There will be up to two medals awarded each year in the following categories:

- The Metabolomics Society Medal is for mid-career members of the Society and is open to those members who have been awarded a PhD 10-15 years prior to the closing date for nominations in each round. In 2026 this means your PhD must have been awarded between 2011 and 2016.
- The President's Award recognizes outstanding achievements in metabolomics. It is available for Society members who have been awarded a PhD no more than 5-10 years prior to the closing date for nominations in each round. In 2026 this means your PhD must have been awarded between 2016 and 2021.

See https://metabolomicssociety.org/awards/career-medals/ for further details and the application form. The application closing date is February 25, 2026.

**Please get nominating and remember the closing date for all applications is February 25, 2026.**

Back to top

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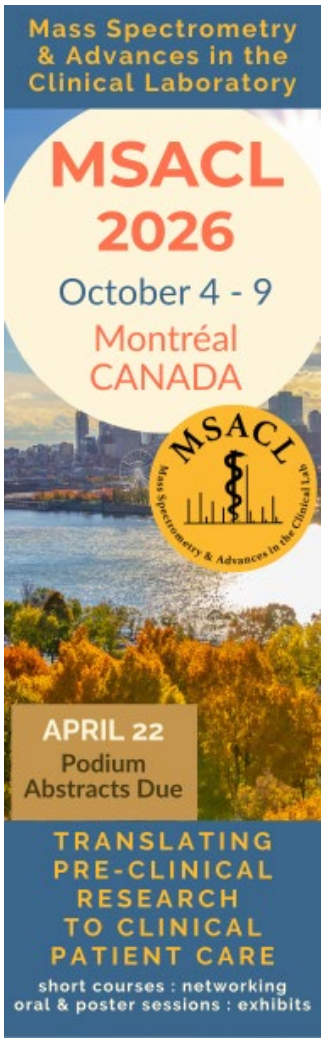


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## Spotlight Article

*****Sponsored Content*****

## Bruker LSMS

**Authors:**

- Frédéric Vaz, Principal Investigator and Clinical Biochemist, Amsterdam UMC
- Yorrick Jaspers, Postdoctoral Scientist, Amsterdam UMC
- Michel Van Weeghel, Manager Core Facility Metabolomics, Amsterdam UMC

Amsterdam UMC is one of the leading academic medical centers in Europe, dedicated to advancing patient care, conducting innovative research and educating the next generation of medical professionals. The translational research environment at Amsterdam UMC allows discoveries at the bench to reach the bedside more quickly, ensuring that metabolomics findings translate into clinical relevance and patient benefit.


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**1. Can you describe the current focus areas and key findings of your metabolomics and lipidomics research?**

Our research uses 4D metabolomics and lipidomics to capture a comprehensive view of metabolic dysregulation in complex diseases. We study genetic conditions such as inborn errors of metabolism and acquired disorders impacting metabolic pathways. Using models like adrenoleukodystrophy (ALD), we can investigate lipid dysregulation and metabolic anomalies to identify biomarkers that have so far eluded detection. Combining high-resolution analytical techniques with targeted approaches allows us to map metabolic alterations in detail, offering new insights into disease mechanisms and potential therapeutic targets.

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**2. What are the main challenges in metabolomics research that you encounter?**

Confident annotation of metabolites and lipids is a persistent challenge. Biological samples are inherently complex, and isomeric compounds make identification difficult. Standardization across labs also remains a barrier to clinical diagnostic implementation as differences in methodology can undermine reproducibility. Interpreting large, multi-dimensional datasets requires not only technical skill but also deep biochemical understanding and expertise that is sometimes missing in technically focused labs. Integrating metabolomics and lipidomics with other omics fields, such as genomics and proteomics, adds another layer of complexity that demands advanced bioinformatics solutions.

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**3. How has your lab approached these technical and biological limitations?**

We combine several strategies including advanced analytical platforms, including Bruker's timsMetabo, sophisticated software tools and close collaboration between analytical chemists, bioinformaticians, and clinicians. Our integration with bioinformatics platforms supports data visualization and annotation, while rule-based frameworks reduce false identifications. We also

emphasize translational research, maintaining a short feedback loop with clinical investigators to ensure biological relevance. Investing in multi-disciplinary teams and expertise is crucial to addressing both technical and biological interpretation gaps.

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**4. What significant changes and technological advances have you observed in the metabolomics field recently?**

In the past few years there have been remarkable advances in instrumentation, data acquisition speed, and resolution, particularly with the integration of ion mobility spectrometry with mass spectrometry. This approach adds a crucial separation dimension, greatly enhancing detection and annotation of isomeric metabolites. Alongside technological progress, we expect to see computational approaches such as artificial intelligence (AI) and machine learning (ML) increasingly employed to handle complex datasets, improve annotation confidence, and identify novel metabolic patterns.

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**5. How has the timsMetabo instrument impacted your metabolomics research?**

The integration of trapped ion mobility spectrometry (TIMS) with high resolution mass spectrometry (MS) in the Bruker timsMetabo provides a significant leap forward in the measurement of known biomarkers and the exploration of new metabolic signatures, addressing many limitations of traditional methods.

Its ability to separate isomers, isobars, and reduce chimeric spectra enhances confidence in metabolite identification. The instrument balances high throughput with deep analytical coverage, enabling sensitive and selective profiling of small molecules and lipids even in complex samples. This has accelerated our research into both known biomarkers and novel metabolic signatures, especially in challenging disease models. The multidimensional data, including accurate mass, retention time, and collision cross-section, improves annotation reliability and supports automated, rule-based workflows, streamlining data analysis and interpretation.

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**6. How do you envision the future of metabolomics research and its application?**

Looking ahead, we see metabolomics evolving towards even higher spatial and temporal resolution. Exploring metabolic variation at the cellular or tissue level offers new opportunities to understand disease heterogeneity and microenvironmental effects more precisely. Integrating multi-omics datasets and clinical phenotypes will be crucial for translating metabolic signatures into actionable clinical diagnostics and therapeutics. Technological advances, alongside AI-driven data analysis, promise to address current challenges in throughput, annotation, and interpretation, where efforts towards standardization and robust quality control will pave the way to metabolomics becoming a routine clinical tool. Ultimately, these developments will improve disease diagnosis and monitoring, and unlock personalized treatment by revealing metabolic insights at unprecedented resolution.

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**7. What are your research goals, and what barriers remain?**

Our research goals are to enhance the resolution and throughput of lipidomics and metabolomics workflows, particularly for spatially resolved analyses. We aim to overlay molecular findings with clinical phenotypes to better analyze lipid alterations within tissue sections or isolated cell populations. We are seeking to deepen mechanistic understanding of metabolic diseases,

linking molecular changes to clinical phenotypes and therapeutic responses. Remaining barriers include comprehensive metabolite annotations, harmonization across labs, and the management of increasingly complex multi-omics data. Continued investment in interdisciplinary collaborations, bioinformatics tools, and AI-based computational methods will be crucial steps forward in realizing the full promise of metabolomics and lipidomics in research and clinical practice.

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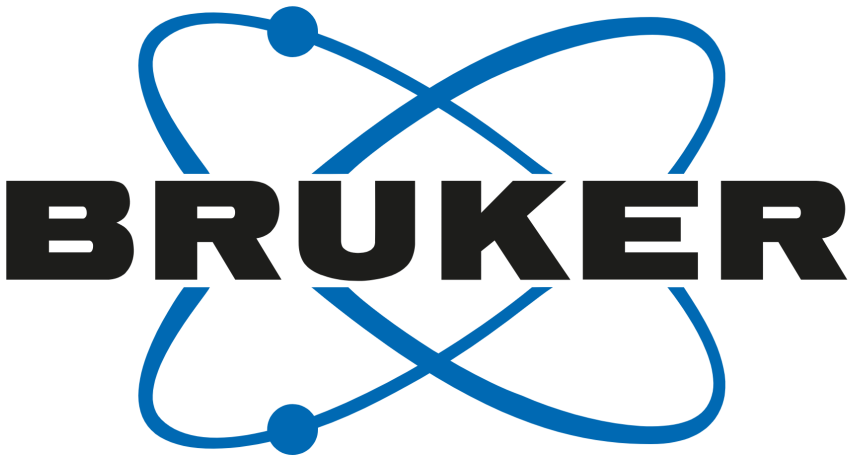
For more information on the timsMetabo, click here or contact Bruker.




Back to Top

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## MetaboReads

### Microbiome metabolism and functional pathways in host outcomes

The strongest microbiome papers in this set treat microbes as biochemistry rather than as a census. In cancer immunotherapy, pathway-level signals such as the methylerythritol 4-phosphate route and riboflavin biosynthesis track with distinct immune programs and patient outcomes. In the gut, a defined microbial product, hexadecanedioic acid, is positioned as an effector that improves fatty liver pathology, while a probiotic stabilizes community functions even when antibiotics disrupt composition. Outside the intestine, corneal repair is linked to a cholesterol sulfate axis that shifts when commensals are removed, extending microbiome influence to epithelial wound healing. Tools such as MICOMWeb make functional hypotheses easier to test at scale, but many associations still stop short of direct perturbation of the implicated pathways or metabolites.

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Bacteroides uniformis-generated hexadecanedioic acid ameliorates metabolic-associated fatty liver disease.

Zhang and colleagues in GUT MICROBES showed that depletion of Bacteroides uniformis and disruption of fatty acid and amino acid metabolism are defining features of metabolic-associated fatty liver disease, and that restoring this organism or its metabolite can blunt disease progression. In a prospective cohort of 120 cases and 120 matched controls, paired shotgun metagenomics and plasma metabolomics discriminated disease status and steatosis severity with high accuracy (AUC 0.93). Fecal transfer from patients induced metabolic-associated fatty liver disease-like phenotypes in antibiotic-treated mice, whereas B. uniformis administration reduced intestinal fat absorption and limited adipose-derived free fatty acid influx to the liver. Mechanistic multi-omics implicated portal delivery of the B. uniformis product hexadecanedioic acid, which suppressed IRE1 alpha-XBP1s signaling and downstream lipogenesis and ferroptosis, positioning a specific microbe-metabolite axis as a therapeutic entry point.

Saccharomyces boulardii CNCM I-745 mitigates antibiotic-induced gut microbiome functional alterations independently of the host.

Huang and colleagues in GUT MICROBES found that Saccharomyces boulardii CNCM I-745 can directly buffer antibiotic-driven functional collapse of gut microbial communities, with downstream consequences for immune tone. Using static and dynamic in vitro gut models under amoxicillin/clavulanic acid or vancomycin, they paired quantitative microbiome profiling with targeted metabolomics to track bacterial biomass and metabolic outputs. Under amoxicillin/clavulanic acid, S. boulardii partially preserved community function and restored production of the immunoregulatory metabolites propionate and indole-3-propionic acid. Microbiota conditioned by S. boulardii reduced pro-inflammatory cytokine secretion from human PBMCs and intestinal mucosal tissue ex vivo, supporting a microbiome-mediated mechanism of probiotic benefit during antibiotic exposure.

Microbial Metabolic Pathways Guide Response to Immune Checkpoint Blockade Therapy.

Mimpen and colleagues in CANCER DISCOVERY showed that microbiome functional capacity, rather than taxonomic membership, provides a more stable and mechanistically informative predictor of immune checkpoint blockade response across cancers. Across pan-cancer metagenomic datasets from treated patients, they identified conserved community-level pathways associated with response, notably the methylerythritol 4-phosphate pathway. In patient-derived tumor organoids, pathway-linked activity promoted V delta 2 T cell-mediated antitumor responses, whereas riboflavin biosynthesis signatures tracked with resistance and induced MAIT cell-mediated immune suppression. Concordant gut metabolomics connected higher riboflavin levels to worse survival in patients with abundant intratumoral MAIT cells, tightening the causal chain from microbial metabolism to immune cell programming and clinical outcome.

MICOMWeb: a website for microbial community metabolic modeling of the human gut.

Fresno and colleagues in GUT MICROBES introduced MICOMWeb, a browser-based platform that lowers practical barriers to microbial community metabolic modeling and makes flux balance analysis accessible as a functional hypothesis generator. The site removes the need for prior Python expertise, provides curated and user-defined diet models, and supplies compute to run simulations using community composition from shotgun metagenomics or 16S data. Benchmarking across three published datasets showed a constant runtime dominated by the most diverse sample and substantially reduced RAM use and total execution time relative to MICOM, with reported improvements ranging from several-fold to more than 200-fold depending on dataset size. By shifting modeling from bespoke scripting to a reproducible web workflow, MICOMWeb should accelerate functional interpretation and enable tighter iteration between in silico predictions and experimental validation.

The Microbiome Modulates Corneal Wound Healing via the Induction of Cholesterol Sulfotransferase Pathway.

Ogawa and colleagues in FASEB JOURNAL showed that commensal bacteria influence corneal epithelial repair by constraining a cholesterol sulfotransferase axis that, when induced, slows wound closure. In mice, systemic antibiotic treatment delayed corneal healing and increased cholesterol sulfate and the cholesterol sulfate-synthesizing enzyme SULT2B1, as defined by untargeted lipidomics and qPCR. SULT2B1 knockout accelerated healing and increased recruitment of neutrophils and eosinophils, while topical cholesterol sulfate delayed closure and recapitulated the antibiotic effect. In vitro scratch assays in human corneal epithelial cells suggested that cholesterol sulfate slows repair by inhibiting the DOCK2-Rac pathway, extending microbiome-host crosstalk to a clinically relevant ocular surface phenotype.

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## Immune-cell bioenergetics in sepsis and autoimmunity

Both studies point to a shared liability of inflammatory disease: immune cells run short on metabolic flexibility. In sepsis, metabolomics of circulating and splenic immune cells shows broad suppression of amino acid, nucleotide, and lipid metabolites, and mitochondrial transfer moves many of those signals toward sham profiles. In lupus, a large meta-analysis converges on depleted branched-chain and aromatic amino acids with consistent lipid remodeling, a pattern that fits mitochondrial and redox strain reported across cohorts and platforms. Metabolite panels will have more clinical value when they are tied to immune function readouts, not treated as stand-alone biomarkers. Interventions aimed at mitochondrial performance will need pharmacodynamic markers specific enough to separate restored respiration from nonspecific shifts that accompany inflammation resolution.

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Mitochondrial Transplantation Restores Immune Cell Metabolism in Sepsis: A Metabolomics Study.

Chung and colleagues in INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES found that mitochondrial transplantation can partially reverse the immune-cell metabolic paralysis of sepsis, restoring central carbon and lipid programs toward a sham-like state. Using a rat polymicrobial sepsis model, they applied GC-TOF-MS metabolomics to peripheral blood mononuclear cells and splenocytes and observed clear separation of sham, sepsis, and treated groups by multivariate analyses. Sepsis suppressed metabolites across amino acid, carbohydrate, and lipid metabolism, including aspartate, glutamate, AMP, and myo-inositol, consistent with mitochondrial failure. Transplanted mitochondria shifted these metabolites toward sham levels and reactivated pathways spanning the tricarboxylic acid cycle, nucleotide metabolism, and lipid remodeling, providing biochemical support for mitochondrial-based metabolic therapy.

Metabolomics in systemic lupus erythematosus: A systematic review and meta-analysis.

Barrera-Hernandez and colleagues in SEMINARS IN ARTHRITIS AND RHEUMATISM showed that systemic lupus erythematosus is associated with a reproducible metabolomic signature dominated by depleted branched-chain and aromatic amino acids and remodeling of fatty acid profiles. Their systematic review, spanning PubMed, Web of Science, Scopus, and Cochrane through November 2024, included 46 human observational studies totaling 2,238 patients and 1,761 controls. Meta-analysis indicated lower isoleucine, leucine, and tryptophan and higher methionine in lupus, alongside higher oleic acid and lower capric acid. Qualitative synthesis further highlighted reduced tricarboxylic acid intermediates, accumulation of acylcarnitines, and oxidized lipid mediators consistent with mitochondrial stress and redox imbalance, providing a focused basis for biomarker and pathway prioritization.

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## Metabolic signatures of aging, chronotype, and schizophrenia

Aging biology, circadian preference, and schizophrenia all come with metabolomic shifts; the hard part is sorting physiology from exposure. In aged mice, integrated proteomics and metabolomics in pancreas narrows beta-cell decline to networks that support amino acid handling and redox balance, including arginine biosynthesis and the pentose phosphate pathway. In older adults, evening chronotype associates with NAFLD and with specific amino acid and lipid features, and mediation models propose candidates that may sit on the path from circadian behavior to liver disease. The schizophrenia review puts study design front and center, because antipsychotics reshape many of the same pathways used to define disease signatures. Interpretation will hinge on longitudinal sampling with medication, sleep timing, and clinical state measured as carefully as the metabolome.

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Integrative proteomics and metabolomics analysis of the mechanism of pancreatic β-cell dysfunction in aged mice.

Pan and colleagues in FRONTIERS IN ENDOCRINOLOGY showed that pancreatic beta-cell dysfunction in aging is accompanied by coordinated proteomic and metabolomic remodeling that converges on amino acid handling and redox-supporting pathways. Compared with young mice, aged mice had higher fasting glucose and a higher insulin resistance index, while HOMA-beta was reduced, consistent with declining beta-cell function. LC-MS/MS quantified 3,795 proteins and metabolomics identified 65 significantly altered metabolites, with integrated analysis highlighting pathways including arginine biosynthesis and the pentose phosphate pathway. Aspartate and glutamine were linked to the aging phenotype and islet function in the integrated dataset, nominating tractable biochemical nodes for mechanistic work and potential biomarker development in age-related diabetes.

Chronotype, serum metabolome, and nonalcoholic fatty liver disease in middle-aged and older adults: Association and potential mediation analyses.

Hu and colleagues in EXPERIMENTAL GERONTOLOGY found that evening chronotype is associated with higher odds of nonalcoholic fatty liver disease in middle-aged and older adults, and that this behavioral trait maps onto coordinated amino acid and lipid alterations in the serum metabolome. In 744 participants assessed with the Morningness-Eveningness Questionnaire, untargeted high-resolution LC-MS profiling identified 81 metabolite features associated with chronotype and 251 features distinguishing NAFLD from non-NAFLD. Pathway analyses implicated arginine biosynthesis, histidine metabolism, alanine-aspartate-glutamate metabolism, arginine and proline metabolism, and beta-alanine metabolism as metabolically relevant neighborhoods linking chronotype and liver status. Mediation models nominated seven metabolites, including Asparaginyl-Proline and a diacylglycerol feature, as partial mediators accounting for about 12 to 21% of the chronotype-NAFLD association, reinforcing the clinical relevance of circadian alignment while underscoring the need for longitudinal causal work.

Metabolic Plasticity in Schizophrenia: Clinical Rehabilitation Meets LC-MS Metabolomics and Neurofeedback.

Trubalski and colleagues in INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES argued that schizophrenia is marked by systemic metabolic dysregulation across energy, amino acid, lipid, and redox pathways, and that metabolomics can provide an objective layer for evaluating rehabilitation strategies. They synthesize recurrent themes from prior studies, including disruption of the tryptophan-kynurenine axis, arginine and nitric oxide metabolism, phospholipid and sphingolipid remodeling, reduced brain glutathione, and elevated lactate consistent with mitochondrial stress. The authors highlight that antipsychotic exposure itself reshapes broad metabolite domains, complicating biomarker discovery and motivating study designs that separate disease biology from treatment effects. They propose that progress will require longitudinal, multimodal cohorts integrating LC-MS profiles with imaging, neurofeedback metrics, and clinical trajectories to move from associative panels toward actionable stratification.

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## Metabolic fingerprints of low-dose metal exposure

The exposure studies here show why metabolomics is useful in environmental health: it can register biological response before overt disease is obvious. Chronic cadmium at environmentally relevant levels links cognitive deficits in aged mice to a more oxidizing systemic redox state and to shifts in brain lipid mediators and acylcarnitines. In Taiwanese residents, arsenic speciation coupled to urinary metabolomics separates exposure chemistry from physiology, with children carrying far higher inorganic arsenic and showing metabolite patterns consistent with weaker methylation capacity and oxidative stress. Exposure measurement quality sets the ceiling for metabolomic interpretation; speciation and timing matter as much as platform choice. Causal claims will be stronger when these signatures are paired with targeted assays of mitochondrial function and lipid signaling.

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Cadmium exposure at low environmental levels induces cognitive decline in aged male mice.

Lim and colleagues in NEUROTOXICOLOGY showed that chronic exposure to cadmium at environmentally relevant levels can accumulate in the aged brain and precipitate cognitive decline with a characteristic disruption of redox and lipid signaling pathways. Aged male C57BL/6J mice received 3.3 mg/L cadmium in drinking water for 12 weeks, and cognition, plasma thiol/disulfide state, hippocampal histology, and high-resolution mass spectrometry-based metabolomics were assessed. Cadmium impaired Y-maze performance, reduced neuronal density in hippocampal CA1, and shifted systemic redox toward a more oxidizing state. Brain metabolomics revealed increased hydroxytetradecanoic acid and decreased N-oleoylethanolamine, broad reductions in bioactive lipids and select acylcarnitines, and compensatory increases in pyridoxal phosphate and lipoamide, linking low-dose exposure to neurometabolic fragility in aging.

Arsenic species exposure and urinary metabolic profiling in children and elderly residents near a petrochemical complex in Taiwan.

Yuan and colleagues in ENVIRONMENTAL GEOCHEMISTRY AND HEALTH showed that residents living near a petrochemical complex exhibit higher urinary inorganic arsenic burdens accompanied by metabolomic shifts consistent with impaired methylation capacity and heightened oxidative stress, with children appearing most vulnerable. In 81 children and 79 older adults, four urinary arsenic species were quantified by HPLC-ICPMS and metabolites profiled by GCxGC-TOFMS alongside questionnaire data. Children in the high-exposure area had about 20-fold higher As3+ and 10-fold higher As5+ concentrations, while older adults showed more modest increases, and high exposure was associated with worse methylation indicators in both age groups. Metabolite patterns included down-regulation of methylation pathway intermediates and up-regulation of oxidative stress-related metabolites, supporting the use of combined speciation and metabolomics for monitoring early biological effects of exposure.

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## Early development and neonatal metabolite trajectories

Duck embryos and very preterm infants share one feature: early development is sensitive to metabolic context. The duck study captures the first 48 hours after diapause exit and ties incubation temperature to coordinated changes in yolk and albumen metabolites, including signals in tryptophan and branched-chain amino acid pathways. In preterm infants, birth mode and feeding map onto both community composition and the balance of host versus microbe-derived tryptophan metabolites, with indole derivatives tracking taxa such as Bifidobacterium. Both papers treat metabolites as developmental inputs rather than passive correlates. The case will be strongest when these profiles are linked to functional endpoints, such as hatch uniformity and viability in avian systems or immune maturation markers in infants.

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Temperature-driven metabolic shifts in duck egg components during early embryogenesis: from diapause to active developmental phase.

Zuo and colleagues in ITALIAN JOURNAL OF ANIMAL SCIENCE found that the temperature-triggered exit from embryonic diapause in duck eggs is accompanied by coordinated metabolite shifts in both yolk and albumen during the first 48 hours of incubation. Untargeted metabolomics identified 17 differentially abundant metabolites in yolk and 22 in albumen, including increased arachidonic acid and reduced N-acetylserotonin in yolk and elevated ketoleucine in albumen. KEGG enrichment implicated tryptophan metabolism, branched-chain amino acid biosynthesis, and ABC transporter pathways, consistent with reactivation of signaling, antioxidant capacity, and nutrient allocation during embryonic resumption. The dataset proposes concrete metabolic levers for refining incubation practices and for testing how diapause control intersects with developmental timing and hatch uniformity.

Longitudinal analysis of fecal tryptophan metabolites and microbiome composition in very preterm infants: impact of birth mode and feeding type.

Wieser and colleagues in GUT MICROBES found that early-life exposures in very preterm infants, particularly birth mode and feeding type, are coupled to distinct trajectories of microbial colonization and bioactive tryptophan metabolism during the first month of life. In 53 infants born before 30 weeks of gestation, they measured 21 fecal tryptophan metabolites longitudinally and profiled the microbiome by 16S rDNA sequencing. Cesarean delivery and supplemented feeding were associated with elevated host-derived kynurenine metabolites, whereas breastfeeding was linked to reduced Proteobacteria and increased Staphylococcus. Bifidobacterium abundance correlated positively with the AhR ligand indole-3-lactic acid, while Staphylococcaceae showed negative associations with indole derivatives, outlining metabolite-mediated routes by which nutrition could shape mucosal development and immune calibration.
Plant, food, and natural-product metabolomics from quality traits to bioactivityMetabolomics earns its keep in plant and natural-product science when it is used to explain a trait, not just to list compounds. In tomato and wheat, metabolic and multi-omic data are used to account for sweetness, carotenoid value, and storage-driven maturation of processing quality, pointing to shifts in carbon partitioning and amino acid networks. In seeds, chemically mediated synchrony is supported by targeted validation of a candidate signal, moving a population phenotype toward a molecular mechanism. Dark tea and Nymphaea work connect class-level chemistry to sensory or assay readouts, while Bacillus regulation studies show how genetics can raise antibiotic scaffold yield. Across these papers, structure confirmation and quantitative validation remain the bottleneck; the strongest cases move from annotated features to specific molecules and testable causal models.

Unravelling Egyptian blue Lily (Nymphaea nouchali) organs' metabolome via UHPLC/PDA/ESI-QTOF-MS and in relation to their antioxidant and anti-cholinesterase effects.

Younis and colleagues in SCIENTIFIC REPORTS showed that organ-resolved UHPLC/PDA/ESI-QTOF-MS profiling of Egyptian Nymphaea nouchali reveals a rich, class-diverse secondary metabolome that tracks with antioxidant and anticholinesterase bioactivity. Across flower, leaf, and stem they annotated 185 metabolites spanning 10 chemical classes, and reported 72 compounds newly described in Egyptian Nymphaea including ellagitannins, patuletin glycosides, naringenin-related flavonoids, spermidine alkaloids, and 33 lipids. Flowers showed the strongest activity across DPPH, ABTS, nitric oxide, and hydrogen peroxide scavenging assays and acetylcholinesterase inhibition, consistent with higher abundance of flavonoids, anthocyanins, and alkaloids. Chemometric analyses (PCA, HCA, and OPLS-DA) resolved organ-specific signatures that can guide compound isolation and mechanistic validation of candidate neuroprotective agents.

Metabolome analyses of two varieties of Anhua dark tea.

Liu and colleagues in INTERNATIONAL JOURNAL OF FOOD PROPERTIES showed that varietal identity strongly shapes both nonvolatile chemistry and aroma-active volatiles across Anhua dark tea processing, yielding distinct sensory and potential health-related profiles. Across withering and kneading, pile-fermentation, and drying and second kneading, they profiled volatile and nonvolatile metabolomes of Zhuyeqi and Baihaozao and identified 427 metabolites that differed between varieties across stages. Zhuyeqi was enriched in glycerophospholipids, isoflavonoids, purines, and related compound classes, with higher epicatechin, neochlorogenic acid, phenylacetic acid, and cis-carveol, and pathway enrichment implicated flavonoid biosynthesis and amino acid and lipid metabolism. Volatile analysis identified 43 differentiating compounds and, using odor activity metrics, attributed a broader set of high-impact aroma contributors to Zhuyeqi, suggesting that genotype and processing interact to amplify desirable flavor chemistry.

Eggplant Rootstock Grafting Enhances Tomato Fruit Sweetness and Nutritional Value via Metabolic Reprogramming.

Ruan and colleagues in FOOD SCIENCE & NUTRITION found that grafting a tomato scion onto selected eggplant rootstocks can reprogram fruit metabolism to increase sweetness and carotenoid value without worsening acidity. Untargeted metabolomics and targeted assays showed substantial increases in fructose and glucose, with a significant rise in lycopene that was strongest with the ZheQie117

rootstock. Key organic acids linked to sourness were not elevated, while most free amino acids, including the umami-associated glutamate, declined, indicating a selective reshaping rather than a global metabolite inflation. Pathway signals pointed to enrichment of sulfur-containing glucosinolate biosynthesis and other energy-linked metabolites, suggesting that rootstock choice can tune flavor chemistry and defense-related metabolism in a commercially actionable manner.

Integrative physiological, transcriptomic, and metabolomic analyses reveal novel insights into quality maturation in wheat during after-ripening period.

Tian and colleagues in FOOD RESEARCH INTERNATIONAL found that wheat after-ripening is underpinned by a staged metabolic and transcriptional program that precedes, and plausibly drives, later stabilization of key processing-quality traits. Over 120 days of storage at 25 degrees C, germination and redox-related enzyme activities shifted most strongly in the first 60 days, while glutenin content, gluten index, solvent retention capacity, disulfide bonding, and farinograph properties stabilized later, around 80 days. Integrated transcriptomics and metabolomics implicated starch and sucrose metabolism, nitrogen metabolism, and amino acid metabolism, with up-regulation of genes including TPP, GAD, PAL, PD, ASL, NAGK, and AGM. Concordant metabolite changes, including increased trehalose, D-gluconic acid, and phenylalanine and decreased sucrose, glutamate, and tyrosine, support a model in which carbon partitioning and linked networks refine gluten and starch functionality during quality maturation.

Mutual perception among conspecific seeds enhances germination synchrony.

Dong and colleagues in BMC BIOLOGY found that seeds of the invasive plant Ambrosia trifida engage in chemically mediated mutual perception that accelerates and synchronizes germination at high density. Increasing seed density or adding seed extracts boosted germination rates and shortened germination time, and aggregated seeds germinated earlier and more synchronously than isolated seeds. Widely targeted metabolomics detected 527 compounds in seed extracts, with enrichment of shikimate- and phenylpropanoid-class secondary metabolites among pathway-associated features. Quantitative assays implicated angelicin as a functional signal that enhances synchrony across concentrations, providing a molecular foothold for understanding cooperative germination and for designing invasion management strategies.

Decoding the regulatory role of AmiC in amicoumacins production through transcriptomics and metabolic profiling in Bacillus subtilis fmb60.

Hu and colleagues in WORLD JOURNAL OF MICROBIOLOGY & BIOTECHNOLOGY showed that amiC is a positive regulatory node for amicoumacin antibiotic biosynthesis in Bacillus subtilis fmb60, with measurable consequences for yield and antibacterial activity. Overexpression of amiC increased total amicoumacin production and enlarged inhibition zones against Staphylococcus aureus and Escherichia coli, whereas deletion reduced yield to 23.5% of wild type. Metabolic profiling confirmed coordinated effects across multiple amicoumacin derivatives, and transcriptomics of the knockout identified 68 differentially expressed genes enriched for flagellar assembly, chemotaxis, and two-component signaling. The results support a model in which loss of amiC enhances motility and regulatory signaling, diverting metabolic flux away from secondary metabolism, and they position amiC as a tractable target for metabolic engineering.

Back to Top

# Metabolomics Events

Back to top

## MANA SODAMeet

### February 10, 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**

## 2026 Groningen Semantic Metabolomics ELIXIR Workshop

### February 16 - 17, 2026

**Venue: Groningen, Netherlands**

Join the next ELIXIR RCI-M Metabolomics Workshop — a unique opportunity for the metabolomics community to shape reproducible, comparable, integrable and FAIR metabolomics data. Participants will take part in hands-on sessions and learn how to leverage tools (EBI MetaboLights), formats (mzQC, mzTab-M) and semantic resources (Ontologies, OLS). Whether you are a researcher, developer, or data manager, you will have the opportunity to contribute to the next generation of interoperable standards and artefacts, and see how to adopt and evolve them in practice.

Registration is **open now.**

**Register now**

## Metabolomics Day 2026

### February 17, 2026

**Venue: Edmonton, Alberta, Canada**

The event bringing together researchers, professionals, and students in the field of metabolomics. It is a one-day symposium offering a platform to explore the latest advancements, share innovative research, and foster collaborations through **keynote presentations, poster sessions, and networking opportunities**.

Abstract Submission Deadline: **February 3, 2026**
No registration fee

Visit the website for more details

## World Critical Care & Anesthesiology Conference 2026 (WCAC26)

### March 6 - 7, 2026

**Venue: Bangkok, Thailand**

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

Visit the website for more details

## 7th Annual Canadian Metabolomics Conference

### April 30 - May 1, 2026

**Venue: Toronto, Ontario, Canada**

The 7th Canadian Metabolomics Conference (CanMetCon) 2026 will be taking place at York University Cornerstone Centre, Toronto, Ontario. The conference is themed "**Cancer Metabolomics**" and will feature feature plenary talks from leading Canadian and international metabolomics experts.

Early-bird registration is **open** and abstract submission is **coming soon.**

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.
**Coming Soon:** Abstract Submission and Registration details

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**

## Metabolomics Jobs

### Metabolomics Jobs

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| 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 |

Back to top

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Back to top



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