MetaboNews

This month in metabolomics

November, 2025
Vol 15, Issue 11

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:

MetaboInterview
Nathan Ghafari

Spotlight Article
SHARP Metabolomics

Metabolomics Society News

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

General Enquiries

info@metabolomicssociety.org

Members Corner

Board of Directors: Message from Warwick (Rick) Dunn, President

Dear Metabolomics Society Members and metabolomics friends,

The first snow of the winter has fallen in the UK (quite early in the season), and it reminded me of winter conferences and snow; Metabomeeting 2017 in Birmingham in the UK was very snowy but all the more enjoyable. I hope Metabomeeting 2025 in London is not as snowy in December.

The Metabolomics 2026 conference will also be hosted in the winter, but I am reassured there will be no snow. As previously announced, Metabolomics 2026 will be hosted in late June in Buenos Aires. We wanted to share the *very likely* conference dates of June 21-24, 2026, please place in your calendars and start thinking about sponsorship, workshop proposals and abstract submissions. Personally, I would like to thank the following for all the considerable work they are undertaking to make this conference work for all – the local organisers (Maria Eugenia Monge, Monica Cala and Ian Castro Gamboa), our conference committee chair (Aurelia Williams), the scientific organising committee (too many names to

include!) and the Snap team. One of my goals as President was to diversify conference locations and this will be the first Society conference in South America.

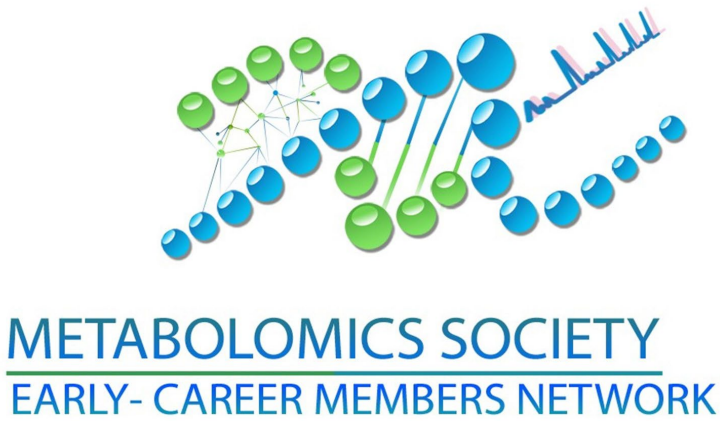
Plans are already in place for the 2027 conference in Asia and we have received three strong proposals which are currently being reviewed. Thank you to the three teams who submitted the proposals.

In other news, the Board of Directors have approved the bylaw changes to ensure greater geographical diversity of the Board. This is an important change to ensure the global metabolomics community is represented on the Board; previously there has been cases of a majority of Directors being from one continent. The new bylaws will ensure we have at least one Director from each of six geographic regions/continents. Thank you to all members who provided feedback to the changes.
The Board have also constructed a short-term financial sustainability task group to review and provide recommendations to the board on options to maintain or improve the financial sustainability of the society. More news on this will follow next year.

This may be my last message before the December holidays. I would like to wish all a happy and relaxing time away from work and I hope you all return in January refreshed and re-energised

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

Early-career Members Network (EMN)



November Webinar
The EMN committee extends its gratitude to Dr. Yamilé López Hernández from The Metabolomics Innovation Centre (TMIC), Canada and the Autonomous University of Zacatecas, Mexico for the November webinar entitled "Advancements in Clinical Metabolomics: Overcoming Challenges and Translating Research into Healthcare Applications". The webinar recording will be available on the Metabolomics Society website: https://metabolomicssociety.org/resources/multimedia/emn-webinars-2025/.

December Webinar
The last webinar of the year will be hosted on Monday, 15th December 2025, 14:00 UTC (15:00 CET) and we are happy to host **Dr. Marcos Y. Yoshinaga** from Universidade Cruzeiro do Sul, Brazil and founder of PinguisLab for a talk entitled: "*Bridging Research and Industry with Precision Lipidomics*". Registration is available via the following Zoom link: https://zoom.us/meeting/register/xsQ3NZQcSV6CzaefM5tGtg.

Keep an eye on your inbox for the e-blast and make sure to follow us on social media: **X @EMN_MetSoc** and **LinkedIn**! We strive to ensure geographical diversity in our webinars and would like to invite researchers, especially those from Africa and Asia, to participate in our webinars. If you are interested, or want to recommend someone from your network, please reach out to info.emn@metabolomicssociety.org.

International Affiliates' Corner

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

Australian Lipid Meeting 7 & 5th International Lipidomics Society Conference Perth, Western Australia

October 18 – 21, 2026 | Perth, Western Australia
We are delighted to announce the **joint conference** of the **Australian Lipid Meeting 7 (ALM7)** and the **5th International Lipidomics Society (**iLS**) Conference**, taking place October 18-21, 2026 in Perth, Western Australia.

This special event unites two major gatherings in lipid research, bringing together researchers, scientists, clinicians and industry leaders from around the world to share discoveries, promote collaborations and shape the future of lipidomics.

Conference Page
For detailed information (Venue, Program, Speakers) please visit the official conference website and don't forget to sign up to receive the latest updates: https://www.alm-ils-2026.org

Sponsorship Opportunities: https://www.alm-ils-2026.org/sponsors
Workshop Expression of Interest: https://www.alm-ils-2026.org/workshops

For any enquiries, please contact admin@alm-ils-2026.org

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

18th Scientific Days of RFMF in Lille
Join us in Lille, May 19-22, 2026, for the 18th Scientific Days of the French-speaking Network of Metabolomics and Fluxomics. Eleven years after its last edition in the region, the RFMF returns to the dynamic capital of Hauts-de-France.

Lille, at the crossroads of French and Flemish cultures, offers a vibrant setting with its rich heritage, cosmopolitan spirit, and strategic location—just 90 minutes from Paris, London, Brussels, or Amsterdam. Known for its scientific vitality, cultural energy, and warm hospitality, Lille is the ideal host city for this symposium.

Come share discoveries, foster collaborations, and be inspired in a city where science, innovation, and conviviality meet.

More details and registration to follow soon: https://18-js-rfmf-2026.sciencesconf.org/

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

The **20th BBBS Webinar Series**, organised by **RFMF and RFMF Junior**, will be held on **December 18th, 2025 (3:00-4:30 pm, GMT+2)**.

This edition will focus on **Plant Metabolism and Biochemistry**, chaired by **Téo Hebra** (*Prague, CZ*) and **Pierre Pétriacq (*Bordeaux, FR*),** and will feature a **keynote lecture by Henriette Uthe** (*Leibniz Institute of Plant Biochemistry, Halle, Germany*).

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

|MC:SUBJECT|

Metabolomics Association of North America (MANA)
Visit https://metabolomicsna.org

Email: mana@metabolomicsna.org
LinkedIn: @MANA (Metabolomics Association of North America)

X: @MetabolomicsANA

The 7th Annual Conference for MANA at the Banff Centre for Arts and Creativity in Alberta, Canada, was a great success! Our scientific program this year intertwined plenary talks, late-breaking and vendor lightning talks, poster sessions, interactive forums and parallel sessions highlighting advances in technologies and their application in clinical, agricultural, exposome, and other fields. The program allowed for ample time to network and enjoy the mountains. At our townhall meeting, we also eagerly announced our next location for MANA 2026: University of California in Davis, California, USA! MANA 2026 will be held September 8 through 11.
As always, please check the MANA website for the latest details, and our job board for open positions and scientists looking for job opportunities in metabolomics.

Metabolomics South Africa

Visit www.metabolomics-sa.co.za

Metabolomics South Africa (MSA) to host the 1st African Metabolomics Conference – March 2026

Metabolomics South Africa (MSA), an affiliate of the International Metabolomics Society, is proud to announce the **1st African Metabolomics Conference**, to be held from **March 11–13, 2026**, at the Misty Hills Hotel and Conference Centre, South Africa. Under the theme **"Metabolomics in Motion: Advancing Science for Africa's Future,"** this landmark gathering will convene global and African leaders in metabolomics, systems biology, AI, health, agriculture, and environmental science. With a dynamic program of plenary talks, workshops, exhibitions, and student-led sessions, the event aims to foster innovation, capacity building, and collaboration across the African continent and beyond.

Conference website: https://metabolomicsafrica2026.co.za/

Since its establishment in 2018, MSA has emerged as a leading platform for advancing metabolomics in Africa. MSA has built a thriving community of researchers through national symposia, training workshops, and technical courses in LC-MS, NMR, and imaging-based metabolomics. With over 300 memberships across the continent (with majority membership in South Africa), MSA supports career development via its journal club, student mentoring, and cross-sector partnerships. The 2026 conference marks a strategic evolution of these efforts, amplifying Africa's

scientific voice in metabolomics (on the continent and globally) and laying the foundation for long-term research networks, policy integration, and innovation-driven impact.

Fidele Tugizimana and Aurelia Williams
President and Vice-President, Metabolomics South Africa (MSA)
On behalf of the Organizing Committee
Chairperson & Convenor of the 1st African Metabolomics Conference, South Africa

Thailand Metabolomics Society (TMS)
Visit https://thailand-metabolomics.org/

Thailand Metabolomics Society
(TMS)

The 3rd Thailand Metabolomics Association Conference Highlights Thailand's Expanding Metabolome–Microbiome Community

The Thailand Metabolomics Association (TMA), together with Khon Kaen University through the National Phenome Institute and the Hub of Talent in Microbiome Medicine and Microbial Technology for One Health (MMOH), successfully hosted the **3rd TMA Conference** on **10–12 November 2025** at the Khon Kaen University Science Park. The event welcomed **185 participants** from universities, research institutes, hospitals, and industry—reflecting the rapid expansion and growing cohesion of Thailand's metabolome–microbiome research community.

The conference aimed not only to showcase frontier research, but also to strengthen Thailand's scientific capacity and infrastructure in metabolomics, microbiome science, and integrated phenomics, with strong support from national and international partners.

The three-day programme featured a balanced mix of **plenary lectures, symposia, and poster sessions**. Distinguished speakers included **Prof. Jeremy Nicholson**, **Asst. Prof. Jianhong Ching**, **Assoc. Prof. Hiroshi Tsugawa**, **Assoc. Prof. Jia Li**, **Prof. Zhigang Liu**, **Prof. Huiru Tang**, **Prof. Ron M.A. Heeren**, **Dr. Anne K. Bendt**, and **Assoc. Prof. Sunjae Lee**, among others. Their talks spanned molecular phenomics, multi-omics integration, computational MS, gut–immune interactions,

spatial metabolomics, clinical translation, and One Health applications.

Scientific sessions were organized around two major themes:

• **Metabolomics:** Covering natural products, food and nutrition, plant metabolomics, and clinical metabolomics. Presentations highlighted applications in functional food characterization, crop metabolism, biomarker discovery, and precision medicine.

• **Microbiome:** Focusing on agricultural and environmental microbiomes, food- and drug-associated microbiomes, biotechnology, and clinical microbiome research. Talks demonstrated how microbiome science supports sustainable agriculture, environmental health, food safety, and microbiome-based therapeutics.

With a strong international faculty and active participation from researchers across Thailand and abroad, the 3rd TMA Conference underscored both the **current strength** and **future potential** of Thailand's metabolomics and microbiome landscape. The meeting reaffirmed a shared vision: leveraging metabolome–microbiome sciences to advance **precision health**, **sustainable food systems**, **environmental resilience**, and **One Health** for the region.

Back to top

MetaboInterview

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

Nathan Ghafari

Nathan Ghafari is a PhD student working in Lekha Sleno's group in the chemistry department at the University of Québec in Montréal (UQAM). His research focuses on method development of both untargeted and targeted metabolomics workflows using LC-MS/MS, applied to a variety of biological sample and disease models.

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

I started working in metabolomics during my bachelor internship, when I was in France, with a side project that involved spectral library creation for metabolites identification via NMR. I was very interested in combining both analytical chemistry and biology. It wasn't really planned, but it made sense as I kept going.

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

One of the main projects I'm working on right now focuses on a rare disease called Hunter syndrome (MPS II). We're using both targeted and untargeted LC-MS/MS methods, as well as proteomics, to study metabolic changes in the liver of a mouse model. The goal is to better understand how the disease affects liver metabolism and if a treatment called enzymatic replacement therapy (ERT) has any impact on metabolome perturbations. It's a very interesting project since it deals with a rare disease that's still not well understood, and there's not much data available on its metabolic effects, especially from a multi-omics perspective.

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

The potential that metabolomics has to reveal biological changes that other methods might miss. I like using powerful analytical techniques to study biological processes and understand how they change in disease. It's a compelling way to link data with biology.

4. What insights did you gain from analyzing bile acid profiles, and how do they enhance our understanding of PCOS pathology or therapy?

Studying bile acids in PCOS really makes sense, as they are linked to many aspects of metabolism that are known to be strongly impacted by PCOS (insulin sensitivity, cholesterol metabolism or lipid degradation). By studying these metabolites, we were able to better understand the mechanisms of a treatment which included the combination of a conjugated bile acid (TUDCA) with an anti-diabetic agent (metformin) and look at specific impact on bile acid metabolism.

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5. What were the most striking metabolic shifts observed between the treated and untreated PCOS groups?

We observed that certain metabolite groups, like amino acids, acylcarnitines, and bile acids, showed significant changes in the PCOS mouse model. These variations have also been reported in human patients, which supports that this mouse model is relevant for studying the disease at the metabolome level, reflecting similar metabolic disruptions seen in humans. Interestingly, many of these changes were not corrected by the treatment, however the bile acid perturbations were reversed.

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6. Why did you choose LC-MS/MS for your metabolomics work, and what do you see as its main strengths?

LC-MS/MS is a versatile and sensitive method that can detect many different metabolites from multiple pathways in one analysis. In our experience, combining complementary chromatographies and ionization polarities really increase our metabolome coverage.

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7. What challenges have you encountered when working with complex biological samples (like plasma or feces), and how did you overcome them?

Working with complex biological samples like feces is challenging as it’s a very

complex matrix that can contain many interferences which can cause signal suppression, or contamination of the instrument. To address this, optimizing the extraction process was essential, we tested multiple protocols, solvent combinations, and starting sample amounts to improve metabolite recovery and reduce background noise.

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8. What advice would you offer to early-stage scientists interested in applying metabolomics to their research?

I think the most helpful thing is to ask questions and talk with people already working in the field; discussing with others really helps to better understand how metabolomics can be useful in your research and gives insight into the common challenges that we encounter in this field.

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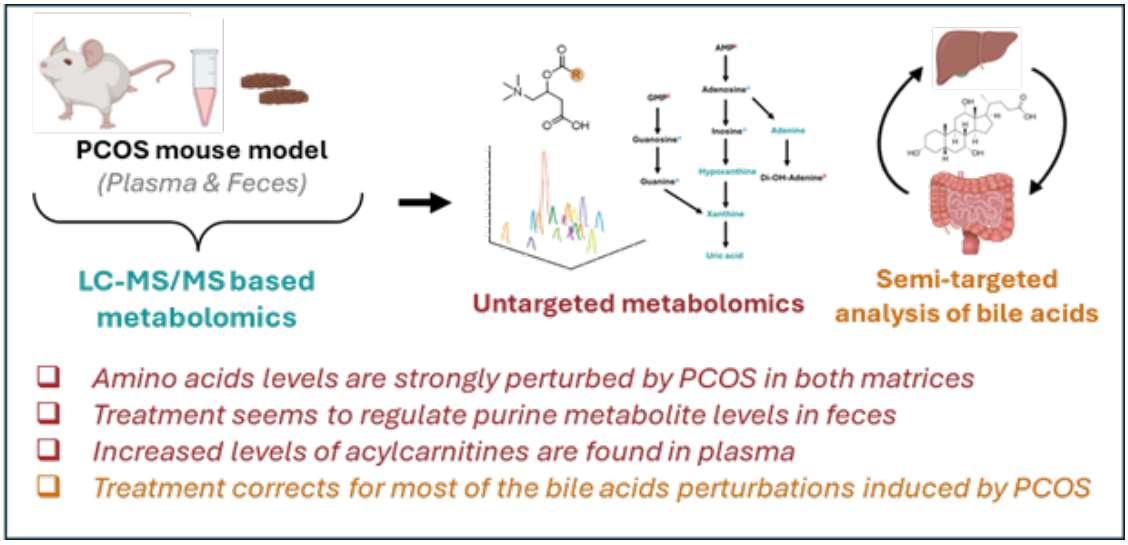
9. Are there other areas of metabolomics or environmental health that you're excited to explore in the future?

I'm interested in eventually using complementary techniques, such as ion mobility, applied to metabolomics.



Back to Top

Spotlight Article

SHARP Metabolomics Platform: Precision Metabolomics from Minimal Volumes

The Need for Small Sample Metabolomics

Metabolomics offers powerful insights into biological systems through the analysis of biofluids like blood and urine. But when working with rare specimens, small animal models, or scarce clinical materials, collecting large sample volumes isn't always possible.

Small sample metabolomics now makes it possible to perform comprehensive, quantitative analysis from minimal material, increasing study sensitivity, and revealing new insights into metabolic pathways, disease mechanisms, and biological variation.

The SHARP Platform: Power Meets Precision

TMIC's Li Node, at University of Alberta, offers the SHARP Metabolomics Platform, a quantitative, highly accurate and reproducible platform that delivers maximum insight from small sample volumes.

The Small-Scale Highly Accurate and Reproducible Platform Metabolomic Platform (SHARP) provides an advanced service that empowers researchers working with minimal amounts of various types of samples, such as serum, plasma, cells, etc, by delivering high-sensitivity metabolome profiling through advanced liquid chromatography-mass spectrometry (LC-MS). By applying TMIC's signature Chemical Isotope Labeling (CIL) LC-MS technology, this platform enhances metabolite detection and ensures confident compound identification, bridging the gap between analytical power and sample availability.

What Makes SHARP Different?

- Low Sample Volume: Advanced Chemical Isotope Labeling LC-MS technology designed to analyze **serum/plasma samples as small as 4 µL and cell samples with as few as 5,000 cells**. Ideal for working with precious or scarce samples.
- Comprehensive Metabolome Coverage: Optimized separation and ionization enhance metabolite detection and high-confidence metabolite identification.
- High Accuracy and Precision: Unique "one-to-one" internal standard approach enables superior quantification.
- Cutting-Edge Instrumentation: Powered by the Thermo Scientific Vanquish NEO UHPLC system integrated with the Orbitrap Exploris 240 Mass Spectrometer.

|MC:SUBJECT|

MetaboReads

Diabetes risk, pathophysiology, and environmental determinants

These studies collectively frame diabetes as a disorder shaped by intersecting pharmacologic, biological, and environmental forces. In obesity, mechanistic work in animal models shows that GLP-1 receptor agonism improves adipose tissue function and insulin sensitivity via cyclooxygenase-2 dependent remodeling, directly addressing pathways that underlie type 2 diabetes. Large cohort data demonstrate that hemoglobin glycation index refines prediction of incident diabetes and prediabetes, capturing inter-individual variability in glycation that is not apparent from HbA1c alone. Prospective pregnancy data extend this theme to gestational diabetes, linking higher neonicotinoid insecticide exposure to increased gestational diabetes risk and identifying metabolomic mediators along taurine and hydroxypalmitic acid pathways. Together, these papers highlight how detailed metabolic phenotyping can sharpen diabetes risk stratification and reveal modifiable drivers of hyperglycemia across the life course.

Activation of cyclooxygenase-2 signaling mediates liraglutide-induced adipose lipolytic activity

Li and colleagues in EUROPEAN JOURNAL OF PHARMACOLOGY showed that liraglutide improves adipose tissue homeostasis in high fat diet induced obese mice through

cyclooxygenase 2 dependent mechanisms. They found that chronic liraglutide treatment reduced body weight, fat mass, and insulin resistance while attenuating adipocyte hypertrophy. In both obese adipose tissue and differentiated 3T3 L1 adipocytes, liraglutide upregulated browning and lipolysis markers, including PGC1α, UCP1, and ATGL. Untargeted metabolomics demonstrated increased COX 2 signaling and prostaglandin levels in subcutaneous adipose tissue from treated animals. Pharmacologic inhibition of COX 2 abolished liraglutide induced effects on adipogenesis, lipolysis, and cold induced thermogenesis, indicating that COX 2 activity is required for the full metabolic benefits of GLP 1 receptor agonism.

Hemoglobin glycation index can be used as a predictor of diabetes mellitus and prediabetes: a cohort study

Bai and colleagues in BMC ENDOCRINE DISORDERS found that hemoglobin glycation index is an independent predictor of incident diabetes and prediabetes in a large middle aged and older Chinese cohort. Using data from 3,963 participants in CHARLS followed for four years, they showed that higher baseline hemoglobin glycation index was associated with greater risk of developing both prediabetes and diabetes after multivariable adjustment. Dose response modeling using restricted cubic splines indicated a linear relationship between hemoglobin glycation index and risk across its distribution. Subgroup analyses identified a particularly strong association for diabetes in individuals aged 45 to 60 years, with odds ratios approaching four in the highest hemoglobin glycation index strata. The authors propose that hemoglobin glycation index could serve as a pragmatic biomarker to identify individuals at high glycemic risk who might benefit from early intervention.

Serum neonicotinoid insecticides levels and gestational diabetes mellitus: mediation by plasma metabolomic alterations

Wen and colleagues in ENVIRONMENTAL POLLUTION found that higher early pregnancy serum concentrations of selected neonicotinoid insecticides are associated with increased risk of gestational diabetes mellitus and that specific metabolomic changes partially mediate this link. In a nested case control study of 164 gestational diabetes cases and 328 matched controls, they observed significantly higher levels of imidacloprid, imidacloprid olefin, and desmethylclothianidin in cases. Conditional logistic regression and mixture modeling approaches indicated that each log unit increase in these compounds and their mixture was related to substantially elevated gestational diabetes risk, with desmethylclothianidin emerging as a key contributor. Untargeted metabolomics and mediation analysis identified taurine and 2 hydroxypalmitic acid as metabolites that significantly mediated the association between neonicotinoid mixtures and gestational diabetes, albeit with modest mediation proportions. These findings suggest that common pesticide exposures may perturb intermediary metabolism in early gestation in ways that predispose to impaired glucose regulation.

Diet, microbiota, and the metabolome across species and life stages

Across diverse contexts, these studies illustrate how specific dietary components and the

gut microbiota converge on shared metabolic pathways to influence host physiology. In neonatal mice, a human milk derived Bifidobacterium strain protects against necrotizing enterocolitis by reshaping the intestinal community and augmenting anti inflammatory tryptophan metabolites. In older adults with mild cognitive impairment, targeted probiotic supplementation improves cognitive performance alongside increases in indole derivatives and beneficial taxa, pointing to a tractable gut brain axis. In healthy adults, short term vitamin C intake delivered as supplements, raw produce, or juice induces distinct patterns of vitamin C kinetics and urinary metabolites that likely reflect differences in intestinal handling and microbial metabolism. Together, these papers reinforce that nutritional interventions leave a reproducible metabolic imprint, offering biomarkers that can bridge mechanistic work in animal models with human interventional trials.

From microbiota to metabolomics: how Bifidobacterium infantis YLGB-1496 shields neonates from necrotizing enterocolitis

Li and colleagues in FOOD & FUNCTION showed that a human milk derived Bifidobacterium longum subsp. infantis strain, YLGB 1496, protects neonatal mice from experimental necrotizing enterocolitis through coordinated shifts in microbiota and serum tryptophan metabolism. In a preventive model, oral administration of YLGB 1496 reduced mortality, attenuated intestinal damage, and dampened TLR4 mediated inflammatory responses. Microbiota profiling revealed marked increases in Lactobacillus and Bifidobacterium abundance during the preventive phase in treated animals. Untargeted serum metabolomics demonstrated enrichment of tryptophan derived metabolites including indole 3 acetic acid, L formylkynurenine, and 5 hydroxyindole 3 acetic acid, which are plausible ligands for AHR dependent anti inflammatory pathways. Correlation analyses linked Bifidobacterium enrichment to enhanced intestinal tryptophan metabolism, supporting a mechanism in which microbial and metabolite changes jointly confer protection against necrotizing enterocolitis.

Efficacy and Safety of Lactobacillus delbrueckii subsp. lactis CKDB001 Supplementation on Cognitive Function in Mild Cognitive Impairment: A Randomized, Double-Blind, Placebo-Controlled Clinical Trial

Baek and colleagues in NUTRIENTS showed that 12 weeks of Lactobacillus delbrueckii subsp. lactis CKDB001 supplementation improves cognitive performance in older adults with mild cognitive impairment. In a randomized, double blind, placebo controlled trial of 100 participants, the probiotic group exhibited greater improvements than placebo in global cognition, memory subscales, trail making performance, and Stroop reaction times. Fecal taxonomic profiling indicated increased relative abundance of beneficial microorganisms, particularly within Lactobacillaceae and Bifidobacteriaceae, and a pronounced expansion of Lactobacillus. Metabolomic analysis of fecal samples revealed higher levels of indole derived metabolites such as 5 hydroxyindole 3 acetic acid, indole 3 lactic acid, and indole 3 glycol in the active group. The intervention was well tolerated, and the authors propose that modulation of the gut microbiota and its indole metabolite output underpins cognitive benefits mediated through the gut brain axis.

Comparative Bioavailability of Vitamin C After Short-Term Consumption of Raw Fruits and Vegetables and Their Juices: A Randomized Crossover Study

Choi and colleagues in NUTRIENTS found that vitamin C provided as fruit and vegetable juice yields higher short term bioavailability than an equal dose delivered as powdered supplement or raw produce, while also eliciting distinct urinary metabolomic responses. In a randomized crossover study in twelve healthy adults, all three forms of vitamin C intake increased plasma and urinary vitamin C over 24 hours, but the juice condition produced the highest plasma area under the curve. Proton nuclear magnetic resonance spectroscopy of urine showed increased excretion of mannitol, glycine, taurine, dimethylglycine, and asparagine, alongside decreases in choline and dimethylamine, with patterns varying by intake form. Notably, urinary mannitol rose only in the morning, suggesting time dependent changes in osmolyte handling or microbial fermentation products. Despite these metabolomic shifts, antioxidant activity assessed by ORAC and TRAP showed only transient improvements, indicating that bioavailability and systemic antioxidant effects are not strictly concordant.

Multi-omics of therapy response, resistance, and chronic tissue remodeling

This theme spans chronic infections, cardiopulmonary myopathy, affective disorders, radiotherapy, and leukemia, yet a common thread is the use of multi omics to map how tissues remodel under therapeutic pressure and chronic stress. In chronic wounds, transcriptomic and metabolomic approaches reveal biofilm specific gene networks and support the development of RNA based diagnostics and nanomaterial therapies. Across cardiopulmonary disease, psychiatry, oncology, and hematology, proteomics and metabolomics highlight tissue specific vulnerabilities, from mitochondrial insufficiency in skeletal muscle to cytokine driven chemoresistance niches and radiosensitivity linked to amino acid and lipid metabolism. Together, these studies illustrate how mechanistic insight at the pathway level can identify druggable targets, refine biomarker panels, and inform more individualized treatment strategies.

Transcriptomic insights into biofilm dynamics and therapeutic targets in chronic wound infections (MIMET 107281)

Pendor and colleagues in JOURNAL OF MICROBIOLOGICAL METHODS reviewed transcriptomic and related omics studies that delineate biofilm formation, chronic wound pathogenesis, and emerging therapeutic interventions. Focusing on Pseudomonas aeruginosa PAO1 in ex vivo porcine skin wound models, they summarize RNA sequencing evidence that surface adhesion genes such as lapA are upregulated, while denitrification genes including nirS are downregulated during biofilm establishment. The authors discuss how targeting denitrification through nitric oxide induction and deploying agents such as silver nanoparticles, lactoferrin, exopolysaccharides, metal based nanozymes, and cerium or zinc containing microneedle patches can disrupt biofilms and enhance healing. They highlight how transcriptomics, metabolomics, electrochemical biosensors, and peptide nucleic acid fluorescent in situ hybridization have improved detection and characterization of biofilm associated infections, including mixed species communities that impair wound

closure more severely than single species biofilms. The review concludes that integrating RNA based diagnostics, molecular therapies, and advanced biomaterials will be essential for translating omics insights into clinically effective, biofilm targeted wound care.

Proteomic and metabolomic profiling nominates druggable targets and biomarkers for pulmonary arterial hypertension-associated myopathy and exercise intolerance in male monocrotaline rats

Abreu and colleagues in JOURNAL OF HEART AND LUNG TRANSPLANTATION showed that pulmonary arterial hypertension in monocrotaline treated male rats induces muscle fiber type specific structural and metabolic remodeling that can be dissected by integrated mitochondrial proteomics and metabolomics. They reported that diseased rats had markedly impaired exercise capacity, with mild atrophy restricted to type II fibers in quadriceps but affecting both type I and II fibers in soleus, alongside fibrotic infiltration in both muscles. Quadriceps exhibited reduced mitochondrial density and proteomic signatures of impaired oxidative phosphorylation and fatty acid metabolism, coupled with decreased triacylglyceride storage. In contrast, soleus showed evidence of proteasome deficiencies and disturbed phosphatidylcholine and phosphatidylethanolamine homeostasis rather than pronounced mitochondrial loss. Serum metabolite and lipid profiles nominated dimethylarginine, cysteine, and specific triacylglycerides as candidate biomarkers of exercise intolerance, and the authors highlight mitochondrial biogenesis and proteasome activation as potential therapeutic targets in pulmonary arterial hypertension associated myopathy.

Epigenetic aging and DNA methylation biomarker changes following ketamine treatment in patients with MDD and PTSD: a pilot study

Dawson and colleagues in TRANSLATIONAL PSYCHIATRY found that a course of ketamine infusions in patients with major depressive disorder or posttraumatic stress disorder is associated with reductions in several DNA methylation based measures of biological age in addition to symptomatic improvement. In twenty individuals receiving six infusions of 0.5 milligrams per kilogram ketamine, scores on the PHQ 9 and PCL 5 scales decreased as expected after treatment. Epigenetic clock analyses showed that biological age estimates derived from OMICmAge, GrimAge V2, and PhenoAge were lower following ketamine compared with baseline. Examining epigenetic biomarker proxies and surrogate protein markers, the authors identified methylation changes that paralleled shifts in established clinical biomarkers. The study suggests that ketamine can acutely modulate aging related methylation signatures and that refined epigenetic clocks may serve as sensitive readouts of biological response in treatment resistant affective disorders.

Novel strategies for investigating radiotherapy sensitivity mechanisms: integrative multi-omics and surface-enhanced Raman spectroscopy (SERS)

Li and colleagues in CHEMICAL ENGINEERING JOURNAL demonstrated that surface enhanced Raman spectroscopy guided multi omics profiling can reveal metabolic pathways associated with acquired radioresistance in A549 lung cancer cells. They engineered DNA

coated gold silver core shell nanorods optimized for SERS sensitivity, stability, and reproducibility, and generated radioresistant A549 cells through repeated low dose irradiation totaling 60 Gy. Raman omics signatures were corroborated by amino acid metabolism assays, non targeted metabolomics, and KEGG pathway analysis, which together pointed to changes in amino acid, lipid, purine, and nucleic acid metabolism as determinants of radiosensitivity. Specific alterations included downregulation of 5 hydroxytryptamine with abnormal tryptophan metabolism, disrupted fatty acid metabolism influenced by 5 aminolevulinic acid, and oxidative damage to phospholipids and nucleic acids. The authors argue that SERS integrated with metabolomics and transcriptomics offers a promising framework for discovering molecular targets and metabolic vulnerabilities to personalize radiotherapy.

Integrated metabolomic and transcriptomic analysis identifies adipogenic differentiation of mesenchymal stem cells as a driver of chemoresistance in acute myeloid leukemia

Pan and colleagues in JOURNAL OF EXPERIMENTAL & CLINICAL CANCER RESEARCH showed that adipogenic differentiation of mesenchymal stem cells promotes chemoresistance in acute myeloid leukemia cells through coupled metabolic and signaling reprogramming. Using an indirect co culture model, they demonstrated that acute myeloid leukemia cell lines grown in the presence of adipogenic mesenchymal stem cells were less sensitive to daunorubicin and cytarabine in vitro and in vivo. Nuclear magnetic resonance based metabolomics revealed altered glycolysis, glutamine metabolism, and lipid metabolism in co cultured acute myeloid leukemia cells consistent with a stress resistant phenotype. RNA sequencing identified activation of PI3K Akt signaling and elevated interleukin 6 as key features of the protective microenvironment, and pharmacologic inhibition of Akt with MK 2206 partially reversed chemoresistance. The study highlights adipogenic remodeling of the bone marrow niche as an important driver of drug resistance and nominates metabolic and cytokine pathways as targets to enhance acute myeloid leukemia treatment efficacy.

Plant defense, agricultural metabolomics, and pesticide responses

These papers collectively show how multi omics approaches can be leveraged to fortify crops, manage contaminants, optimize livestock production, and understand pesticide impacts across trophic levels. In medicinal and forage plants, integrated transcriptomic and metabolomic analyses uncover specific genes and metabolites that confer disease resistance or coordinate the production of pharmacologically important compounds. Microbial inoculants in the rhizosphere emerge as powerful tools to both immobilize toxic metals and biofortify selenium, while a rumen protected choline intervention illustrates how metabolic profiling can be used to link nutrient supplementation to improved carcass traits in ruminants. Fumigants such as ethyl formate are shown to impose substantial metabolic stress on insect pests, and work on fruit ripening links fatty acid catabolism to desirable and off flavor volatile profiles, offering a chemical roadmap for managing sensory quality. Together, these studies exemplify how detailed metabolic phenotyping can support more sustainable and precise agricultural practice.

[Multi-omics insights into the molecular basis of powdery mildew resistance and root metabolic variation in Astragalus membranaceus var. mongholicus]

Guo and colleagues in SCIENTIFIC REPORTS used integrated transcriptomic and metabolomic analyses to identify candidate genes and metabolites underlying powdery mildew resistance in Astragalus membranaceus var. mongholicus. Working with a highly resistant germplasm under natural field inoculation, they profiled root gene expression and metabolite accumulation across multiple time points after infection. Differential expression analysis, weighted gene co expression network analysis, and LASSO regression converged on six upregulated genes enriched in lipoic acid, sphingolipid, and carbon metabolism pathways. Eight discriminatory metabolites, including L tartaric acid and ornithine, were selected as potential regulatory biomarkers linked to resistance. The authors propose two key regulatory pathways connecting transcriptional and metabolic changes, providing theoretical and technical support for breeding new powdery mildew resistant Astragalus cultivars.

[Rhizosphere alkalization and microbial sulfur pathways drive Cd detoxification and Se enrichment in geogenically contaminated soil]

Wang and colleagues in JOURNAL OF HAZARDOUS MATERIALS showed that an alkalizing Stenotrophomonas strain can simultaneously reduce cadmium bioavailability and enhance selenium accumulation in crops grown on geogenically contaminated soils. Hydroponic and soil pot experiments demonstrated that inoculation with Stenotrophomonas sp. H225 increased solution and rhizosphere pH by about 0.44 to 0.47 units, reduced cadmium content in edible plant tissues by roughly half, and increased selenium uptake nearly fourfold while doubling plant biomass at the highest inoculum density. Electron microscopy and spectroscopic analyses indicated that microbially derived hydrogen sulfide promoted cadmium immobilization through cadmium sulfide precipitation. Metabolomic and transcriptomic profiling revealed activation of alkaloid and organosulfur pathways under combined cadmium and selenium stress and showed that rhizosphere communities were reshaped with enrichment of Gammaproteobacteria. The study provides the first evidence that an alkalizing microbe can concurrently mediate heavy metal detoxification and micronutrient enrichment, suggesting a pragmatic approach to improving food safety and nutritional quality.

[Untargeted metabolomic analysis of dietary rumen-protected choline supplementation in fattening lambs]

Yun and colleagues in FRONTIERS IN VETERINARY SCIENCE showed that long term rumen protected choline supplementation remodels the serum metabolome of fattening lambs and enhances carcass traits. In a 122 day feeding trial, lambs receiving 5 grams of rumen protected choline per kilogram of dry matter had higher hot carcass weight and slaughter rate compared with controls. Untargeted LC MS based metabolomics identified broad changes spanning lipid, amino acid, vitamin, and carbohydrate metabolism, with clear separation of groups in partial least squares discriminant analysis. Triacylglycerol, L methionine, plasmenylcholine, taurocholate, 1 acyl sn glycero 3 phosphoethanolamine, and

1 acyl sn glycero 3 phosphocholine emerged as candidate biomarkers associated with improved production metrics. The study supports rumen protected choline as a tool to modulate energy and lipid metabolism in ruminants in ways that translate into measurable gains in meat yield.

Integrated metabolomic and transcriptomic analysis reveals the coordinated regulatory mechanisms of artemisinin and flavonoid mediated by AaMYB8 in Artemisia annua

Han and colleagues in INTERNATIONAL JOURNAL OF BIOLOGICAL MACROMOLECULES revealed a coordinated transcriptional program, centered on the glandular trichome specific transcription factor AaMYB8, that links artemisinin and flavonoid biosynthesis in Artemisia annua. By comparing high and low artemisinin chemotypes using integrated metabolomics and transcriptomics, they observed positive correlations between artemisinin content and flavonoid levels at both the metabolite and gene expression levels. Joint analysis identified several transcription factors that activated promoters of artemisinin biosynthetic enzymes while simultaneously upregulating flavonoid synthase genes, pointing to shared regulatory modules. Functional studies showed that overexpression of AaMYB8 increased artemisinin content, whereas its repression decreased artemisinin and associated flavonoids. These findings support metabolic engineering strategies that co optimize artemisinin and flavonoid production to strengthen Artemisia based therapies against malaria.

The fumigant ethyl formate exposure induces metabolic changes in the citrus mealybug, Planococcus citri (Risso) (Hemiptera: Pseudococcidae)

Lee and colleagues in ECOTOXICOLOGY AND ENVIRONMENTAL SAFETY found that exposure to the fumigant ethyl formate induces pronounced metabolic and lipidomic disturbances in the citrus mealybug Planococcus citri. Using liquid chromatography quadrupole time of flight mass spectrometry, they profiled metabolites in adults exposed to lethal LCt10 and LCt50 regimens and observed activation of central carbon metabolism, amino acid metabolism, and nucleotide pathways. Energy mobilization through glycolysis, gluconeogenesis, and the tricarboxylic acid cycle was accompanied by upregulation of detoxification related pathways, including cytochrome P450 and glucuronate interconversion. In contrast, glycerolipid, glycerophospholipid, and sphingolipid metabolism were suppressed, consistent with disruption of membrane integrity and redox homeostasis. The authors conclude that ethyl formate exerts its insecticidal effects by simultaneously driving energy demanding detoxification and compromising membrane associated lipid metabolism.

Investigating the aroma transition during rapid mango ripening driven by dynamic catabolism of fatty acids

Wang and colleagues in FOOD CHEMISTRY showed that dynamic catabolism of linolenic and linoleic acids governs the transition from desirable to off flavor volatile profiles during rapid mango ripening. Volatilomics profiling across immature, ripe, and overripe stages identified 151 volatile compounds, with 23, including (E,Z) 2,6 nonadienal and geraniol,

contributing most strongly to aroma. Immature fruit were characterized by C6 aldehydes such as (E) 2 hexenal that impart green notes, whereas overripe fruit accumulated volatiles like (E) 2 nonenal and (Z) 4 heptenal associated with waxy and off odors. During ripening, linolenic acid metabolism generated key aldehydes that define characteristic mango aroma, while in overripe fruit linolenic flux declined and linoleic acid decomposition increased by nearly half, driving off flavor formation. These results provide a mechanistic link between fatty acid oxidation pathways and sensory attributes, informing strategies to manage flavor quality in industrial mango processing.

Natural product resources and health: from chemodiversity to clinical outcomes

The final theme highlights how systematic characterization of natural product resources can translate into tangible health benefits. Work on Brazilian cyanobacteria exemplifies how metabolomics integrated with bioassays can prioritize strains and molecular features linked to antibacterial, cytotoxic, and antileishmanial activities. A regional multi omics compendium of medicinal species from the pan Shennongjia region organizes tens of millions of molecular entities within a phylogenetic framework and validates their therapeutic relevance through focused case studies. In reproductive endocrinology, a traditional multi component herbal formula is dissected using metabolomics and network pharmacology to reveal pathways by which it improves oocyte quality and in vitro fertilization outcomes in women with diminished ovarian reserve. Together, these initiatives move beyond single compound discovery toward platform resources and mechanistic insights that connect chemodiversity to clinical endpoints, showing how conservation, taxonomy, and omics based chemistry can be aligned with human health.

Chemodiversity of Cyanobacteria from Brazil Investigated by Metabolomics and Bioassays

da Silva and colleagues in ACS OMEGA used untargeted metabolomics combined with bioassays to survey the chemodiversity and bioactivity of cyanobacterial strains collected across Brazil. Nineteen cultured strains were extracted, prefractionated, and tested for antibacterial, cytotoxic, and antileishmanial activities while the same fractions were characterized by UHPLC high resolution tandem mass spectrometry. Computational tools including NP Analyst and Global Natural Products Social Molecular Networking integrated bioactivity data with LC MS features to prioritize candidate metabolites associated with strong phenotypic effects. Strains from the genera Calothrix and Phormidium yielded particularly rich sets of high priority molecular features that correlated with potent bioactivity. The study positions Brazilian cyanobacteria as promising reservoirs of novel natural products and showcases a scalable workflow for aligning metabolomic fingerprints with functional screening.

Omics-based profiling and therapeutic potential of natural components in pan-Shennongjia medicinal herbs

Song and colleagues in CHINESE MEDICINE constructed a multi omics resource that catalogs natural components and therapeutic potential of medicinal species from the

biodiverse pan Shennongjia region. They integrated 405 representative species, corresponding to 323 traditional Chinese medicine materials, into a genus and species level phylogenetic tree and identified clade specific enrichments at the family level. Case studies of Chrysanthemum indicum var. aromaticum and Dendrobium flexicaule showed environment driven diversification of polysaccharide and volatile terpenoid profiles, respectively, illustrating adaptive metabolomic specialization. The Shennongjia Herbs Multi Omics Components database aggregates over 20 million molecules, including small RNAs, small peptides, secondary metabolites, and carbohydrates, and was validated through targeted analyses of secondary metabolites and small RNAs in Coptis chinensis and small peptides in Scolopendra subspinipes mutilans. This regional scale omics compendium provides a foundation for conservation and sustainable utilization of pan Shennongjia medicinal resources and a platform for systematic mining of valuable natural products.

Integrating network pharmacology and metabolomics to elucidate the mechanism of action of Yangluan formula for treating of diminished ovarian reserve

Wang and colleagues in JOURNAL OF CHROMATOGRAPHY B-ANALYTICAL TECHNOLOGIES IN THE BIOMEDICAL AND LIFE SCIENCES demonstrated that the Yangluan Formula improves in vitro fertilization outcomes in women with diminished ovarian reserve and used metabolomics and network pharmacology to investigate its mechanisms. Compared with untreated patients with diminished ovarian reserve, women receiving the herbal formula showed higher two pronuclear fertilization rates, increased numbers of cleaved embryos, and more high quality day 3 embryos, approaching outcomes seen in women with normal ovarian reserve. Untargeted metabolomics of follicular fluid, analyzed with MetaboAnalyst, identified four key metabolites and implicated pathways in glycine, serine, alanine, and threonine metabolism. Network pharmacology and molecular docking linked Yangluan Formula compounds to targets such as monoamine oxidase A and B, myeloperoxidase, xanthine dehydrogenase, and phosphodiesterase 3A. The authors propose that modulation of amino acid and redox pathways via these targets contributes to improved oocyte competence and embryo development in diminished ovarian reserve.

Back to Top

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Metabolomics Events

Back to top

Bits & Bites #9: Compound ID in nontargeted analysis by integrating MS, MS/MS, retention time, and biological likelihood

December 4, 2025

Venue: Online

The course is taught by Dr. Oliver Fiehn, UC Davis and requires no prior programming experience.

Short description of the course: Metabolomics data can only be interpreted if metabolites are correctly identified. Confidence in metabolomic data reports requires a transparent strategy for combining different types of information. Accurate mass and MS/MS is often not sufficient, because many types of isomeric compounds exist. UC Davis offers Mass.Wiki to match user data against a standardized repository that includes retention time predictions and matches against biological specimens in UC Davis data, GNPS, MetabolomicsWorkbench, and MetaboLight repositories. After introductory remarks, participants will work in compound annotations, including for currently unidentified compounds that we explore in 'Fuzzy Searches'.

Check for more details

EBRAINS Summit 2025

December 8 - 11, 2025

Venue: Brussels

The EBRAINS Summit 2025 will feature scientific talks with leading experts, a public day, a

science slam, poster sessions, and a science market exhibition - all focused on advancing digital neuroscience. This year's programme includes a special joint day with the International Neuroinformatics Coordinating Facility (INCF).

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

Visit the website for more details

MANA SODAMeet

December 9, 2025

Venue: Online

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

Learn more and register here

2nd ASMS Winter Conference

Mass Spectrometry in Microbial Sciences

January 29 - February 1, 2026

Venue: Santa Fe, New Mexico, United States

The conference will showcase leading work in the development (instrumentation, methods, data analysis, etc.) and application (natural products discovery, biotransformation,

microbiome research, etc.) of mass spectrometry to microbial systems. Join the conference for a unique opportunity to gather mass spectrometrists and forward-thinking microbiologists.

Abstract submission deadline: **December 12, 2025**
Registration deadline: **December 19, 2025**

Learn more and register here

World Critical Care & Anesthesiology Conference 2026 (WCAC26)

March 6 - 7, 2026

Venue: Bangkok, Thailand

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

Registration deadline: **December 10, 2025**

Metabolomics in Life Science 2026

January 27 - 28, 2026

Venue: Vävenscenen, Umeå, Sweden

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

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

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

Join the web seminar

Visit the website for more details

2026 Prague Metabolism and Signaling Symposium

June 24 - 27, 2026

Venue: Prague, Czech Republic

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

Check for more details

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Job Title	Employer	Location	Source
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Research Scientist 4	G-27 Division of Environmental Health Sciences	Albany, New York, USA	Metabolomics Society
Postdoctoral Fellow – Metabolomics, Proteomics, Exposomics, and Biology	Metabolomics & Systems Biology Laboratory (Huan Lab), Department of Chemistry, University of British Columbia	Vancouver, BC, Canada	University of British Columbia
Post-Doctoral Research Fellow	MITACS and Nova Medical Testing Inc	Edmonton, AB, Canada	University of Alberta
Senior Research Scholar - Mass Spectrometry Metabolomics	North Carolina State University	Raleigh, NC, USA	North Carolina State University

Back to top

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Back to top