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MetaboNews

This month in metabolomics

February, 2026

Vol 16, Issue 2

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



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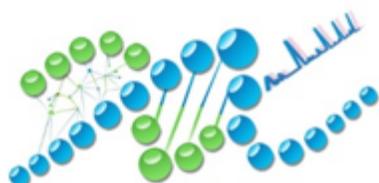
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METABOLOMICS SOCIETY
EARLY-CAREER MEMBERS NETWORK

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

General Enquiries

info@metabolomicssociety.org

Conference Corner



Join us in Buenos Aires!

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

June 21 – 24, 2026

www.metabolomics2026.org

Abstract Submission Open!

Abstract submission is open – plan to submit your work soon. Submissions for oral abstracts will be accepted through March 5. Poster abstracts will continue to be accepted through May 14. Take a moment to [review the webpage](#) for abstract guidelines, themes, sub-topics and scoring rubric.

There are several Travel Awards available to support all types of participants. Review [the details](#) online before submitting your abstract. Most awards also have a membership requirement, meaning you need to be a member of the Society as of March 21, or you need to register for the conference as a Non-member by this date.

Registration Coming Soon

The Society is transitioning to a new platform, thank you for your patience as we are under construction. Conference registration and Society memberships will be available online very soon. In the meantime, you can view the [registration fees](#) and important dates on the website.

Additional details regarding membership will be provided shortly.

See you in Argentina!

Members Corner

Board of Directors

Message from Warwick (Rick) Dunn, President

Dear Metabolomics Society Members and metabolomics friends,

Organisation of the annual conference in Buenos Aires in late June is progressing well and I hope to see many of you there. One of my goals as President was to ensure the society represents all members geographically and so it is a pleasure the society will hold its first conference in South America.

We have a range of great speakers from across the globe and at different career stages. As plenary speakers we have Marta Cascante and Jessica Lasky-Su who were awarded Honorary Fellowships in 2025 as well as Mariana Simões Larraz Ferreira, Huiru Tang and Fidele Tugizimana. As keynote speakers we have Ricardo R. da Silva, Antonia García, Isabel Garcia Perez, Jia Li, Edwin Madala, J. Rafael (Rafa) Montenegro Burke and Louis-Félix Nothias.

Thank you to all our sponsors who have committed to the conference already, your support helps us provide benefits to the society members at the conference. There are multiple types of sponsorship available. see here for further information –<https://www.metabolomics2026.org/index.cfm?pgid=530>.

The portal for submission of abstracts for oral and poster presentations is open and will close on March 5th for oral submissions but will stay open until May for poster presentations. Go to <https://www.metabolomics2026.org/index.cfm?pgid=603> to submit your abstracts.

The conference website is available at <https://www.metabolomics2026.org/>.

On a separate note. I was recently asked to speak at a Schwartz Round with a topic of 'Space to breathe'. On reflection I realised I have two major spaces to breathe, one is beautiful downtown Bramall Lane where Sheffield United play their home football games and the other is walking anywhere in nature (though hopefully with a view from a mountain summit). I also realised that maintaining a good work-life balance is difficult and has to be worked at. To all our members, remember to maintain a balance and enjoy the delights of South America in June.

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)

Virtual Networking Event

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

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

EMN Webinars

January Webinar

The EMN committee extends its gratitude to the speakers **Prof. Masanori Arita** from National Institute of Genetics, **Dr Shohei Nakamukai** from RIKEN Center for Sustainable Resource Science, and **Dr Eisuke Hayakawa** from Kyushu Institute of Technology for the January webinar entitled "*Advancing Data Sharing, Prediction, and Reuse in Metabolomics*". The webinar recording is available on the MetSoc website: <https://metabolomicssociety.org/resources/multimedia/emn-webinars-2026>

February EMN Webinar — Register Now!

The EMN Committee is excited to welcome **Prof. Alessandra Sussulini** (UNICAMP, Brazil; Head of LaBIOmics) and **Dr Henrique Caracho Ribeiro** (Postdoctoral researcher at Örebro University, Sweden) for our Thursday, 26 February webinar (13:00 UTC). Prof. Sussulini will present metabolomic studies in neuropsychiatric disorders, highlighting bipolar disorder, and discuss how natural psychoactives (including ayahuasca and cannabis) may modulate key metabolic pathways relevant to depression and Alzheimer's disease. Dr Ribeiro will then introduce systems biology approaches to brain disorders, showing how integrated omics and computational modelling can support mechanistic insights and the development of diagnostic/prognostic prediction models. Register here: https://zoom.us/webinar/register/WN_xGQBOHAWTqGANruiZVpyuw

Membership News for 2026

The Society is transitioning to a new membership platform this month. If you have an existing membership, your membership will be transferred to the new system. You will have one profile to manage all Society interactions, including conference registration, abstract submission, and voting in elections.

The new system will also offer a multi-year membership of 3 years (for full membership only), which will save the renewal step for you, and reduce the number of reminders in your Inbox, a great option all around!

Look for an e-mail with your renewal options when your membership approaches expiration, and thank you for your patience while we transition to the new system.

International Affiliates Corner



Réseau Français de Métabolomique et Fluxomique (RFMF)

Visit <http://www.rfmf.fr/>

RFMF Greetings for 2026

Dear members of the Francophone Network of Metabolomics and Fluxomics (RFMF),

At the start of this new year, the RFMF Board of Directors would like to express our gratitude. Thank you for your trust, your commitment, and the energy you bring to our network. Thanks to you, the RFMF continues to offer inspiring events, foster ambitious projects, and strengthen ties between the metabolomics and fluxomics communities, both within the Francophonie and internationally.

May 2026 be a bright and stimulating year: filled with discoveries, experiences, collaborations, and memorable moments. We wish you health, happiness, and success, always driven by the curiosity and passion that advance science.

Let's maintain this collective momentum: together, let's continue to build, share, and grow our community, supporting the emergence and flourishing of young talent in metabolomics around us.

Looking Back at 2025: A Landmark Year for Our Community (Thanks to You!)

- The RFMF organised its **17th Scientific Conference in Paris**: a special "20th anniversary" edition, vibrant and expertly organised by a stellar local team. We named **Patrick Giraudeau** as the **2025 Honorary Member** for his contributions, dedication, and work in NMR metabolomics. [Thomas Brunet](#) received the **Rolin-Portais Thesis Prize** for the quality of his research. **281 participants** joined us in Paris.
- We enabled **19 young researchers** to attend training through **Travel Grants** (MetSoc 2025, RFMF Scientific Conferences, and others) and/or **Training Grants**, and we **funded 3 events** led by our community members.
- A **YouTube channel** is now available to access all our recorded webinars—search for "**RFMF_official**" on YouTube.
- The first RFMF **thematic school**, organised by Pierre Pétriacq, took place in Sète. Focused on plant metabolome annotation, it brought together **31 participants**.

2026: New Developments and Upcoming Information

- A **revamped website** featuring an **interactive skills map** and a **calendar listing all events** (training, conferences related to our fields). Visit the **RFMF website** to explore these resources.
- A **partially renewed Junior Board**. We warmly thank all outgoing members for their contributions to our network. Special thanks to Marine Leterte, an exceptional president, Loïc Le Gregam, and especially our "Swiss Army knife" from Toulouse, Amandine Rocher, for her outstanding dedication and unwavering support.

...and Continuity:

- A **second thematic school** on metabolomics in the health sector (Autumn 2026).
- Our **18th Scientific Conference** will be held in Lille from **20–22 May 2026**, with a preliminary day of workshops on **19 May**. The local team is preparing an exceptional programme with outstanding speakers.
- **RFMF Webinars** will take place twice in 2026, in April and October (dates to be confirmed).
- The **Rolin-Portais Thesis Prize (€500)**: Don't hesitate to apply or encourage your students to do so (submit applications to rfmj.junior@gmail.com by **28 February 2026**; details on the RFMF website).
- The **mentoring programme** is back for its 5th edition. Don't miss the launch workshop at our upcoming Lille Conference! We are also looking for mentors to support our young researchers. Contact Corentine Goossens, the programme coordinator.
- The **open mailing list** remains available for sharing job offers, information, and community updates (subscribe/unsubscribe [here](#)).
- A **week-long Workflow4Metabolomics training** will be held in person from **20–24 April in Rouen** (workflow4metabolomics.org/W4E2026).

Memberships for 2026 are now open. They grant access to travel and training grants, as well as discounted rates for our scientific conferences. Renew yours on the "[Become a Member](#)" page of our website.

All these initiatives are carried out in close collaboration with the dynamic and enthusiastic Junior Board. Feel free to reach out to us (Board and Junior Board) for support with your projects.

We wish you another wonderful year in 2026 and look forward to seeing you soon for great

science (and great food!).

The Board Members

[Audrey Le Gouellec](#) President

[Pierre Pétriacq](#) Vice President

[Justine Bertrand-Michel](#) Secretary

[Florence Mehl](#) Treasurer

[Touboul David](#)

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And the RFMF Junior Board

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[Ghina Hajjar](#) Vice President

[Nathalie Lacrampe](#) Treasurer

[Thomas Brunet](#) Secretary and Communications Officer

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[Jeremy Monteiro](#)

[Rochelle Kouakou](#)

[Axelle Bourez](#)

Picture taken for the CA² in Grenoble in January 2026



The Juniors' Corner

Are you a junior research fellow planning to attend the next #MetSoc conference in Buenos Aires? --The RFMF is pleased to announce that you can apply for a travel grant to support your trip!

Requirements:

- Be aged 33 or under
- Be up to date with RFMF membership fees
- Be a master's or doctoral student, post-doctoral researcher or non-permanent scientific or technical staff member
- Plan to attend the conference and present a poster or oral presentation on metabolomics or fluxomics.

Guidelines:

You will be asked to submit the following:

- Your CV (maximum 3 pages).
- A cover letter (maximum 2 pages) detailing the work to be presented and the reasons why you chose this conference.
- The abstract of the communication (poster or oral) submitted
- A description of the budget needed to cover travel expenses (registration, travel, lodging). Note that a maximum of €1,000 can be awarded.

Deadline: 21 April 2026

To apply and for more information, please visit our website <https://www.rfmf.fr/bourse-de-voyage/>

#bourse_de_voyage #travel_award #metabolomics #lipidomics #fluxomics



Latin American Metabolic Profiling Society (LAMPS)

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

Dear LAMPS Members,

The 22nd Annual Conference of the Metabolomics Society ([Metabolomics2026](#)) will be held for the first time in Latin America. To support the participation of **graduate students and postdocs residing and studying/working in Latin American countries**, the Latin American Metabolic Profiling Society (LAMPS) will award travel grants to cover registration fees.

Travel grant awardees will be announced on March 25, 2026. Gender balance, equitable geographical and minority representation will be taken into consideration.

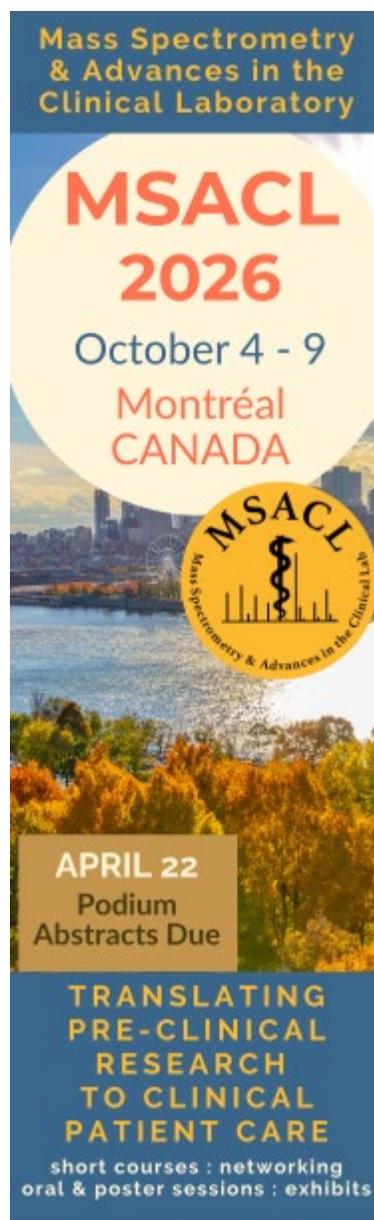
Guidelines and requirements:

- Deadline: March 8, 2026.
- Send the following information to lampsnetwork@gmail.com using as e-mail subject "Travel Grant Metabolomics 2026".
- The graduate student/postdoc must be residing and studying/working in a Latin American country.
- The graduate student/postdoc must have submitted an abstract for oral or poster presentation. Please, attach the submission proof.
- The awardees will have two days to communicate the acceptance of the travel grant after the notification.
- The awardees must be [members of the Metabolomics Society](#) or become members before accepting the travel grant.

- Attach a short CV (Maximum 1 page).
- Attach a <300-word letter indicating your motivation for attending Metabolomics 2026. This letter must have the approval or endorsement of your advisor.

Looking forward to seeing you all in June in Buenos Aires!

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[Perspectives](#)

Dr. Mary-Ellen Harper



Mary-Ellen Harper PhD is a Full Professor in the Department of Biochemistry, Microbiology and Immunology in the Faculty of Medicine at the University of Ottawa. She is also the Director of the University of Ottawa's Institute of Systems Biology, and for 6 years has directed an NSERC CREATE Graduate Training Program in metabolomics, Metabolomics Advanced Training and International Exchange. 'MATRIX'. Dr. Harper's undergraduate degree was in Human Clinical Nutrition (Guelph); graduate degree was in Biochemistry (Ottawa) and postdoctoral training was in Biochemistry (Cambridge, UK). Her research focuses on metabolic diseases mainly obesity and diabetes, with studies in model systems and clinical populations. In 2021 she was awarded the Diabetes Canada Lifetime Achievement Award. Dr. Harper holds a Tier 1 Canada Research Chair in Mitochondrial Bioenergetics and Metabolic Health, and has published 212 peer-reviewed papers, and supervised 35 graduate students and 12 postdoctoral fellows. Her research is currently funded by CIHR, NSERC, Mitacs, Connexus, and the University of Ottawa Heart Institute.

We asked her about the growing significance of metabolomics, and her career in metabolic research:

1. How has your understanding of metabolic disease mechanisms evolved over 30 years, and how has metabolomics reshaped this perspective?

It has evolved a lot! This is largely because the field of metabolomics developed extensively since 1995 when I was first hired as an Assistant Professor. Metabolomics is extremely valuable as it provides a systems-level view of biochemical pathways, enabling researchers to move beyond isolated gene/protein studies. Metabolic diseases have complex origins and metabolomic approaches have greatly helped to advance our understanding of these diseases and many others. In the research done by my group, I

continue to learn new things about unique metabolites and pathway activities. Early in my career, we focused on single proteins or pathways. The Human Genome Project (completed in 2003) shifted attention to genetics, but researchers soon realized genes alone couldn't explain complex diseases like obesity and diabetes. These diseases usually have multigenic origins with many genes contributing to risk; genetic factors are important, and metabolic factors compound this risk.

Metabolomics began to be much more established in the early-to mid 2000s, and the development of high throughput analytical platforms and data analysis software like MetaboAnalyst, launched in 2009, were key. Metabolomics was a game-changer in metabolic biochemistry -it revealed how interconnected pathways can drive insulin resistance (e.g., fatty acid and branched chain amino acid catabolism in the context of mitochondrial dysfunction). Our first forays into metabolomics were in ~2008 in collaboration with Dr. Oliver Fiehn at the West Coast Metabolomics Center at University of California (Davis) as we were collaborating with his colleague, Dr. Sean Adams. Metabolomics is the youngest of the major omics approaches that are key to systems biology research. It, like other omics approaches are 'hypothesis-generating' and opened our eyes to novel mechanisms to explore in metabolic diseases. Systems biology approaches allow the integration of data from multi-omics approaches such as genomics, transcriptomics, proteomics and metabolomics. At the University of Ottawa Institute of Systems Biology (OISB), we promote research training and collaborations in multi-omics approaches.

2. What are the major challenges for those who want to conduct metabolomic research for the first time?

Metabolomics is inherently multidisciplinary, requiring expertise in analytical chemistry, biostatistics, bioinformatics, as well as the biological sciences. Thankfully however, much of the research is done as a 'team-sport' together with metabolomics experts in core facilities at universities and institutes. For example, at the University of Ottawa, one of the 26 cores is the Metabolomic Core Facility (MCF), which provides cutting-edge targeted metabolomics, untargeted metabolomics and stable isotope tracing analyses (SITA) to the uOttawa research community and other academic and industrial partners. Potentially interested researchers can meet with staff to discuss needs and suitable methodologies. The MCF has made a huge difference to uOttawa biomedical research, especially that in the area of metabolic diseases, and there are exciting plans for new infrastructure/capabilities in the MCF. So, while there is a steep learning curve, there are usually enthusiastic and well-informed scientists in an institution's metabolomics center or

core, if they are fortunate enough to have one. It is very important that you enter your metabolomic projects with a very well-defined research objective and that you invest a lot of effort into study design. Then it is important to identify the most suitable analytical platform and data analysis tools. No single analytical platform or method can capture the entire diversity of metabolites in biological samples, so it's important to choose the best approach. Another thing that helps to get over initial hurdles is taking workshops and courses in metabolomics. In 2018 we were fortunate to receive graduate training program funding for metabolomics through an NSERC CREATE award. Together with Université de Montréal and McGill University we have trained over 40 graduate students as well as some undergraduate students and postdoctoral fellows. One of the new courses that we established as part of this program was a Metabolomics 'Base Camp', an intensive two-week graduate course in theoretical and practical aspects of metabolomics. We plan to sustain this course for many years to come.

3. Can you describe pivotal discoveries in your career that had a major impact in metabolic disease research?

So much of what we all do is about building on the previous work of others. I've always been fascinated by how fluxes through interrelated pathways are controlled, and by metabolic 'inefficiencies'. Inefficiencies, such as 'futile cycles' often have beneficial physiological functions that are initially not understood. This has been the case for uncoupled mitochondrial oxidative phosphorylation in tissues throughout the body, which now is thought to be associated with the adenine nucleotide translocator. In brown adipose tissue (BAT) it is associated with uncoupling protein 1. In BAT it is clear that the function is thermogenesis, but in other tissues it is poorly understood but may be important for redox and oxidative stress control. I worked on BAT thermoregulation in my PhD, and my group still works in this area. In my postdoctoral training in Martin Brand's group at Cambridge we studied the mechanisms of inefficient mitochondrial metabolism in other tissues, such as the liver. The findings from his laboratory c.1990 were quite pivotal in showing that mitochondrial inefficiencies were real (not an artifact within the experimental system), and were regulated for example by thyroid hormones. Energy transduction mechanisms in mitochondria are more inefficient in hyperthyroid than hypothyroid states. The idea that inefficiencies in metabolic pathways could be beneficial was initially thought to be counter-intuitive, but now makes sense. One of the approaches that we used in the early days was metabolic control analysis, which allows researchers to identify the distribution of control of flux within pathways. This can now be combined with stable-isotope tracer analysis (SITA) to identify the major sites of flux control in pathways in healthy and diseased states as well as sites affected by drug treatment in cells, tissues, organoid

systems, etc. The rapid emergence of bioinformatics and computational biology/AI is also having a major impact on our capacity to analyse large omics data sets and to model and text hypothesized metabolic processes.

4. Where do you see metabolomics having the greatest impact in metabolic disease research over the next decade?

I think that emerging applications could include nutrition-personalized interventions, and metabolic strategies that will hopefully improve treatments for a wide range of diseases that are normally not thought of as 'metabolic diseases', including cancer and neurodegeneration, for example. Metabolism becomes disordered in many diseases and can contribute significantly to pathology. So targeting metabolic dysfunction can help to minimize disease development, or in the case of tumour cells, targeting the unique metabolic processes can be used to selectively disadvantage or kill those cells. The application of metabolomics in research, including biomarker discovery should significantly advance precision nutrition and medicine (e.g., real-time metabolomic feedback (e.g., postprandial lipidomics) for personalized diets). In our work with adults with obesity and type 2 diabetes we have focused on interindividual variability in treatment responses and used metabolomic and lipidomic approaches to demonstrate the marked differences from person to person. Clearly, one size does not fit all. So we think that in the future there will be better personalized approaches for the prevention and treatment of metabolic diseases. Finally, we are very excited about applying single-cell metabolomics to map metabolic heterogeneity within tissues, biopsies and advanced organoid models to improve the understanding of intercellular communication and interdependencies. For example, tumor cells can rely heavily in non-cancer cells in their environment for metabolites to survive. To cut off this supply of metabolites from tumors is one way to target and kill cancer cells. Integrating bioinformatics and AI to decipher these complex datasets will be pivotal. Overall, I expect that metabolomics will become the backbone of 'systems medicine' within a decade or so.

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[Conference Spotlight](#)

7th Annual Canadian Metabolomics Conference



Metabolomics of Health and Disease

Don't forget to register for the 7th Annual Canadian Metabolomics Conference (CanMetCon 2026), taking place **April 30–May 1, 2026**, at the **York University Cornerstone Centre** in Toronto, Ontario.

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

The conference theme, “**Metabolomics of Health and Disease**,” will be explored through plenary lectures from leading Canadian and international experts, including Oliver Fiehn and Sebastian Böcker, alongside invited speakers such as Rafa Montenegro-Burke, David Wishart, Derek Wilson, Jason Acker, and more.

Abstract Submission

Abstract submissions are now open for:

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

We are accepting abstracts in the following thematic areas:

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

Submission deadline: March 20, 2026

Submission Form: <https://forms.gle/BP2vyLn2LFrBZunZ7>



April 30th - May 1st, 2026



York University Cornerstone Centre
Toronto, Canada

The 7th Canadian **Metabolomics** Conference 2026

Metabolomics of Health and Disease

Plenary Speakers:



Dr. Oliver Fiehn
University of California, Davis



Dr. Sebastian Boecker
Friedrich-Schiller-Universität
Jena

Featured Speakers:

- Dr. Jason Acker (University of Alberta)
- Dr. Daina Avizonis (McGill University)
- Dr. Christoph Borchers (McGill University)
- Dr. Rafa Montenegro Burke (University of Toronto)
- Dr. Philip Britz-McKibbin (McMaster University)
- Dr. David Goodlett (University of Victoria)
- Dr. Rachel Gregor (University of Toronto)
- Dr. James Harynuk (University of Alberta)
- Dr. Tao Huan (University of British Columbia)
- Dr. Hartland Jackson (University of Toronto)
- Dr. Thomas Kislinger (University of Toronto)
- Dr. Mohit Kapoor (University of Toronto)
- Dr. Liang Li (University of Alberta)
- Dr. Courtney Toth (University of Toronto)
- Dr. Thomas Velenosi (University of British Columbia)
- Dr. Dajana Vuckovic (Concordia University)
- Dr. Derek J Wilson (York University)
- Dr. David Wishart (University of Alberta)
- Dr. Jianguo (Jeff) Xia (McGill University)



Scan for full details:



Visit the [official conference website](#) for full details, registration, and the complete speaker list.

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MetaboReads

Food bioactives and engineered functional ingredients

These papers use metabolomics and allied omics in the way the field most needs: not to decorate a nutraceutical claim, but to narrow plausible mechanisms. Across phytochemicals, whole-food interventions, and fermentation-modified ingredients, the strongest studies tie metabolic change to a defined target or pathway, whether that is xanthine oxidase, IL-17 signaling, mitochondrial homeostasis, or specific fatty acid programs. What makes this group persuasive is the move from compositional richness to functional specificity. The implication is straightforward: food-derived interventions become scientifically interesting when the chemistry, the host response, and the mechanistic readout are all brought into the same frame.

[Integrated Analysis of Proteomics and Metabolomics Uncovered the Anti-Inflammatory Mechanisms of Baicalin in CIA Rat FLS.](#)

Wang and colleagues in *Current Issues in Molecular Biology* showed that baicalin suppressed inflammatory activity in fibroblast-like synoviocytes from collagen-induced arthritis rats. Integrated proteomic and metabolomic analyses identified retrograde endocannabinoid signaling as the principal shared pathway altered by treatment. Baicalin reduced multiple NADH dehydrogenase subunits together with GRIA2 and GABRA5, while increasing gamma-aminobutyric acid and phosphatidylcholine and decreasing phosphatidylethanolamine. The combined dataset linked baicalin exposure to changes in inflammatory signaling and mitochondrial-associated metabolism in CIA rat FLSs.

[Urate-lowering effect of delphinidin-3-glucoside in red kidney beans via binding to the FAD site of the XO enzyme.](#)

Chen and colleagues in *Journal of Advanced Research* found that delphinidin-3-glucoside from red kidney beans lowered urate by acting directly on xanthine oxidase. Composition-target-metabolic network analysis, molecular dynamics, and surface plasmon resonance placed the compound at the FAD site rather than the catalytic center of the enzyme. This binding pattern was associated with disrupted electron transfer across xanthine oxidase redox centers and lower uric acid production in biochemical, cellular, and mouse models. Treatment was also accompanied by broader metabolic shifts involving methionine, proline, and folate pathways.

[Cuscuta chinensis Lam. extracts ameliorate type 2 diabetes by regulating metabolism and gut microbiota.](#)

Zhou and colleagues in *iScience* found that *Cuscuta chinensis* extracts improved glycemic control in rats with type 2 diabetes while also altering metabolic and microbial profiles. Chemical analysis showed that the extracts were rich in flavonoids and phenolic acids. Treatment lowered blood glucose, improved body weight, and partially corrected broader metabolic disturbance. Integrated metabolomics and 16S sequencing linked these effects to changes in unsaturated fatty acid biosynthesis, including oleic acid and alpha-linolenic acid pathways, together with shifts in gut

microbial composition.

[Microbial Consortium Fermentation Remodels the Metabolite Profile and Enhances the Biological Functionality of Stevia rebaudiana Leaves.](#)

Chu and colleagues in *Foods* found that a *Bacillus subtilis*-*Candida utilis* fermentation system substantially changed the chemical profile of *Stevia rebaudiana* leaves. After optimization of temperature, time, inoculum ratio, and moisture, the fermented material showed higher chlorogenic acid, increased total phenolics and flavonoids, and stronger antioxidant capacity than the unfermented control. Untargeted metabolomics showed broad remodeling across phenolic acids, flavonoids, and terpenoids, including the appearance of new bioactive compounds. In a laying-hen model, the fermented material was also associated with measurable antioxidant and anti-inflammatory effects.

[Multi-Omics and Molecular Docking Reveal That Oats and Oat Bran Alleviate Chronic Colitis Via IL-17 Pathway Modulation.](#)

Duan and colleagues in *Nutrients* found that whole oats and oat bran alleviated chronic colitis in mice through metabolite and transcriptomic changes linked to inflammatory signaling and barrier repair. Untargeted metabolomics identified ursodeoxycholic acid, 3-(3-hydroxyphenyl)propionic acid, and avenanthramide C as key treatment-associated metabolites. Molecular docking linked these metabolites to IL-17 pathway proteins including IL-17A, TRAF6, and ACT1. Transcriptomic and RT-qPCR analyses also showed modulation of IL-17, PI3K-Akt, and TNF signaling, together with higher expression of tight junction proteins and lower inflammatory cytokine levels.

Host-microbe and tissue-scale metabolic remodeling

This month's papers in this theme show that disease-associated metabolism is spatially patterned, organ-coupled, and often inseparable from microbial ecology, with bile acids, indole metabolites, amino acid flux, and lipid classes shifting in context-dependent ways. The recurrent lesson is that a single circulating biomarker rarely captures the biology that matters. Better disease models will need to treat metabolism as a distributed system rather than a uniform whole-body signal.

[Maternal diet-induced hypercholanemia alters gut microbiota and metabolome in adult female Western diet-fed offspring.](#)

Ovadia and colleagues in *Experimental Biology and Medicine* found that maternal hypercholanemia altered the later microbial and metabolite response of adult female offspring to a Western diet. In a mouse model of gestational cholestasis, offspring exposed in utero to excess cholic acid developed a distinct cecal bile acid and microbiota profile under obesogenic feeding. The usual Western-diet increase in secondary bile acids was attenuated in exposed offspring. Several bile acid species, including cholic acid and dehydrocholic acid, were also reduced relative to controls.

[Hidradenitis suppurativa was associated with consistent metabolic shifts across moderate and severe disease.](#)

Vorcakova and colleagues in Archives of Dermatological Research found that moderate and severe hidradenitis suppurativa shared a stable systemic metabolic signature. NMR profiling of blood samples showed hyperglycemia, nonketotic acidosis, elevated branched-chain amino acids, reduced branched-chain keto acids, and higher circulating succinate, phenylalanine, and tyrosine relative to controls. Most of these changes varied little between the moderate and severe groups. The dataset therefore placed metabolic dysregulation across the disease range examined rather than only in the most advanced cases.

[Multi-omics reveal the key role of gut microbiota metabolism in adenine-induced chronic kidney disease.](#)

Xin and colleagues in Toxicology and Applied Pharmacology found that adenine-induced chronic kidney disease in mice was accompanied by coordinated disruption across gut microbial structure, microbial metabolites, circulating metabolites, and renal tissue chemistry. Integrated analysis identified 94 co-regulated metabolites, including increased indolelactic acid, decreased indole-3-propionic acid, and marked remodeling of taurine-conjugated bile acids. Correlation analyses linked Lactobacillus with several upregulated metabolites and Taurinivorans muris with inverse bile-acid patterns. Spatial metabolomics in the kidney further connected local phospholipid disorganization with inflammatory renal injury.

[Metabolome Atlas of Brain Reveals Regional Shared and Unique Metabolic Drifts in Response to Type 2 Diabetes in Male Mice.](#)

Zhou and colleagues in FASEB Journal found that type 2 diabetes produced region-specific metabolic changes across the brain in male mice. Combined metabolomic and lipidomic profiling identified 673 metabolites across seven anatomical regions, with the hypothalamus and olfactory bulb showing the largest shifts. No single differential metabolite was shared across all regions. Recurrent cross-region patterns included higher triacylglycerols, lower fatty acids and diacylglycerols, increased primary amides, and reduced N-acylethanolamines.

Biogenic therapeutics and supportive interventions

A notable strength of this section is that the authors do not rely on the novelty of a natural source as evidence in itself. Instead, they test defined preparations in demanding in vivo settings and ask whether measurable functional gains follow, from tumor control to wound closure to reduced treatment toxicity. That shift matters, because translation will depend less on origin stories than on formulation, dosing, and mechanistic clarity. These studies move in that direction, even when the underlying biology remains only partly resolved.

[Bilberry \(*Vaccinium myrtillus* L.\) Peel-Enriched Pomace as Natural Anticancer Agents: Preclinical Evidence from Breast Carcinoma Models Supporting Preventive and Personalized Treatment Strategies.](#)

Dvorska and colleagues in *Journal of Nutrition* found that bilberry peel-enriched pomace affected breast carcinoma models across preventive, treatment, and in vitro settings. Chemical profiling distinguished a phenolic-rich methanolic fraction from a hexane fraction enriched in unsaturated triacylglycerols and triterpene acids. In vivo, bilberry interventions reduced tumor volume, proliferation markers, oxidative stress, and stemness-associated signals. Treatment was also associated with changes in apoptotic markers, selected histone modifications, promoter methylation, microRNA profiles, and several metabolites.

[Orange-Derived Extracellular Vesicles: Characterization and Therapeutic Applications in Normal and Diabetic Wound Healing in In Vivo Models.](#)

Gai and colleagues in *Cells* found that extracellular vesicles isolated from orange juice accelerated wound healing in both healthy and diabetic mice when delivered in hydrogels. Tangential flow filtration produced vesicles with physicochemical and molecular characteristics comparable to those obtained by ultracentrifugation. In vitro, the vesicles promoted cell migration, endothelial tube formation, cell proliferation, and resistance to hyperglycemic or cytokine-driven oxidative stress. These effects were accompanied by faster wound closure in the in vivo models.

[Serine synthesis and transport mediate the synergistic and detoxifying effects of lienal peptides on cisplatin.](#)

Ding and colleagues in *Frontiers in Pharmacology* found that lienal peptides enhanced the antitumor effects of cisplatin while reducing treatment-related toxicity in a lung cancer model. In Lewis lung carcinoma-bearing mice, the peptides improved survival, reduced renal and hepatic injury, and partially corrected cisplatin-associated metabolic disruption. The mechanistic analyses centered on serine metabolism, which was altered by tumor growth and combination treatment. The data linked the adjunctive effect to microbial serine synthesis and SFXN1-mediated serine transport in tumor cells.

Cancer metabolism, toxic exposure, and lipid dependency

Metabolic rewiring is the unifying language of this theme, but the papers use it for different purposes: to expose a therapeutic vulnerability, to explain an exposure-driven pathology, or to trace a route by which tumors gain metabolic advantage. Lipid handling sits at the center of all three studies, whether through storage, uptake, beta-oxidation, or autophagic trafficking. That convergence is useful, because it places tumor biology and toxicology on shared mechanistic ground. It also suggests that lipid metabolism remains one of the more tractable interfaces between discovery science and intervention.

[Multiomic integration reveals tumoral heterogeneity of lipid dependence within lethal group 3 medulloblastoma.](#)

Bernardi and colleagues in *Cancer Cell* showed that group 3 medulloblastoma contains marked heterogeneity in lipid dependence across tumors. Across 384 patient samples profiled by

methylome, transcriptome, proteome, phosphoproteome, and metabolome, the authors identified proteomic subtypes with distinct lipid-handling programs. In vivo inhibition of the MYC-FASN-SCD axis triggered compensatory uptake of exogenous fatty acids rather than sustained metabolic collapse. The integrated dataset also linked MYC to lipid storage and to dependence on lipid droplet-mitochondria communication.

[6:2 Chlorinated Polyfluoroalkyl Ether Sulfonate \(6:2 Cl-PFAES\), a PFOS Alternative, Impairs Testosterone Synthesis in Leydig Cells by Targeting Lipophagy via the SIRT1-FOXO1-RAB7 Axis: An In Vitro and In Vivo Study.](#)

Jiang and colleagues in Environmental Science & Technology found that 6:2 Cl-PFAES reduced testosterone synthesis by disrupting lipophagy in Leydig cells. In exposed mice and primary Leydig-cell assays, the compound lowered sperm counts and testosterone levels and produced histologic injury in testicular interstitial tissue. Transcriptomic and metabolomic analyses converged on autophagy and lipid-metabolism pathways. Follow-up experiments localized the effect to a SIRT1-FOXO1-RAB7 axis that regulates lipophagic flux.

[Chronic exposure to environmentally relevant doses of butyl benzyl phthalate promotes development of breast tumor Via the tricarboxylic acid cycle and fatty acid \$\beta\$ -oxidation.](#)

Chen and colleagues in Journal of Hazardous Materials found that chronic exposure to environmentally relevant doses of butyl benzyl phthalate accelerated breast tumor growth in mice and promoted proliferation in 4T1 cells. Tumor volumes increased substantially at both tested exposure levels. Metabolomic and lipidomic analyses indicated enhanced hydrolysis of glycerolipids to fatty acids, increased fatty acid beta-oxidation, and greater flux of acetyl-CoA into the tricarboxylic acid cycle. The reported metabolic changes were also associated with increased substrate availability for pyrimidine synthesis and energy production.

Clinical stratification, biomarkers, and analytical performance

These papers are less concerned with pathway discovery than with discrimination, calibration, and clinical usefulness. One develops a sharper analytical platform for cardiovascular metabolite profiling, one links pain phenotypes to future renal risk in diabetes, and one shows that multiomics can add far less to prediction than the field sometimes assumes. That last point is especially valuable. A mature omics literature needs papers that improve measurement, papers that identify clinically relevant signatures, and papers that define where added complexity does not yet pay off.

[Association between Multisite and Site-specific Chronic Pain, Analgesic Use, Metabolic-Proteomic Profile, and Incident Chronic Kidney Disease in Diabetes.](#)

Yang and colleagues in Anesthesiology found that chronic pain, particularly when present at multiple sites, was associated with higher future risk of chronic kidney disease in people with diabetes. In more than 20,000 UK Biobank participants followed for a median of 13.2 years, each additional pain site increased CKD risk, and opioid use among those with chronic pain showed an additional adverse association. Secondary multiomic analyses identified a recurring signature

across the pain phenotypes most strongly linked to CKD: higher chromogranin-A, higher glycoprotein acetyls, and a lower omega-3-to-total-fatty-acid ratio. Protein-network analysis further connected these associations to TNF- and EGFR-centered pathways.

[Integrated GC-MS/MS Metabolomics in Cardiovascular Disease: Targeted Nitro-Oleic Acid Quantification Meets Untargeted Profiling.](#)

Elshoura and colleagues in Analytical Chemistry found that an optimized GC-MS/MS workflow improved targeted quantification of nitrated fatty acids while also supporting untargeted metabolomic profiling in acute myocardial infarction. The method used 17-BrHDA as an internal standard together with optimized derivatization to improve precision. Applied to patient plasma, the assay separated infarction cases from controls in multivariate analyses and detected higher nitro-oleic acid in acute myocardial infarction. The study also showed that alkylation and silylation captured complementary metabolite classes within the same analytical framework.

[Value of Multiomics Over Clinical Risk Factors in Hypertension Prediction.](#)

Vuori and colleagues in Hypertension found that, in a well-characterized population cohort, multiomics added only modestly to prediction of incident hypertension beyond standard clinical risk factors. Among nonhypertensive FINRISK participants followed for 18 years, the best-performing models combined clinical variables with a systolic blood pressure polygenic risk score. The resulting gain in AUC over the clinical model alone was small. Neither NMR metabolite profiling nor gut microbiota data improved prediction when added to the clinical model in this dataset.

Agricultural and ecological metabolomics

These studies place multi-omics in explicitly applied settings where the endpoint is control, resilience, or crop quality rather than clinical diagnosis. Even so, they avoid the common mistake of stopping at broad physiological description. By tying organismal outcomes to oxidative stress, mitochondrial disruption, microbial succession, antioxidant balance, and defense-gene programs, both papers generate mechanisms that can inform intervention. This is a reminder that agricultural metabolomics is at its best when it is as mechanistic as it is practical.

[BAM 15 Exerts Molluscicidal Effects on *Pomacea canaliculata* Through the Induction of Oxidative Stress, Impaired Energy Metabolism, and Tissue Damage.](#)

Wang and colleagues in *Molecules* found that BAM 15 was toxic to the invasive golden apple snail across adult, subadult, and juvenile life stages, with juveniles showing the greatest sensitivity. Proteomic and metabolomic profiling indicated disruption of energy metabolism together with a pronounced oxidative-stress response. Follow-up assays showed reduced mitochondrial membrane potential, increased lipid peroxidation and hydrogen peroxide, depletion of NADPH, and visible damage in head-foot tissue. The measured changes linked exposure to ATP depletion, reactive oxygen species accumulation, and progressive tissue injury.

[Multi-omics analysis revealed the comprehensive regulatory pattern of chestnut development on pathogenic defense.](#)

Chen and colleagues in *Scientia Horticulturae* found that chestnut development was accompanied by a coordinated and changing defense program against postharvest pathogens, with *Alternaria* identified as the dominant fungal threat. Sampling across burs, seeds, shells, and kernels at 10-day intervals supported an integrated microbiome, transcriptome, metabolome, and defense-compound analysis. Non-enzymatic antioxidants such as polyphenols, flavonoids, and tannins declined over time, while enzymatic defenses including SOD, POD, and CAT increased. Network analysis linked this shift to plant-pathogen interaction genes and phenylpropanoid-pathway components.

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NIH Metabolomics SIG Webinar - Dr. Susan Sumner

March 9, 2026

Venue: Online

Dr. Susan Sumner from the University of North Carolina will discuss "The Internal Exposome in Precision Medicine and Precision Nutrition". Dr. Sumner's laboratory is using untargeted metabolomics of the internal exposome to reveal how exposures perturb our normal metabolic state, and how these perturbations are associated with states of health and wellness. Using a nutritional pharmacology/toxicology workflow, the high-information metabolomics/exposome data

is evaluated to design intervention strategies: such as needs in exposure reduction, or the formulation of nutrient cocktails that could protect against adverse exposures, or augment the beneficial impact of medical treatments. Applications in areas of drug addiction, inflammation, and pregnancy complications will be presented in the context of informing nutritional guidance. Ultimately, the nutritional pharmacology/toxicology approach will have a significant impact on public health by reducing environmentally related disease burden, or augmenting the beneficial impact of specific treatments (U2CES030857, U24CA268153).

[Join the web seminar](#)

MANA SODAMeet

April 14, 2026

Venue: Online

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

[Join the web seminar](#)

7th Annual Canadian Metabolomics Conference

(CanMetCon)

April 30 - May 1, 2026

Venue: Toronto, Ontario, Canada

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

CanMetCon is actively working on integration with various other omics disciplines to cultivate a more expansive and nuanced perspective for research in the realm of multi-omics. Recognizing

the interconnected nature of genomics, transcriptomics, proteomics, and other omics domains, the conference aims to forge synergies that transcend traditional disciplinary boundaries. This year conference is themed “**Metabolomics of Health and Disease**” and will feature plenary talks from leading Canadian and international metabolomics experts.

Early Bird registration is **Open**.

Abstract submission deadline is **March 20, 2026**.

[Check for more details](#)

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

June 15 - 19, 2026

Venue: In person, London Hammersmith

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

Early Bird registration is until **May 15, 2026**.

Three bursaries are available for this course which cover the early bird fee.

[Register now](#)

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.

Abstract submission and registration details is coming soon.

[Check for more details](#)

2026 Prague Metabolism and Signaling Symposium

June 24 - 27, 2026

Venue: Prague, Czech Republic

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

[Check for more details](#)

The 1st Congress of Instrumental Analysis (CAI2026)

July 21 - 24, 2026

Venue: Salamanca, Spain

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

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

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

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

[Visit the website for more details](#)

MANA 2026

8th Annual Conference

September 8 - 11, 2026

Venue: UC Davis, California, USA

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

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

Workshop and Interactive Forum submissions will start in March and close on **May 4, 2026**

Abstract submissions will open mid-April and close for oral presentations on **June 8, 2026**, for poster presentations will close on **June 15, 2026**.

Early bird registration will open mid-July.

[Check for more details](#)

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

September 14 - 18, 2026

Venue: Granada, Spain

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

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

[Visit the website for more details](#)

Benelux Metabolomics Days 2026

September 22 - 23, 2026

Venue: Antwerpen, Belgium

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

Abstract submission for oral presentations is open.

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

[Visit the website for more details](#)

5th Nordic Metabolomics Conference 2026

September 28 - 30, 2026

Venue: Uppsala, Sweden

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

Abstract submission for oral and poster presentations deadline - **May 11, 2026**

Travel awards deadline - **May 11, 2026**

Early bird registration deadline - **June 30, 2026**

[Check for more details](#)

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Senior Metabolomics Bioinformatician	Syngenta Jealott's Hill International Research Centre	Bracknell, United Kingdom	Metabolomics Society
Research Associate – Environmental Analytical Chemistry	Algoma University	Sault Ste. Marie, Ontario, Canada	Metabolomics Society
Research Scientist 4	G-27 Division of Environmental Health Sciences	Albany, New York, USA	Metabolomics Society
Post-Doctoral Research Fellow	MITACS and Nova Medical Testing Inc	Edmonton, AB, Canada	University of Alberta

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