MetaboNews

This month in metabolomics

March, 2025
Vol 15, Issue 3

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

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Metabolomics Society News

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

General Enquiries

info@metabolomicssociety.org

Conference Corner

We hope to see you in Prague this June for Metabolomics 2025!

Website: www.metabolomics2025.org
Hosted by: The Metabolomics Society
When: June 22-26, 2025

Abstract Submission

We received an overwhelming number of abstracts to be considered for oral presentation. Thank you to everyone for submitting your work!

There's still time to submit a poster abstract, please check the website for details.

Registration & Workshops

The early bird registration rate is only available until April 1. Take advantage of the discounted early rates, register today! Receive an extra discount by renewing or becoming a member of the Metabolomics Society BEFORE registering for the conference.

Workshop sign-up will be available on April 15. If you register now, you can login to your registration to add complimentary workshops when they are posted. Workshops have limited capacity, be sure to sign-up on April 15 to save your spot.

Book Accommodations

Visit the Hotel Information page for hotels close proximity to the Prague Congress Centre. If you're interested in booking the Holiday Inn, located next door to the PCC, book your reservation soon, as the hotel will be releasing rooms between now and the conference. The earlier you book, the better!

Visa – Do you need one?

Details for entry into Czech Republic are available on the website. Most attendees will not require a visa, based on your country of residence. If you do need a Visa, you should apply now.

For **all travelers** to Czechia, you are required to have a passport that is more than 6 months from expiration and has at least 2 blank pages.

Calling Student Photographers!

There's an opportunity to share your photography skills during the conference and receive travel funds. See the bottom of the Awards page for details.

Members' Corner

Board of Directors

Dear Metabolomics Society Members and metabolomics friends,

As many of you will know - reviewing abstracts, grant applications, scientific papers and fellowship applications is a routine and frequent job in academia. This review process has been focused a lot in the last four weeks with my Metabolomics Society hat on.

I have just finished reviewing 34 abstracts submitted for oral presentations at Metabolomics 2025 in Prague. This is an enjoyable process as any reviewer is lucky to see novel and new research, sometimes before it is available anywhere else. The abstracts this year have certainly whetted my appetite, and I am already looking forward to the conference. In total, 448 oral abstracts (!!!!!!) were submitted across a diverse range of the sciences from technology developments to applications in humans and other mammals, plants, microbes, exposomics etc. Each abstract is reviewed and scored by multiple members of the organizing and scientific committees. If you missed the deadline for oral presentations then please do consider submitting an abstract for a poster presentation (see https://www.metabolomics2025.org/abstract-submissions).

A second review process was required by the organizing committee in February to choose the workshops for the conference. There were many important and interesting topics suggested and unfortunately there were many more applications than workshop slots available. If you submitted a workshop proposal this year and were unsuccessful then please consider submitting in future years.

The final enjoyable review process was for applications submitted for annual Metabolomics Society awards. Again, there were many more applications than available awards and so not all applicants can be winners but we do recommend unsuccessful applicants to reapply in future years if you still fulfil the criteria. Two hugely deserving female members of our community have been awarded ***Honorary Fellowships*** in recognition of their outstanding contributions to the metabolomics community. I will announce these during Metabolomics 2025 in Prague and so use this as an excuse to register for the conference now.

The Metabolomics Society Medal is for mid-career members of the society and is open to those members who have been awarded a PhD 10-15 years prior. The 2025 awardee is **Hiroshi Tsugawa** from *Tokyo University of Agriculture and Technology in Japan.*

The President's Award recognizes outstanding achievements in metabolomics. It is available for Society members who have been awarded a PhD no more than 5-10 years prior. The 2025 awardee is **Tao Huan** from the University of British Columbia in Canada.

Both awardees will present their research as a keynote speaker in Prague. Congratulations to the recipients!

All the very best,

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

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TMIC The Metabolomics Innovation Centre

CanMetCon

McGill University

The 6th Canadian Metabolomics Conference 2025

Clinical Metabolomics

Plenary Speakers:

Mary-Ellen Harper
University of Ottawa

"Leveraging metabolomics and systems biology approaches in the clinical translation of cellular bioenergetics research"

Gary Siuzdak
Scripps Research

"Sifting through Analytical Artifacts: Untargeted Activity Metabolomics and Data Mining Yield Gold."

Erin Baker
University of North Carolina

"Exploring Lipidomic Perturbations Due to Chemical Exposures"

Featured Speakers:

- Stephane Bayen (McGill University)
- Christoph Borchers (McGill University)
- Lorraine Brennan (University College Dublin)
- Philip Britz-McKibbin (McMaster University)
- Michael Chen (University of British Columbia)
- David Goodlett (University of Victoria)
- James Harynuk (University of Alberta)
- Tao Huan (University of British Columbia)
- Liang Li (University of Alberta)
- Tom Metz (Pacific Northwest National Laboratory)
- Matej Oresic (Örebro University & University of Turku)
- Lekha Sleno (Université du Québec à Montréal)
- Ines Thiele (University of Galway)
- Dajana Vuckovic (Concordia University)
- David Wishart (University of Alberta)
- Jianguo (Jeff) Xia (McGill University)

New Residence Hall, McGill, Montreal **April 24-25th, 2025**

Early-Career Members Network (EMN)

EMN Webinars 2025

March Webinar

The march EMN webinar occurred on Tuesday, 25th March 2025, 8:00 UTC (9:00 CET) featuring **Prof. Dr. Kyo Bin Kang** and **PhD candidate Huong T. Pham** from the Sookmyung Women's University, Seoul, Korea. The talk was about "*Untargeted Metabolomics for Natural Products: Not only for Discovery but also for Functional Analysis*", focusing on microbial metabolomics. We would like to thank both speakers for their nice presentation and discussion!

EMN Networking TG

The EMN-MetSoc, in collaboration with Metabolomics South Africa, is thrilled to invite you to an exclusive online networking event focused on "Career Paths and Transitions" for Early Career Researchers (ECRs) working in metabolomics. Join us for an insightful discussion featuring Herna de Wit (OmniSci Consulting, SA), Marli Dercksen (Center for Human Metabolomics, SA), Olli Kärkkäinen (Afekta Technologies Ltd. & University of Eastern Finland), and Efficient Nsikayezwe Ncube (Tshwane University of Technology, SA), as they share their experiences and advice on different pathways including academia, industry, government/clinical settings, and alternative careers. When: APRIL 10 | 14.00 to 15.30 PM CET. Registration is available via the following link: https://zoom.us/meeting/register/ruKcOmLsS4mZ5rbjdXtvvg.

International Affiliates' Corner

Réseau Français de Métabolomique et Fluxomique (RFMF)

Visit http://www.rfmf.fr/

17th RFMF Meeting in Paris, France

The organizing committee of the 17th edition of the French Speaking Network of Metabolomics and Fluxomics (RFMF) meeting will be happy to welcome many of you from June 10 to 13 in Paris. This year, the local organising committee is composed of research teams from the Laboratory of Molecular Chemistry (LCM – Ecole Polytechnique) and NMR of Biological Substances group at the Faculty of Fundamental and Biomedical Sciences (Univ. Paris Cité). These groups have been developing projects in metabolomics and fluxomics for several years, and are strongly invested

members of the scientific community of the RFMF.

The 17th Scientific Days of the RFMF will take place on the Saint-Germain-des-Près Campus at Université Paris Cité, in one of the most beautiful amphitheatres of the Campus overlooking a monumental reception hall in which the meeting will take place. This fully accessible site will contribute to the tradition of conviviality and human and scientific exchanges cherished by the RFMF members. Located on some twenty campuses and research sites throughout the Paris region, the University of Paris Cité was born in 2019 from the union of the Université Paris Descartes, Université Paris Diderot (Paris 7) and the Institute of Earth Physics of Paris (IPGP). This multidisciplinary university ranks 5th in the world for innovation, driven in particular by its research in the field of Health Sciences. Since 2024, it has chosen "Planetary Health" as its signature.

The 17th RFMF Scientific Days will be a unique opportunity to bring together academic and industrial researchers interested in the most recent analytical developments explored in this field, from instrumentation to data processing, as well as their applications to the study of current biological or medical issues. The upcoming RFMF meeting will once again provide a valuable opportunity for our vibrant community to come together and share ideas.

The main program of the conference will include plenary lectures by internationally renowned researchers, and contributory oral papers, flash papers, with a special session dedicated to young scientists and poster sessions. The following speakers have already accepted our invitation to give a lecture: Elaine Holmes (Imperial College), Michael Witting (Technical University of Munich), Erwan Poupon (Université Paris-Saclay), Jennifer Kirwan (Berlin Institute of Health) and Alia Dellagi (AgroParisTech, Institut Jean-Pierre Bourgin).

Save the date and do not forget to register here. We hope to see many of you there ;)

RFMF thematic school on the annotation of plant metabolomes in Sète, France
The RFMF is launching new training and networking initiatives centered around thematic schools for researchers, which will take place annually. The first edition in 2025 will be dedicated to the annotation of plant metabolomes, featuring theoretical sessions in the morning and practical sessions in the afternoon. You can already save the date in your calendars: it will take place from September 8 to 12, 2025, in Sète, in this beautiful Mediterranean region. Stay tuned as more information will be coming soon ;)

Latin American Metabolic Profiling Society (LAMPS)

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

Dear LAMPS Members,
We invite you to submit nominations for the **Board of Trustees** of our society. This represents a significant opportunity to contribute to the advancement and governance of our society, and we encourage your active engagement in this vital process.

Who is eligible?
To be eligible for nomination, candidates must meet the following criteria:

- To be a researcher with at least three years of residency in Latin America with a publication record in metabolomics.
- To be endorsed by a LAMPS Founding Member. You can find the list of Founding Members and their contact information here: https://jwist.github.io/lamps/team.html

Nomination form: Form

Nomination deadline: The nomination period will remain open until **March 31, 2025**.

After this date all nominees will be put to a vote by all LAMPS members. Since our charter requires that at least three seats of the Board will be allocated to Founding Members, LAMPS members will also have to vote for three Founding Members to integrate it. The four nominees with the highest number of votes representing different Latin American countries, together with the three most-voted Founding Members will form the new Board. In case the four new seats cannot be covered by nominees from different countries, these will be allocated to Founding Members.

If you require additional information, please do not hesitate to reach out. We look forward to your participation in this important process of renewal and strengthening of our community.

Best regards,
LAMPS Founding Members

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

web https://metabolomicsna.org
email mana@metabolomicsna.org
LinkedIn @MANA (Metabolomics Association of North America)

MANA has been quite busy in the start of 2025 with conference and other events planning, revamping parts of our website, and firming up our new registration process. Here are some important events/news:

MANA 2025 – Banff | September 2 – 5, 2025 - Save the Date!
Abstract submissions for **MANA 2025** are opening soon! This year's conference will be held at the **Banff Centre** in beautiful **Banff, Alberta, Canada**. Start preparing your abstracts early—**space will be limited**!
MANA 2025 will feature our signature high-quality scientific program, along with some exciting new **outdoor engagement activities**. The Banff Centre, also home to the world-renowned Banff Mountain Film Festival, offers stunning views and access to nature, all just a short walk from the historic town of Banff, Bow Falls, and Tunnel Mountain. World-famous destinations like the Banff Upper Hot Springs, Cave and Basin National Historic Site, and Moraine Lake are just a quick drive away.
Check our conference website at https://mana2025.metabolomicsna.org/ frequently for updates!

MANA Virtual Symposium: "From Metabolomics to Mechanism".
May 8th, 2025 - Save the Date!
Metabolomics is a powerful tool to probe biological phenotypes that provides a perspective not possible with other 'omics approaches. Translating metabolomic phenotypes to mechanistic understanding is difficult, requiring experimental iteration, innovation, and orthogonal approaches. In this symposium, field leaders will present their work in a "metabolomics first" manner, describing how their research developed from early metabolomics observations to true biological mechanisms. Click here for registration.

MANA Virtual Job Fair coming up in April!
The MANA Early Career Members are hosting its bi-annual virtual job fair in April! More details to follow. Check our main website for the latest details.

New MANA membership system - click here to become a member! (membership needs to be updated annually starting this year)
Benefits of membership include eligibility to apply for awards, discount on our annual conference, discount on publication fees for MANA special issues, starting interest groups, and more! Visit here for more details.

As always, remember to visit our website for the latest and remember to also visit our job board for open positions and scientists looking for job opportunities in metabolomics.

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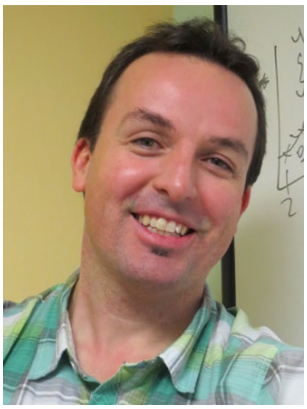
Perspectives

In our *Perspectives* section, we take some time to sit down with experienced and decorated researchers in the field of metabolomics to gain their insights on both the evolution of the field and its future directions.

For our third Perspective, we're excited to feature Dr. Philip Britz-McKibbin, who reflects on the evolution of metabolomics and innovations driving large-scale population health research



Dr. Philip Britz-McKibbin received his PhD in analytical chemistry (2000) from the University of British Columbia under the supervision of David D. Y. Chen, followed by a *Japan Society for Promotion of Science* post-doctoral research fellowship in the renowned group of Shigeru Terabe at Himeji Institute of Technology (2001-2003). He started his independent career in 2003 at McMaster University, and is currently a *Professor* at the Department of Chemistry and Chemical Biology, and an affiliate member of the Department of Pathology and Molecular Medicine. He is also an affiliate member of the Metabolomics Innovation Centre (TMIC) – Canada's national laboratory for metabolomics research and innovative analytical services. His work has been funded by NSERC, CIHR, CFI, Genome Canada and Cystic Fibrosis Canada, and involves innovative collaborative research projects that have strong translational

potential in clinical medicine and public health.

Reflecting on your journey, what is the most valuable piece of advice you would give to a new researcher entering the field of metabolomics?

I would recommend that new researchers entering the field of metabolomics to learn the fundamental aspects of analytical chemistry and bioinformatics while striving for data transparency and high ethical standards given a reproducibility crisis in scientific research. Also, it is all too easy these days to rely on a plethora of vendor specific or open-access software tools for data pre-processing in untargeted metabolomics that are often sub-optimal, which one can blindly use as it is convenient but may lead to false discoveries especially in metabolite/lipid annotation or identification. Further, implementing design of experiments during method optimization as well as applying rigorous method validation are critical to generate reliable metabolomic data that is reproducible. Lastly and most importantly, try not to follow trendy research that compromises your integrity – be innovative and follow your curiosity!

What advice would you offer to researchers, institutions, or organizations looking to adopt metabolomics technologies to improve their own work?

My recommendation when adopting metabolomic technologies is to invest more in people than infrastructure. It is all too commonplace to witness new instrumentation that is underutilized and poorly serviced without regular preventative maintenance. The development of standardized operating protocols while ensuring adequate staff training are essential to improve both the productivity and quality of data in metabolomics research especially when instruments are used by multiple users. Participating in round robin studies and analyzing certified reference materials can also help support good laboratory practices when using cutting-edge metabolomics technologies.

What are the largest barriers currently facing the wider adoption of metabolomics, particularly in the context of large-scale population studies (like your recent publication on serum metabolomics for insights into early childhood development)? Are there limitations to how metabolomics can be implemented in large cohort research?

In my experience, there are several major barriers to large-scale metabolomic analysis in epidemiological or clinical research, including low sample throughput, high operating costs, as well as complicated data pre-processing. Moreover, prospective cohort studies

that require batched analysis of thousands of samples over long periods of time are also more prone to long-term signal drifts and bias especially when using ESI-MS methods. We have addressed these obstacles by developing a multiplexed separation platform based on multisegment injection-capillary electrophoresis-mass spectrometry (MSI-CE-MS) that can analyze up to 13 independent samples within a single analytical run, including a quality control or reference sample. This not only improves sample throughout by more than an order of magnitude, MSI-CE-MS offers a 'greener' platform given savings in both infrastructure and operating costs that consume less energy and organic solvent than conventional LC separations. Recently, we have introduced a new software tool for automated data pro-processing of metabolomic data using MSI-CE-MS referred to as PeakMeister that make use of migration time indices to reliably and more rapidly select peaks and annotate sample positions in spite of large shifts in migration time in CE.

How has the collaboration across disciplines—such as with your colleagues in Brazil, nutrition experts, and researchers—contributed to the evolution of metabolomics?

Two common inquiries raised by our collaborators when performing large-scale metabolomic studies has been budget and timeline. In essence, how to perform high quality metabolomic analyses fast but at low costs when dealing with large numbers of samples. Also, overall metabolome coverage is an important consideration. For example, we have recently completed a 12,000 sample international cohort study using standardized MSI-CE-MS technology that represents our largest study to date. We previously applied MSI-CE-MS to verify tobacco smoking, including secondhand smoke exposures in self-reported never smokers in the Prospective Urban-Rural Epidemiological (PURE) study by measuring the sum total of up to seven nicotine metabolites in urine. These demands in nutritional epidemiology and rapidly expanding exposomics research have ultimately spurned the development of more efficient data workflows and software tools in our laboratory, such as when exploring large treatment response variations to a single large bolus of vitamin D3 in critically ill vitamin D deficient children.

What research areas or sectors do you foresee as being most impactful for public health in the coming years, and why?

Given an obesity and metabolic health crisis globally and the unsustainable healthcare costs to symptomatic treatment, in my opinion it is critical that public health focuses on

practical yet effective strategies for chronic disease prevention in a more holistic manner. Precision nutrition using high throughput metabolomic technologies offers an exciting approach towards optimizing lifestyle modifications on an individual level to improve health outcomes, including diet quality, stress reduction, physical activity, sunlight exposure and drug deprescription. This paradigm runs counter to conventional public health policies that typically implement a 'one-size-fits-all' model based on interventions for the mythical 'average person' that can lead to negative outcomes in susceptible individuals. Also, more emphasis needs to be focused on improving maternal and childhood health outcomes given the key role that changing environmental exposures play during the earliest stages of human development.

How do you envision current metabolomics research, such as the serum metabolomics study, being applied in the future? Are there specific areas of research that you think researchers should focus on or track for future development?

A key challenge in metabolomics research, and other -omics fields, has been effective clinical translation of research discoveries that leads to measurable benefits to patients as compared to a standard care of practice. We are currently striving to validate a panel of urine-based biomarkers of diet quality that are linked to lower risk for incident clinical events that can provide empower and inform individuals on how best to improve their metabolic health based on their personal preferences. The development of robust user-friendly AI tools to assist individuals to interpret complex metabolomic data sets that is actionable based on optimal food choices and supplement use (if required and if so at what dose) will likely have a key impact on translating metabolomic discoveries to the layperson.

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Spotlight Article

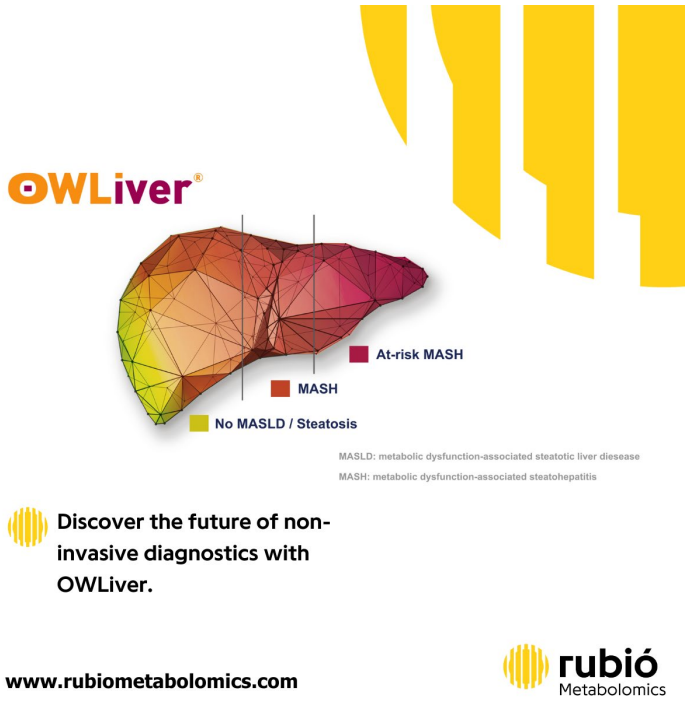
Sponsored Content

DISCOVER THE FUTURE OF METABOLOMICS WITH RUBIÓ METABOLOMICS

Formerly OWL Metabolomics

Spotlight on Innovation: OWLiver® Test & MASEF Score

|MC:SUBJECT|



Advancing the way we diagnose and manage metabolic diseases, **Rubió Metabolomics** brings cutting-edge solutions from the research lab to the clinic.

With the MASEF Score included in **OWLiver® Test**, endorsed by world-leading experts[i], we provide a breakthrough tool for **early detection** and monitoring of **MASLD** (metabolic dysfunction-associated steatotic liver disease)**, including** metabolic dysfunction-associated steatohepatitis (**MASH**).

Our OWLiver® Test, developed and validated against biopsy, is a **non-invasive diagnostic tool** designed to assess all lesional phases of MASLD. This **high-resolution lipidomic analysis** of fasting blood samples leverages UHPLC-MS to measure a targeted panel of lipid biomarkers reflecting **liver fat content, inflammation, and fibrosis**.

Our OWLiver® Test is already transforming care in **Europe (CE-marked)** and the **United States (PLA code *0344U)***. This test integrates lipid concentrations and clinical data to estimate the stage of MASLD. Built on a multicenter, multiethnic study, OWLiver® Test offers reliable insights for patients with a body mass index above 25 kg/m² with or without type 2 diabetes mellitus.

Making knowledge actionable for you through metabolomics

Rubió Metabolomics offers a portfolio of **semi-quantitative** and **quantitative metabolomics platforms**, including Lipidomics, Amino Acids, Polar Metabolites, Bile

Acids, Oxidized Fatty Acids, Lipoprotein Profiling, and Glycoprotein Profiling, with **tailored analysis supported** by **Data Science** for exploratory analysis, preparation, statistical design, predictive modeling, and communication—**discover more**.

Taking Metabolomics into the Clinic

Metabolomics is revolutionizing clinical diagnostics. At Rubió Metabolomics, we ensure to make metabolomics accessible, precise, and impactful. Our methodologies are **endorsed by top hepatology specialists** and backed by **robust scientific validation**.

If you're a clinician, researcher, or healthcare provider looking to bring metabolomics into your practice, let's talk. Discover how we can help you **unlock metabolic insights** that go **beyond standard testing**.

Based in Bilbao, serving health.
Want to know more? Contact us today and join the future of precision medicine.
➡ **www.rubiometabolomics.com / metabolomics@owlmetabolomics.com**

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[i] Noureddin M, Truong E, Mayo R, Sanyal A. J., Martínez Arranz I., Bañales J. M., et al. *Serum identification of at-risk MASH: The metabolomics-advanced steatohepatitis fibrosis score (MASEF)*. Hepatology. 2024;79(1):135-148. doi:10.1097/HEP.0000000000000542

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MetaboInterview

Jun Han

Biography

Dr. Jun Han is the group leader of metabolomics at the Genome BC Proteomics Centre and an adjunct assistant professor in the Division of Medical Sciences at the University of Victoria, BC. He obtained his MS and PhD degrees from China Pharmaceutical University and had 8 years of experience in developing and validating GLP and FDA guideline-compliant analytical methods. Dr. Han received his postdoctoral training at the University of North Carolina at Chapel Hill and the Medical University of South Carolina, where he

acquired extensive expertise in proteomics and metabolomics.

Since 2007, Dr. Han has played a key role in the technical support and execution of metabolomics projects at the node of The Metabolomics Innovation Centre (TMIC) in Victoria, led by Dr. Christoph Borchers in the early years and by Dr. David Goodlett over the past few years, based on successful developments and continuous refinements of hundreds of sample preparation and UPLC-MRM/MS methods for high-sensitivity and high-precision quantitation of metabolites involved in diversifying metabolic pathways or in a compound class-specific way. The developed metabolomic and lipidomic assays have enabled the quantitative measurement of >3000 metabolites and lipids in biological, environmental, and plant samples. Dr. Han has authored or co-authored >110 peer-reviewed research and review publications, including one E-book. He is also the co-inventor of a U.S. patent.

How did you first get involved in metabolomics, and what drew you to focus specifically on quantitative metabolomics assays using UPLC-MRM/MS?

In my earlier career, I gained several years of experience in the development and validation of analytical methods using HPLC-UV and LC-MS for the precise and accurate quantification of pharmaceutical molecules in dosage forms for quality control purposes or in biological samples for drug metabolism and pharmacokinetics studies, all strictly adhering to GLP and FDA guidelines. The experience instilled in me the experimental skills necessary to achieve high precision and accuracy in quantitation, as well as a good sense of the responsibility involved, emphasizing the importance of achieving highly

quantitative measurements for related studies. These also made me realize, even in the early days when I started working on metabolomics, that highly quantitative measurements of endogenous metabolites would be equally important in metabolomics when the results are used for biomarker discovery or for dissecting the changes in metabolic networks within a biological system. LC-MRM/MS has been the gold-standard analytical technology in bioanalysis for decades. This is why, since 2010, when an LC-MS/MS instrument became available for me to work on metabolomics, I have primarily focused my efforts on developing different UPLC-MRM/MS analytical methodologies for quantitative metabolomics, especially in a pathway-specific or compound class-specific manner.

Your work spans a wide variety of metabolic pathways and compound classes. What excites you most about this breadth of focus, and how do you approach the challenge of developing targeted assays for these complex systems?

When I began working on metabolomics, I primarily relied on metabolic fingerprinting in an untargeted manner, using direct infusion-FTMS or UPLC-HRMS, due to the limited or no access to triple-quadrupole mass spectrometers in the early years. As I conducted more untargeted analyses, I found it increasingly difficult to discern the detailed, albeit minor, systemic changes that occurred in specific metabolic networks or pathways across different sample groups using data acquired from untargeted metabolomics only. These had driven me to design and test new and significantly improved UPLC-MRM/MS methods for the quantitative measurement of as many metabolites as possible, located at each node or branching point of different modeled metabolic pathways, such as central carbon metabolism. In this way, scientists would have a detailed understanding of what exactly happened to specific pathways inside cells or the entire biological system in an unbiased way. With the development of hundreds of different combinations of sample preparation protocols, including or excluding pre-analytical derivatization, and the highly diversified UPLC-MRM/MS methods achieved thus far, we have carried out high-precision and high-sensitivity quantification of more than 3,000 metabolites and lipids in a pathway-specific or compound-class manner for more than one thousand metabolomics projects. The developed assays and corresponding metabolomics results have aided numerous researchers and collaborators in their studies. The chemical structures of small-molecule metabolites are highly diverse, while the concentrations of some of the same metabolites in different types of biological or environmental samples can span very wide concentration ranges, up to 10^8 or even higher orders of magnitude. All these necessitate the continued development and application of new analytical methods for quantifying the metabolites in different types of biological or environmental samples.

You've developed methods for quantifying low-abundance metabolites in challenging sample types, such as wildlife hair and seawater. Can you share some of the key challenges you've faced in working with these material-limited samples and how you've overcome them?

The need for the development of new assays and methods in targeted metabolomics has often been driven by demand, as I have experienced.

For example, assay of steroid hormones in animal wildlife hairs had been challenging and time consuming, not just because of the very low concentrations of steroid hormones in the complex matrices of wildlife hairs but also because the time lengthy (24 hours to days) extraction procedures as we see in the literature, which are high-throughput incompatible and difficult to analyze hundreds of hair samples in one batch, while importantly need to ensure high-precision quantitation. Therefore, to develop an assay for both of steroid and thyroid hormones, we designed a procedure combining high-throughput hair homogenization, metabolite extraction and a QuEChERS like protocol in one step for the sample preparation within minutes, followed by a reproducible single-step liquid-liquid extraction, for UPLC-MRM/MS of >30 steroid and thyroid hormones in the hairs with high sensitivity. The analytical strategy enabled the preparation of up to 200 hairs, ready for UPLC-MRM/MS, in just a few hours, requiring only the use of low-mg levels of animal hair, which is difficult to collect in large amounts from wild animals.

Another case is that, when we tried quantitation of dissolved free amino acids in seawater and freshwater, a big challenge lies in very low concentrations (>1M fold lower) of amino acids in natural water than that typically we see in biological samples, while the background contamination levels of proteinogenic amino acids in common chemical reagents and solvents are often higher than that in natural water. To address the challenge, in addition to developing a high-sensitivity UPLC-MRM/MS method that incorporates natural water matrix removal, appropriate reagent, solvent, and labware decontamination procedures were implemented, ensuring the reliable measurement of dissolved free amino acids in natural water.

Over the past few years, we have also seen more and more metabolomics projects for which very limited materials are only available, such as for stem and T cells, to address the challenges for targeted metabolomics, we have spent a lot of efforts in refining some well-developed UPLC-MRM/MS methods or further development of novel UPLC-MRM/MS methods, with significantly improved, 10 to 100-fold higher sensitivity to address the assay challenges.

In your research, you've worked extensively on metabolic pathways like central carbon metabolism, purine-pyrimidine metabolism, and fatty acid beta-oxidation. How do you see these areas contributing to a broader understanding of metabolism and disease?

Untargeted and targeted metabolomics are two distinct approaches used in metabolic pathway analysis, each with its strengths and limitations. Untargeted metabolomics provides a comprehensive snapshot of the metabolome, capturing thousands of metabolites, including unknown compounds. It is particularly useful for exploratory studies where the key players in a pathway are not yet fully understood. It can also reveal interactions between multiple pathways due to its higher metabolome coverage. However, it is often less specific for low-abundance metabolites existing in specific pathways. In addition to the use of advanced bioinformatics tools to deconvolute and identify metabolites relevant to a specific pathway, the quantification is relative rather than absolute, which limits precision for pathway analysis.

To complement untargeted metabolomics, we have developed UPLC-MRM/MS methods and assays for the comprehensive and absolute quantification of nearly all known metabolites in more than 15 metabolic pathways, including central carbon metabolism, purine-pyrimidine metabolism, and fatty acid beta-oxidation, among others, utilizing available authentic compounds of the metabolites. The developed methods are also capable of putative detection and relative quantitation of some metabolites for which standard substances are currently unavailable.

Over the past few years, we have also focused on developing comprehensive, cross-pathway metabolomics and lipidomics assays for human and animal metabolomics studies. Benefiting from precise and absolute quantitation, the results from pathway-specific, compound class-specific, or function-specific assays have helped researchers gain a broader and in-depth understanding of metabolism and disease in a hypothesis-driven yet more comprehensive manner.

What current research initiatives are you most excited about?

While we are developing new metabolomics assays and methodologies, I have found that some metabolites related to human health or genetic diseases have not been well measured due to technological limitations in the past, or their analytical methodologies have not been publicly available. Additionally, a growing number of metabolites have

been identified in recent years, and their biological or physiological significance is increasingly being revealed. For comprehensive metabolomics, particularly for translational research, the development of new, large-scale targeted metabolomics assays, including the analysis of these and many backdoor pathway metabolites, is needed. These inspire us to devise and further develop new techniques and methods to achieve it.

As you work on developing new LC-MRM/MS methods, what improvements, technological or otherwise, do you think need to take place for metabolomics?

Metabolites span a vast concentration range, from low picomolar to high millimolar levels. Low-abundance metabolites often get buried under noise from high-abundance metabolites when hundreds of metabolites are analyzed together in an LC-MRM/MS run, as we have increasingly applied for large-scale metabolomics projects. The improvement of ionization efficiency across diverse metabolite classes, higher-sensitivity triple-quadrupoles or hybrid MS/MS systems and improvement of detection dynamics could push limits of detection lower while maintaining linearity over >5 orders of magnitude. The development and refinement of new and novel higher-sensitivity metabolomics assays are crucial, whether for large human cohorts, environmental exposure studies, or clinical applications.

How do you see metabolomics evolving over the next 5 to 10 years?

The analytical sensitivity, scanning speed, mass resolution and detection dynamics of mass spectrometers continue to improve. We're likely to see the ability to detect and identify more low-abundance yet biologically or patho-physiologically important metabolites that have not been previously identified or quantified and to do so with greater accuracy. Additionally, with the increasing availability of high-quality authentic metabolite compounds, metabolomics results in a more quantitative manner, providing more reliable biological interpretations. This is especially true when quantitative metabolomics is combined with genomics, proteomics, and transcriptomics in a multi-omics approach, providing a holistic view of biological systems. Over the next years, we may see routine metabolic screening as part of physical checks, allowing for the prediction of risks for chronic diseases such as CVD, diabetes and neurodegenerative disorders years before symptoms appear. Metabolomics is also growing in agriculture, environmental science, and synthetic biology. These are the key fields to consider when

developing new metabolomics methods or assays.

In your view, what are the key barriers facing metabolomics today? How can these challenges be addressed?

Metabolomics researchers employ a range of protocols, analytical instruments, and data processing tools. Variability in sample collection, storage, and preparation can introduce inconsistencies, making it hard to compare results across studies or labs. The situations are also further complicated by the quality and chemical stability of standard substances used in quantitative metabolomics. Many endogenous metabolites are chemically unstable and sensitive to light, heat, pH, and oxygen, or some (e.g., the folate cycle metabolic intermediates) can even undergo interconversion during sample storage or processing for metabolomics assays. These often make it challenging to compare results across different studies and could slow down large collaborative projects, undermining trust in the findings. Addressing these challenges requires the standardization of metabolomics practices, but this has remained a significant hurdle.

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MetaboReads

Microbiome & Immunology in Cancer

These studies highlight the interplay of microbes, metabolic pathways, and immune responses in shaping tumor behavior. Whether by uncovering how the gut microbiome influences chemotherapy outcomes, exposing the metabolic basis of therapy resistance, or revealing novel

methods to bolster immunotherapy, they all point to emerging strategies in cancer management that hinge on metabolic and immunological insights.

Gut microbiome modulates the outcome in primary central nervous system lymphoma patients undergoing chemotherapy: an ancillary study from the BLOCAGE trial.

Hernandez-Verdin and colleagues in Neuro-oncology showed that the gut microbiome modulates treatment outcomes in primary central nervous system lymphoma patients undergoing chemotherapy. By analyzing patient samples from the BLOCAGE trial, they found associations between specific bacterial taxa and improved therapeutic response. These microbial patterns also correlated with overall survival rates, suggesting that gut microbiota profiling may guide personalized interventions. Their findings highlight the importance of host–microbe interactions in oncology.

Realigned transsulfuration drives BRAF-V600E-targeted therapy resistance in melanoma.

Borbenyi-Galambos and colleagues in Cell Metabolism found that a reconfiguration of the transsulfuration pathway drives resistance to BRAF-V600E-targeted therapies in melanoma. They observed that this metabolic shift helps cancer cells maintain redox balance and survive under drug pressure. Inhibiting transsulfuration enhanced the efficacy of BRAF inhibitors, suggesting that blocking this pathway could thwart adaptive resistance. This work reveals how metabolic rewiring can limit the success of targeted cancer treatments.

Adipocyte-derived glutathione promotes obesity-related breast cancer by regulating the SCARB2-ARF1-mTORC1 complex

Zhao and colleagues in Cell Metabolism showed that adipocyte-derived glutathione promotes obesity-related breast cancer by regulating the SCARB2-ARF1-mTORC1 complex. Their experiments revealed that excessive glutathione supply from adipose tissue fuels tumor growth and survival. Limiting glutathione transport weakened malignancies in animal models, illuminating a key metabolic crosstalk in obesity-driven cancers. Targeting adipose–tumor interactions may represent a viable therapeutic approach.

Low-dose irradiation of the gut improves the efficacy of PD-L1 blockade in metastatic cancer patients.

Chen and colleagues in Cancer Cell demonstrated that low-dose irradiation of the gut enhances PD-L1 blockade efficacy in patients with metastatic cancer. Mild radiation shifted gut microbiome composition and induced local immune stimulation, synergizing with immune checkpoint inhibitors. This improved tumor control, suggesting that selectively modulating gut ecosystems can strengthen systemic cancer immunotherapies. The study opens new avenues for combining microbiome-targeted strategies with conventional treatments.

Metabolic Diseases & Therapeutic Advances

Metabolic dysfunction underlies not just diabetes, but a range of chronic conditions. These papers illuminate new therapeutic targets—spanning enzymes, immunomodulatory molecules, and adipocyte regulators—that could reshape the trajectory of metabolic and autoimmune

diseases.

[Renalase inhibition defends against acute and chronic beta cell stress by regulating cell metabolism.]

MacDonald and colleagues in Molecular Metabolism showed that inhibiting renalase defends against both acute and chronic beta cell stress by regulating cell metabolism. In their models, renalase suppression helped preserve insulin secretion and cellular integrity in pancreatic islets. Mechanistic analyses linked improved redox balance to better beta cell survival. These findings suggest renalase as a promising therapeutic target in metabolic disorders.

[Gluconolactone restores immune regulation and alleviates skin inflammation in lupus-prone mice and in patients with cutaneous lupus]

Li and colleagues in Science Translational Medicine found that gluconolactone restores immune regulation and alleviates skin inflammation in lupus-prone mice and in patients with cutaneous lupus. By stabilizing regulatory T cells and reducing inflammatory T helper cell activity, gluconolactone lowered lesion severity. Immunophenotyping further revealed balanced cytokine profiles in treated subjects. This work highlights the therapeutic potential of targeting metabolic pathways to control autoimmune diseases.

[Proteomic and Metabolomic Signatures in Prediabetes Progressing to Diabetes or Reversing to Normoglycemia Within 1 Year.]

Barovic and colleagues in Diabetes Care showed that distinct proteomic and metabolomic signatures in individuals with prediabetes can predict who will progress to diabetes or revert to normoglycemia within one year. Their longitudinal study identified pathways related to amino acid and lipid metabolism as key indicators of disease trajectory. Early detection of these molecular markers may facilitate targeted intervention. Such “omics” approaches refine our ability to customize metabolic disease prevention.

[Sugar-sweetened beverage intake, gut microbiota, circulating metabolites, and diabetes risk in Hispanic Community Health Study/Study of Latinos]

Zhang and colleagues in Cell Metabolism discovered that higher sugar-sweetened beverage intake in Hispanic populations correlates with altered gut microbiota and circulating metabolites that heighten diabetes risk. By combining 16S rRNA gene sequencing and metabolomics, they traced how sugar-laden diets can shift microbial communities toward insulin resistance. These changes often preceded overt hyperglycemia. Reducing sugary drinks may thus be a tractable approach to realign the microbiome and mitigate diabetes incidence.

[Blocking Adipocyte YY1 Decouples Thermogenesis From Beneficial Metabolism by Promoting Spermidine Production]

Qiu and colleagues in Diabetes found that blocking adipocyte YY1 decouples thermogenic benefits from overall metabolic health by promoting spermidine production. Although YY1 deficiency increased fat browning, it unexpectedly impaired glucose tolerance and lipid handling. The team traced this adverse effect to dysregulated polyamine metabolism. This study emphasizes the tight coupling between energy expenditure pathways and broader metabolic

networks.

Multi-Omics Approaches to Health & Disease

Multi-omics studies integrate genomic, proteomic, metabolomic, and microbiome data to uncover hidden links between host physiology and disease progression. These four papers illustrate the power of combining datasets over time—from COVID-19 convalescents to gut symbionts—to reveal biomarkers and mechanistic insights across diverse biological systems.

Longitudinal multi-omics analysis of convalescent individuals with respiratory sequelae 6-36 months after COVID-19

Yang and colleagues in BMC Medicine found that longitudinal multi-omics analyses of convalescent individuals with respiratory sequelae following COVID-19 (6–36 months post-infection) revealed persistent immune, metabolic, and microbiome alterations. Specific inflammatory markers and gut microbial profiles correlated with ongoing pulmonary symptoms. Certain metabolite signatures distinguished individuals who recovered better from those with prolonged complications. Their results point to potential therapeutic targets and biomarkers for post-COVID syndromes.

Microbiota-derived short-chain fatty acids determine stem cell characteristics of gastric chief cells

Jeong and colleagues in Developmental Cell showed that microbiota-derived short-chain fatty acids (SCFAs) control the stem cell characteristics of gastric chief cells. By profiling SCFA levels and linking them to epigenetic changes, they observed that these bacterial metabolites influence chief-cell plasticity and regenerative capacity. The study highlights how microbial signals help shape mucosal maintenance and repair. Manipulating SCFA signaling could offer new strategies to treat gastric injury.

Decreased gut microbiome-derived indole-3-propionic acid mediates the exacerbation of myocardial ischemia/reperfusion injury following depression via the brain-gut-heart axis.

Mu and colleagues in Redox Biology demonstrated that reduced concentrations of the gut microbiome-derived metabolite indole-3-propionic acid worsen myocardial ischemia/reperfusion injury in depressed mice. Restoring this metabolite relieved oxidative stress and improved heart function, implicating a brain–gut–heart axis in the pathophysiology. The findings underscore how mental health and specific microbial metabolites can synergistically impact cardiovascular outcomes. Targeting such links may offer novel cardioprotective strategies.

Genome-scale resources in the infant gut symbiont Bifidobacterium breve reveal genetic determinants of colonization and host-microbe interactions.

Shiver and colleagues in Cell revealed genetic determinants of colonization and host interactions in the infant gut symbiont Bifidobacterium breve using genome-scale resources. Through transposon mutagenesis and functional assays, they identified key metabolic and adhesion factors supporting successful gut residence. Their data advance understanding of early-life microbiota assembly and may guide probiotic innovations. This resource-rich approach

spotlights the value of systems-level tools in microbiome research.

Environmental Exposures & Microbial Ecology

Organisms—from bees to humans to microbes in space—exist in environments shaped by chemical, physical, and biological stressors. These studies reveal how exposures to pesticides, metals, oxidants, and microgravity can disrupt or reshape microbial communities and host physiology, offering new insights for mitigating harmful effects.

A gut bacterial supplement for Asian honey bee (Apis cerana) enhances host tolerance to nitenpyram: Insight from microbiota-gut-brain axis.

Zhao and colleagues in Environmental Research found that supplementing Asian honey bees (Apis cerana) with a specific gut bacterial strain enhances tolerance to the neonicotinoid pesticide nitenpyram. Mechanistic analyses indicated that improved detoxification and neural protection were involved. The supplemented bees exhibited fewer toxic effects and improved survival. This approach suggests that microbiome-based interventions may strengthen pollinator health in pesticide-laden environments.

The International Space Station has a unique and extreme microbial and chemical environment driven by use patterns.

Salido and colleagues in Cell showed that the International Space Station harbors a distinctive microbial and chemical environment driven by microgravity and usage patterns. Through comprehensive sequencing and metabolomic profiling, they documented unique shifts in microbial diversity and biofilm formation. These conditions could impact both astronaut health and spacecraft maintenance. Their work underscores the need for tailored solutions to manage microbial ecosystems in space travel.

Associations of prenatal metal exposure with child neurodevelopment and mediation by perturbation of metabolic pathways

Xie and colleagues in Nature Communications found that prenatal exposure to metal mixtures alters metabolic pathways that mediate child neurodevelopment. They connected maternal metal burdens with specific infant metabolite profiles and later cognitive outcomes. Oxidative stress emerged as a critical mediator of toxicity. The findings highlight the importance of reducing maternal environmental exposures to protect developing brains.

Surfactin facilitates establishment of Bacillus subtilis in synthetic communities

Lozano-Andrade and colleagues in ISME Journal demonstrated that the biosurfactant surfactin facilitates Bacillus subtilis establishment in synthetic microbial communities. By monitoring bacterial interactions and metabolomic changes, they found that surfactin promotes adhesion and niche colonization while enabling coexistence with other species. This mechanism could be harnessed to design beneficial consortia in agriculture or waste management. The study exemplifies how bacterial metabolites shape community assembly.

Taurine supplementation alleviates asthma airway inflammation aggravated by HOCl exposure.

Chen and colleagues in Journal of Hazardous Materials found that taurine supplementation alleviates asthma airway inflammation that is exacerbated by HOCl (hypochlorous acid)

exposure. Their experiments demonstrated that taurine's antioxidant properties dampen both oxidative stress and neutrophilic infiltration in lung tissue. This intervention reduced key pro-inflammatory mediators and improved respiratory function in exposed animals. The results suggest that taurine might help mitigate environmentally driven inflammatory diseases.

Novel Biotechnologies & Tools

Finally, these studies exemplify how innovative platforms—from engineered yeast strains to microneedle-based delivery systems—are expanding the frontier of biomanufacturing and targeted therapies. By optimizing metabolic pathways or local drug release, they open doors to sustainable production methods and smarter treatments.

The oleaginous yeast Rhodosporidium toruloides engineered for biomass hydrolysate-derived (E)-α-bisabolene production.

Adamczyk and colleagues in Metabolic Engineering showed that engineering the oleaginous yeast Rhodosporidium toruloides for (E)-α-bisabolene production achieves robust yields from biomass hydrolysates. By refining terpene synthesis pathways and fermentation conditions, they demonstrated an economically viable, bio-based route to this valuable compound. Their strategy advances renewable chemical manufacturing and highlights yeast as a versatile production chassis. This work paves the way for more sustainable commodity and specialty chemical processes.

Microneedles Loaded with Nitric-Oxide Driven Nanomotors Improve Force-Induced Efferocytosis Impairment and Sterile Inflammation by Revitalizing Macrophage Energy Metabolism

Tan and colleagues in ACS Nano demonstrated that microneedles loaded with nitric-oxide-driven nanomotors improve efferocytosis and reduce sterile inflammation by revitalizing macrophage energy metabolism. Their system harnesses NO release to enhance mitochondrial function and promote efficient clearance of damaged cells. This localized approach attenuated inflammatory signaling and accelerated tissue repair in a force-induced injury model. The findings point to a novel therapeutic platform for managing inflammation and supporting wound healing.

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Metabolomics Events

MANA SODAMeet

April 8, 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.

Join the web seminar

X-omics Festival

April 14, 2025

Venue: Nijmegen, Netherlands

The seventh edition of the X-omics festival, themed “The future of multi-omics research is now” will include:

- Keynote lectures: Hear from leading experts in the field of multi-omics.
- Innovative sessions: discover the latest advancements and applications in multi-omics

technologies and data analysis.
- Interactive sessions: participate in engaging discussions and activities.
- Networking opportunities: connect with the multi-omics community and expand your professional network.

Registration is required but free of charge. To secure your spot, complete the registration form here: X-omics festival 2025—Registration.

X-omics festival registration

Bits & Bites #3: Skyline: Getting Started with Targeted Metabolomics Data Processing

April 24, 2025

Venue: Online

The new course is taught by Dr. Christopher Ashwood from Protea Glycosciences. This intermediate course, designed for participants with a basic understanding of LC-MS and method development, focuses on the application of Skyline software. Skyline is a freely available, vendor-neutral software that facilitates targeted qualitative and quantitative analysis of both protein and small-molecule mass spectrometry data. Using hands-on tutorials, participants will learn best practices on analyzing metabolomics LC-MS data with Skyline, including iterative and sensitive targeted method development, small molecule target confirmation at both the MS1 and MS/MS levels, and analyte quantification using internal calibrants and external calibration curves.

Check for more details

6th Annual Canadian Metabolomics Conference (CanMetCon) 2025

April 24 - 25, 2025

Venue: Montreal, QC, Canada

This year's conference will bring together leading researchers, professionals, and students from across the metabolomics field for two days of engaging discussions, presentations, and valuable networking opportunities. The event will feature plenary and keynote lectures from experts, including:

- **Dr. Erin Baker** (University of North Carolina) – "Exploring Lipidomic Perturbations Due to

Chemical Exposures”

- **Dr. Mary-Ellen Harper** (University of Ottawa) – ” Leveraging metabolomics and systems biology approaches in the clinical translation of cellular bioenergetics research”
- **Dr. Gary Siuzdak** (Scripps Research) – “Sifting through Analytical Artifacts: Untargeted Activity Metabolomics and Data Mining Yield Gold”

Additional keynote presentations will include contributions from leading researchers such as **Dr. Lorraine Brennan, Dr. Matej Oresic,** and **Dr. Tom Metz**, and many others, covering a range of topics from Clinical Metabolomics, Computational Metabolomics and Machine Learning, Metabolomics of Nutrition and Health, and Public Health and Population Metabolomics.

To kick off the conference, two hands-on Pre-Conference Workshops "Comprehensive Clinical Omics - From Sample to Result", offering hands-on training in clinical mass spectrometry and data analysis.

Workshop Part 1: Attendees will have the opportunity to train at the Warren Y. Soper Clinical Proteomics Centre, one of Canada's only certified clinical metabolomics laboratories, on the latest techniques in clinical mass spectrometry analysis and data generation.

Workshop Part 2: Participants will learn how to explore this dataset and generate diagnostic insights, with MetaboAnalyst and OmicsAnalyst, two of the most-used and most-cited data analysis tools in metabolomics and multi-omics.

Registration is still open

6th Annual Workshop on Analytical Metabolomics

May 5 - 6, 2025

Venue: Thessaloniki, Greece

The series hosts renowned speakers from academia, industry and regulators advocating the application of holistic analytical approaches in biomarker discovery in life, plant and food sciences. It aims to bring high-level presentations to promote knowledge transfer with a special focus on application in clinical chemistry and diagnostics. Selected presentations will highlight the potential and benefits of bringing metabolomics biomarker discovery closer to clinical practice.

Early-Bird Registration Deadline - **March 31, 2025**

Check for more details

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EMBL-EBI Introduction to Metabolomics Analysis Course

May 20 - 23, 2025

Venue: Hinxton, United Kingdom

This course will provide an introduction to metabolomics through lectures and hands-on sessions, using publicly available data, software, and tools. Participants will become familiar with standardized workflows as well as with the current state of experimental design, data acquisition (LC-MS, MS imaging), processing, and modelling. In addition, they will learn about community standards and sharing in metabolomics, particularly through the use of EMBL-EBI's MetaboLights repository and Galaxy infrastructure. Participants will learn through hands-on tutorials to use tools available for data analysis and data submission. Additionally, case studies will be discussed to show how to employ the week's learning.

Check for more details

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

June 9 - 13, 2025

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.

Deadline to apply for bursary - **April 28, 2025**

Check for more details

21st Annual Conference of the Metabolomics Society Metabolomics 2025

June 22 - 26, 2025

Venue: Prague, Czech Republic

21st Annual International Metabolomics Conference of the Metabolomics Society will be held on June 22-26, 2024 in Prague, Czech Republic. The conference will follow the same pattern as previous years, with Workshops on Sunday and Monday, and the full conference beginning on Monday afternoon and running through Thursday afternoon.
Scientists in academia, government, industry, and others working in the field of metabolomics are invited to submit abstracts in the following scientific themes:

- Metabolomics and Lipidomics in Health and Disease
- Plants, Food, Environment and Microbes
- Technology Advancements
- Computational Metabolomics, Statistics & Bioinformatics

Poster Abstract Submission Deadline - **May 15, 2025**

Check for more details

2025 World Critical Care and Anesthesiology Conference

October 10 - 11, 2025

Venue: Singapore

The 2025 Critical Care Conference and Anesthesiology Congress will host its 9th Edition of the conference in Singapore. The speakers and delegates will get a chance to meet the international faculty members, great networking sessions and explore the magnificent Singapore.

Click here to view more details

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Metabolomics Jobs

Metabolomics Jobs

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Job Title	Employer	Location	Source
Omics Data Scientist	Michabo Health Science Ltd (spin-out company from University of Birmingham)	Birmingham, United Kingdom & hybrid working	Nature Careers
Postdoctoral Scholar - Metabolomics	Lund University	Lund, Sweden	Lund University
Postdoctoral Researcher in Targeted Mass Spectrometry Imaging and Multi-modal Spatial Biology	Karolinska Institute	Stockholm, Sweden	Karolinska Institute
Postdoctoral Studies in the Metabolomics of Asthma	Karolinska Institute	Stockholm, Sweden	Karolinska Institute
1Postdoc Position for LC-MS Metabolomics	Gottfried Wilhelm Leibniz Universität	Hannover, Germany	Hannover, Germany
Postdoctoral Scholar	University of North Carolina at Chapel Hill, Nutrition Research Institute	Kannapolis, North Carolina, US	University of North Carolina at Chapel Hill
Research Associate (Computational Metabolomics, PhD or PostDoc)	Leibniz Institute of Plant Biochemistry	Halle, Germany	Leibniz Institute of Plant Biochemistry
16 PhD positions in Doctoral Training Unit	University of Luxembourg, Luxembourg Institute of Health, and Luxembourg Institute of Science and Technology	Luxembourg	University of Luxembourg

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