MetaboNews

This month in metabolomics

February, 2025
Vol 15, Issue 2

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

In This Issue

This Months Features:

Perspectives
Dr. Erin Baker

MetaboInterview
Ryland Giebelhaus

|MC:SUBJECT|

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

A few quick updates for the upcoming conference in Prague, this is a busy planning time, and we're excited to see you in June!

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

Abstract Submission – Deadline Approaching!

Abstract submission is open and the deadline for oral abstracts is quickly approaching – **MARCH 6**! If you are applying for a travel award, you must submit in the "Oral or Poster" category by the oral abstract deadline.

Poster abstracts will continue to be accepted through May 15.

Registration – Save Money Now!

Take advantage of the discounted early registration rates, now through April 1. 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 in the next few weeks. If you register now, you can login to your registration to add complimentary workshops when they are posted.

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

Words from the Chair – Rick Dunn, President, Metabolomics Society

Dear Metabolomics Society Members and metabolomics friends,

Months seem to fly by for me as I am sure they do for you. We are nearly in March already. March is an important month for me as the day length increases, I celebrate my birthday and MOST IMPORTANTLY I start to consider abstract submission for the annual Metabolomics Society conference, which I should quickly act on with the upcoming deadline of March 6 for oral abstracts.

This year's conference is scheduled for June 22 nd - 26 th in the beautiful city of Prague. Workshops will operate all day Sunday and Monday morning (workshops have been chosen, stay tuned) and will be followed by three and a half days of great science and discussions (and I suspect food and drink). Tomas, David and Natasa along with the scientific organising committee (SOC) are working hard on developing the programme for Metabolomics 2025. Do book your place on workshops early when you register so not to be disappointed!

Now is the time to submit your abstracts for either oral presentations or poster presentations - https://www.metabolomics2025.org/abstract-submissions - as a SOC member I always look forward to reviewing and scoring abstracts as it reminds me of the diversity and high quality of science being performed where metabolomics is applied. All abstracts are reviewed by multiple members of the SOC and all abstracts are blinded (i.e. the reviewers do not see the authors or affiliations information).

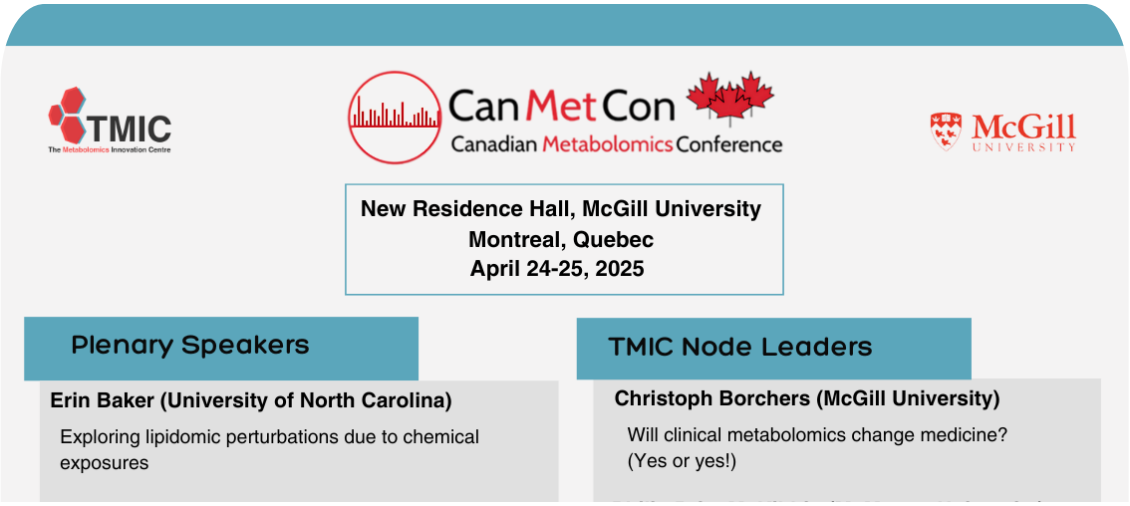
While we are discussing conferences… I had the pleasure to co-chair with Susan Sumner the 2025 GRC metabolomics conference in California in early February. The location in Ventura was great with afternoon walks a must to the beach and pier (along with about a 15 degree rise in temperature compared to the UK!). The science presented was mind blowing and showcased new and unpublished research across human health and exposomics – thanks to all the speakers for their presentations and all of the attendees for constructive discussions. Susan and I passed the baton to Jennifer Kirwan and Liang Liang to chair the next meeting, provisionally scheduled for Feb 28 th – March 5 th , 2027, in Tuscany. The chairs for 2029 were also voted in, Roy Goodacre and Nichole Reisdorph.

The GRC conferences are smaller than the Society's annual conference, with a maximum of 200 attendees. You spend a lot of time, including meals, with other attendees and I really enjoyed speaking to old friends and new friends about their research, careers and the society. One large view I came away with is that the field of metabolomics is hugely lucky to have so many world- leading early-career researchers driving the field forward, hopefully some will become Directors or Officers of the Society

in the future. On that note, there were a number of current and previous Directors at the conference, and we got together for a photo.

All the very best,

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



|MC:SUBJECT|

Early-Career Members Network (EMN)

EMN Travel Bursary

Applications for the 2025 EMN Travel Award are open! Four awards (2 graduate student (PhD or Masters) and 2 post-doctoral researcher) are available which will cover registration fees to Metabolomics 2025 in Prague. Applications will close with the oral

presentation abstract deadline (March 6). Please see https://www.metabolomics2025.org/awards for more information and eligibility. We encourage all eligible early career researchers to apply, especially those with a special interest in supporting EMN and joining the EMN committee in future years.

EMN Webinars 2025

February Webinar

The EMN committee expresses its sincere gratitude to Prof. Dr. Judith Jans and PhD candidate Hannah German from UMC Utrecht, Netherlands, for the insightful webinar on 12th February 2025 entitled "Applications of metabolic flux analysis in the field of inborn errors of metabolism", focusing on clinical metabolomics. The webinar recording will be available on the MetSoc website (https://metabolomicssociety.org/resources/multimedia/emn-webinars-2025/) and YouTube channel (https://www.youtube.com/playlist?list=PLvyBs-HBY5R2o3FbAkGMeX8f4ZwXZ6iTw).

March Webinar

The next EMN webinar will occur 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 EMN committee is delighted to invite you for the talk about "Untargeted Metabolomics for Natural Products: Not only for Discovery but also for Functional Analysis", focusing on microbial metabolomics. Registration is available in the following Zoom link: https://zoom.us/webinar/register/WN_YvTfl3b6RJu3NBGxq8qMvw

Online Presence

Keep an eye on your inbox for email blast and make sure to follow us on our social media accounts: Twitter, Bluesky, and LinkedIn! This year, we especially encourage researchers from South America, Africa and Asia to participate in our webinars. If you are interested, or want to recommend someone from your network, please reach out to us at info.emn@metabolomicssociety.org.

ECR Voices

The EMN “ECR Voices” initiative to spotlight early-career researchers (PhD students, Postdocs, Young Investigators, etc.) on our Twitter/X account is continuing through 2024-2025! You can check out an example here: (https://x.com/EMN_MetSoc/status/1704787637591265456?s=20).

We encourage everyone to participate! You can easily create your own ECR Voice slide

using this link: (https://docs.google.com/presentation/d/1H43FIIp3gmtJMUYS6r-2XVd460N8PjBn/edit#slide=id.p15).

The link contains instructions, templates, and examples from other researchers already featured on our Twitter/X page. It's as simple as making a single PowerPoint slide with a headshot and a few bullet points about yourself! Please consider sharing ECR voices with your network! This year, we would like to invite the researchers especially from South America, Africa and Asia to participate. If you are interested, or want to recommend someone from your network, please reach out to info.emn@metabolomicssociety.org.

Task Groups Corner

International Affiliations Task Group

Next meeting of the international affiliates will be on March 4, 2025 (online), followed by an in-person meeting during the Metabolomics 2025 conference in Prague.

The Affiliates Training Network is starting to take shape. A template was developed for each affiliate of the Metabolomics Society to fill in information about the group/laboratories willing and able to participate in the training network.

International Affiliates' Corner

Nordic Metabolomics Society
Visit www.nordicmetsoc.org

Travel grants for Metabolomics 2025 in Prague:
The Nordic Metabolomics Society is offering four travel grants of 600 EUR each for early-career researchers to attend the 21st Annual Conference of the Metabolomics Society in Prague this year. These awards are for graduate students (Masters or PhD) or within 5 years of obtaining PhD while being in a training position (parental leaves subtracted).

To be eligible, you must be currently studying or working at an organization within the Nordic Metabolomics Society region: Norway, Sweden, Finland, Denmark and Iceland. You apply for the travel grant through the conference website while submitting a

conference abstract in the “Oral or Poster” category by the submission deadline of **March 6**. When submitting your abstract, check the box to be considered for a Nordic Metabolomics Society Travel Award.

Call for Interest: Hosting the Nordic Metabolomics Conference 2026
The Nordic Metabolomics Society is announcing a call for interest to host the upcoming Nordic Metabolomics Conference 2026. We invite interested parties in the Nordic region to submit a letter of interest by 08 May 2025.

Your letter should include:
Proposed Venue: Describe the location and facilities.
Conference Theme: Suggest tentative themes for the conference.
Local Committee Members: List the members of your local organizing committee.
Please send your letters to normetsoc@gmail.com.

Back to top

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 second Perspective, we’re excited to feature Dr. Erin Baker, who shares her thoughts on the field's growth and the lessons she has learned throughout her journey.

Dr. Erin Baker is an Associate Professor at the University of North Carolina and Principal Investigator at The Baker Lab. She earned her B.S. in Chemistry, with a minor in Mathematics, from Montana State University (MSU) in Bozeman, where she conducted undergraduate research in Eric Grimsrud's lab using ion mobility spectrometry (IMS). Dr. Baker furthered her expertise in IMS during her Ph.D. research in Michael Bowers' Group at the University of California – Santa Barbara, where she studied DNA duplexes and quadruplexes using IMS coupled with mass spectrometry (IMS-MS). Following her doctoral work, she joined Pacific Northwest National Laboratory in Tricities, WA,

as a post-doctoral researcher and later as a scientist in Richard Smith's group. Dr. Baker's research interests include the impact of the environment on human health, molecular biomarkers, analytical separations, high throughput screening, mass spectrometry, and ion mobility spectrometry.

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

The most valuable piece of advice I have been given is that there is always work to do, but you need to remember to do one thing you enjoy each day and spend time with those you love. Being a scientist, it is easy to get caught up in your research and all the manuscripts and proposals you need to write. However, as I get older and lose more people from my life, it is so important to have activities outside of work and spend time with those you love. When I think back in time, it is often the fun afternoon I spent with a friend or the chance I had to take my family with me on a work trip that are my favorite memories and help me survive all the craziness. It is not the quick trip where I only saw the inside of a convention center or the all-nighter to finish a proposal that keeps me going. Work always seems to be there waiting no matter how hard we want the stack of reviews to disappear or the manuscripts to just write themselves.

What advice would you give to those looking to integrate metabolomics into their workflows?

Understanding metabolomic changes is such an important puzzle piece to all research questions. When we think of metabolites, it is important to define what we are assessing as different definitions of metabolites exist. For me, metabolites are the intermediates or end products of metabolism which means they can be endogenous primary (essential) or secondary (non-essential) molecules, in additional to xenobiotics which are up taken our bodies and those of other organisms. Furthermore, lipids are technically metabolites, even though they are commonly called out separately in lipidomic measurements due to their insolubility in water. Thus, metabolomic analyses end up evaluating any organic molecule detected in a given organism with a molecular weight between ~50 and ~1500 Da, even though there are a few exceptions in the higher molecular weight range. Analysis of these small molecules therefore allows us to gain so much biological and environmental knowledge. For example, metabolites are the first molecules to respond to environmental and physiological influences as they fluctuate due to changes in nutrition, hydration, stress, etc. That is why fasting is so important in certain studies. Altered metabolite signals therefore provide a rapid assessment of health even before a person

becomes symptomatic. Additionally, metabolite measurements provide both direct and indirect measurements of exposure to harmful chemicals as we can see the metabolized (or unmetabolized) xenobiotic chemical and changes in the endogenous molecules. These indirect endogenous changes are thus fundamental in understanding toxicology if the xenobiotic is quickly excreted before we even know we were exposed. Metabolomic knowledge therefore enhances our understanding of all environmental and clinical studies.

Among the various methodologies and technologies (e.g., LC-MS, GCxGC, NMR), which do you believe will have the greatest relevance or impact in the coming years?

There are so many exciting developments in metabolomic methods and technologies every year. Examples include the use of microfluidics for small sample size analyses, the multidimensional evaluations possible with LC-IMS-MS or GCxGC measurements, and the novel advances in mass spectrometry analyzers, just to name a few. Many times, however, it is not just the creation of a novel technique but finding which application will benefit the most from the new approach. Our recent work using LC-IMS-MS to distinguish halogenated molecules in untargeted analyses is extremely exciting. By combining the different multidimensional separation techniques, we are able to easily identify xenobiotic chemicals, deduce chemical formulas, and prioritize toxicology studies for the xenobiotics found in environmental, biofluid and tissue samples. Since 1000s of features are commonly detected in untargeted analyses for these sample types, LC-IMS-MS is greatly reducing large feature numbers to more manageable lists for further analysis and manual validation, which has not been possible with other techniques to date.

What role do you see for artificial intelligence and machine learning in metabolomics research and applications?

Artificial intelligence will have a great impact on future metabolomics research and applications. In metabolomic studies, we generate so much data that it is impossible to manually assess even a small fraction of it. For example, to obtain broad molecular coverage of a sample we might evaluate it with both positive and negative ionization modes using multiple columns and at times even employing different ionization modes (*e.g.,* ESI versus APCI). Each different assessment multiplies the number of data analyses we must perform, in addition to causing difficulty integrating the molecules detected from the different evaluations. However, by using experimental data to train the

different artificial intelligence tools and algorithms, molecular associations will be attainable that currently are just not humanly possible. Developments in this area are therefore very exciting, and I have told all my students they need to learn how to code as artificial intelligence will be an important part of our future due to the availability of so much experimental data since sample preparation instruments and mass spectrometers are becoming more automated each day.

How do you envision current metabolomics research being applied in the future?

The use of metabolomics for personal medicine is very intriguing to me. Over the last decade there has been extensive talk of the smart toilet and similar devices which would have portable mass spectrometers and be able to rapidly assess changes in our metabolomic profile throughout the day. These types of devices would allow people the ability to monitor their health on a daily basis and get treatments in early stages of conditions and diseases by have their specific molecular information readily available for doctors to assess. The use of metabolomics in wearables is also exciting as the more we know about metabolite changes associated with diseases, the more devices we can design for their rapid assessments. Thus, current metabolomics studies are extremely important for probing metabolite linkages to various conditions and diseases.

What actions do you think are crucial for further growing the metabolomics field?

To further grow the metabolomics field, information sharing and collaborations across different disciplines are crucial! It is only humanly possible to be experts in certain areas, however, to continue making impactful contributions in environmental and health fields we must combine our strengths with those in other disciplines. For example, researchers who create amazing instruments need to work with scientists trying to push developments in novel applications as new platforms should be utilized by evaluating novel samples in order to obtain groundbreaking results. Furthermore, as artificial intelligence becomes more sophisticated, we need to team with computational scientists creating novel tools and algorithms for areas such multi-omic integrations, big data analyses, on-the-fly assessments, and statistical analyses. Data sharing is also critical! By having access to data, people are able to enhance data processing, create large standard libraries, find new molecules, build artificial intelligence tools, and grow molecular networking capabilities. Social media is also playing an important role in advancing the metabolomics field and science in general, as it provides an open forum for researchers to ask questions and have experts quickly weigh in or point people to resources that they might not have known existed. Thus, with collaborations and data

sharing, overall science advancements from the metabolomics field feel endless!

The Baker Research Group

MetaboInterview

Ryland Giebelhaus

Biography

Ryland is just finishing his PhD at the University of Alberta and TMIC, working in Dr. James Harynuk's group. His research focused on applying mass spectrometry-based metabolomics to study physiology and environmental interactions. Ryland completed his BSc (Hons.) at UBC Okanagan, studying phytohormone metabolism in Dr. Susan Murch's lab. A published author in metabolomics and chemometrics, he has received prestigious awards, including the NSERC CGS-M (2021) and

CIHR CGS-D (2023). In July 2025, Ryland will begin his position as Assistant Professor of Chemistry at the University of Victoria.

How did you first get involved in metabolomics, and what motivated you to focus on multidimensional chromatography (gas and liquid) for metabolomics applications?

I first began metabolomics research during my undergrad degree at UBC Okanagan, where I worked under Professor Susan Murch for three and a half years, completing my Honours thesis in her laboratory. My research at UBC Okanagan was primarily focused on liquid chromatography mass spectrometry (LC-MS) based untargeted plant metabolomics, where I used LC-MS to study plant growth regulators in a variety of different species. During this time, I developed a plant growth regulator database, called HormonomicsDB, and used LC-MS metabolomics to understand plant growth regulation and evolution in an ancient living conifer, Wollemi pine.

Through this experience, I became really interested in both developing new technologies for metabolomics and applying metabolomics to solve real problems in physiology and metabolism. I decided I wanted to pursue a graduate degree in a laboratory which would allow me to do both. I ended up joining Professor James Harynuk's laboratory at the University of Alberta, where he is a TMIC Node Leader. Dr. Harynuk's research focuses on developing new technologies for performing metabolomics with comprehensive two-dimensional gas chromatography mass spectrometry (GC×GC-MS). I had not learned much about GC×GC during my undergraduate training, but after hearing about it for the first time I got excited about its applications and advantages in metabolomics over traditional one-dimensional GC.

Your work focuses on the use of multidimensional chromatography. What excites you most about applying this approach to metabolomics, and how do you see it contributing to the advancement of metabolomics?

The goal of untargeted metabolomics is to detect as many metabolites as possible in a single analysis. With current one-dimensional separations – both LC and GC – we can fully resolve about 500 to 1,000 metabolites, if we're lucky. Some data tools, like deconvolution, can deal with coelutions, but this doesn't solve the problem of limited peak capacity. Comprehensive multidimensional separations work by joining two chromatography columns together with a modulator, which is a device which periodically reintroduces effluent from the first column onto the second column. This allows for separation along two different columns in the same analysis, increasing peak capacity

multiplicatively, while improving chromatographic resolution, selectivity, and sensitivity. With GC×GC, we routinely obtain peak capacities above 5,000, often approaching 10,000.

We know the chemical space is massive. For instance, in any given plant leaf there is estimated to be thousands of small molecule metabolites. If we want to truly perform untargeted metabolomics and identify as many metabolites as possible in one single analysis, then multidimensional chromatography is the best tool for the job. The improved resolution and sensitivity are particularly exciting when analyzing complex samples, such as plant material, urine, or stool. I love seeing all the coelutions we resolve, it is beautiful how powerful these separations are at improving chromatographic resolution. I believe multidimensional chromatography will become more mainstream in metabolomics over the next decade as more researchers realize its power, particularly in untargeted metabolomics studies. Broadly, I anticipate multidimensional chromatography in metabolomics will uncover new biomarkers for disease and assist in drug discovery, enabling discoveries that improve the lives of everyone.

Can you share some specific examples or projects you have worked on where this Multidimensional chromatography has provided unique insights into complex biological or environmental samples?

I have developed algorithms for processing GC×GC data, and also applied GC×GC to study numerous complex biological samples. I have developed an algorithm for finding regions of interest within GC×GC chromatograms, an essential preprocessing step for analyzing GC×GC data in untargeted studies, enabling the development of new automated workflows for processing data. I have also used GC×GC to analyze everything from human stool, plants with antibacterial activity, and fecal microbiota transplant formulations. In all these applied studies, GC×GC allowed us to separate hundreds to thousands of metabolites, something that wouldn’t have been possible with GC. This enabled us to generate new hypotheses, and assess the stability of stool and fecal microbiota transplant under different conditions. Additionally, I have experience working with LC×LC at the University of Copenhagen in Denmark, where we used LC×LC to study waste water samples.

What are some of the most significant challenges you face when applying multidimensional chromatography to metabolomics?

There is no free lunch, multidimensional separations are (unfortunately) more challenging than one-dimensional separations. There is more hardware in a multidimensional separation. In GC×GC the column connection can leak, installing columns in the modulator is difficult, and the column often

breaks in the modulator. In LC×LC, there are more connections, therefore more opportunity for leaks, and the separation requires more optimization than an LC separation. When you practice multidimensional chromatography enough you become experienced in handling these challenges, and they become less of an issue, but nonetheless they persist. Vendors are increasing the number of commercial solutions for multidimensional chromatography, reducing the hardware challenges for the user. Processing multidimensional data is also much more complex, with two columns there is retention time shift along both columns. The peaks in multidimensional chromatography are also three dimensional, they can tail along one or both dimensions, which makes peak selection problematic. Aligning multiple chromatograms into a concise peak table also remains a challenge.

In your opinion, how does multidimensional chromatography compare to other techniques in terms of resolving complex metabolomic profiles? Are there specific advantages it has in certain applications?

I believe multidimensional chromatography is the best technique for resolving complex metabolomic profiles, but I may have a bit of a bias. GC×GC and LC×LC are much more sensitive than their respective one-dimensional counterparts. The improved separation also ensures a more pure plug of analyte reaches the mass spectrometer, providing cleaner mass spectra and improving sensitivity. With multidimensional chromatography we can detect peaks that otherwise would be lost in the noise, this is very powerful in untargeted studies. Multidimensional techniques are compatible with mass spectrometry, therefore we don’t lose the ability to have this powerful workhorse detector coupled to our separation. Furthermore, quantification can still be performed with multidimensional chromatography, allowing it to be used in semi-targeted or even targeted metabolomics studies. Multidimensional chromatography could also be considered ‘greener’ than one-dimensional chromatography when accounting for how many separate one-dimensional separations would be required to achieve the peak capacity from multidimensional chromatography.

As you move forward with your research in multidimensional chromatography, what do you see as the biggest breakthroughs or innovations that could further advance its use in metabolomics?

There are opportunities to advance multidimensional chromatography on both the hardware and software side. With hardware, designing new, simpler modulators that don’t use consumables and require less maintenance and downtime is one obvious area where innovations will advance the use of multidimensional chromatography in metabolomics. In a world where high-throughput is desired – at the expense of chromatographic resolution – implementation of technologies to enable faster multidimensional separations will make this approach more attractive to metabolomics users and reduce the cost per sample. There are many commercially available GC×GC solutions from various vendors, as this technology is starting to see widespread adoption in analytical laboratories. However,

LC×LC is a much less mature technique, given this there are far fewer commercial LC×LC systems. As LC×LC becomes more pervasive in analytical laboratories, I anticipate vendors will take a similar approach as they have with GC×GC, allowing multidimensional chromatography to become adopted by more metabolomics laboratories.

Processing the data remains a challenge. During data collection, the nature of multidimensional chromatography necessitates the use of higher acquisition speeds on the detector, however this can introduce noise into the data. There are software challenges related to data size, a single file from an acquisition can be well over 10 GB. Automating processing of GC×GC and LC×LC data is very challenging, current solutions require dozens of user inputs, leading to inconsistent processing between analysts. All these software challenges present a considerable bottleneck for adopting multidimensional chromatography in metabolomics. There are also opportunities to develop and refine softwares to simulate multidimensional separations, and automatically optimize multidimensional separations to maximize separation power. Developing these new software tools, through leveraging machine learning (ML) and artificial intelligence (AI) will remove this bottleneck and increase the uptake of this powerful technology in metabolomics.

What key advancements or research initiatives are you currently pursuing in your lab regarding multidimensional chromatography and metabolomics? How do you envision these initiatives advancing the field?

I am in the process of starting a new laboratory right now, which is exciting as I get to decide the direction of a research program. I'm starting as an Assistant Professor of Chemistry at the University of Victoria (UVic) in Victoria, British Columbia in July 2025. My new group will largely focus on using LC×LC-MS for untargeted metabolomics. Initially, I will be pursuing the development of approaches for performing and implementing quality assurance and quality control (QA/QC) in metabolomics workflows. I am a member of the metabolomics QA/QC consortium (mQACC), and through this, and my own research, I have identified that QA/QC is a critically step in the metabolomics process which we often ignore or take for granted. In untargeted studies, we have a lack of reproducibility, and a lack of standardized QA/QC procedures and methods in metabolomics exacerbates this. My group will be using data-driven approaches, including ML and AI to automate QA and QC practices in metabolomics. These will ensure data fidelity, improve confidence in biological interpretation, and improve reproducibility between metabolomics studies.

Finally, what advice would you give to researchers who are interested in integrating multidimensional chromatography into their metabolomics workflows? What are the key considerations or skills they should focus on developing?

For researchers who desire to maximize peak capacity and detect and identify as many metabolites as possible, integrating multidimensional chromatography into their metabolomics workflows is the best way to achieve this. To perform multidimensional separations, one must have a very good basis of chromatographic theory. With two columns, the separation becomes more complex, and without an understanding of chromatography, optimization and troubleshooting will be challenging. Researchers need to have a solid background in data analysis, and an understanding of how multidimensional data are structured and processed, in order to effectively process their data and interpret their results. I am often surprised how many metabolomics researchers are unaware of multidimensional chromatography, and are therefore unaware of how this powerful technology could make their metabolomics studies more comprehensive and sensitive. As more metabolomics researchers become aware of multidimensional chromatography, and more metabolomics laboratories collaborate with multidimensional separations laboratories, I expect we will see this technology implemented into more metabolomics studies. I, for one, am eager to collaborate with metabolomics researchers who wish to implement multidimensional separations into their metabolomics workflows.

Back to top

MetaboReads

Advances in Metabolomic and Lipidomic Techniques

A variety of recent papers highlight new analytical workflows and computational strategies that expand what metabolomics and lipidomics can accomplish. These developments tackle long-standing challenges like ion suppression, limited sample throughput, and the difficulty of unraveling drug modes of action. They also introduce innovative ways to quantify and interpret small-molecule data—ranging from improved sample prep to aptamer-based metabolite sensing.

[A High-Throughput Integrated Nontargeted Metabolomics and Lipidomics Workflow Using Microelution Enhanced Matrix Removal-Lipid for Comparative Analysis of Human Maternal and Umbilical Cord Blood Metabolomes]

Wu and colleagues in Analytical Chemistry showed that a high-throughput pretreatment workflow based on enhanced matrix removal (EMR)-lipid microelution effectively separates non-lipid metabolites and lipids from small sample volumes. Their method streamlines nontargeted metabolomics and lipidomics into a single sequence, greatly reducing overall sample amount and preparation time. In evaluating maternal and umbilical cord blood, the approach preserved diverse metabolite coverage and even revealed additional features not captured by traditional workflows. The authors emphasize its suitability for both clinical and preclinical metabolomics-lipidomics studies.

[Ion suppression correction and normalization for non-targeted metabolomics]

Mahmud and colleagues in Nature Communications introduced a workflow that combines a stable isotope-labeled internal standard library with companion algorithms to correct for ion suppression in non-targeted metabolomics. This “IROA TruQuant” approach systematically measures ion-suppression effects and normalizes the data, substantially enhancing accuracy and precision across varied LC-MS platforms. In a demonstration, the authors applied their method to study ovarian cancer cell response to l-asparaginase and uncovered metabolic alterations that had previously been masked. Their results highlight how systematic correction of ion suppression can sharpen biological insights in metabolomics.

[Quantifying metabolites using structure-switching aptamers coupled to DNA sequencing]

Tan and colleagues in Nature Biotechnology developed “smol-seq,” a technique that employs structure-switching aptamers (SSAs) to convert metabolite binding events into the release of DNA barcodes, which are then counted by next-generation sequencing. Because each aptamer is specific to a single small molecule, the abundance of freed barcodes directly reflects metabolite levels. This workflow allows parallel measurement of multiple metabolites with high sensitivity and potentially very large throughput. By harnessing the scalability of DNA sequencing, smol-seq opens new doors for population-scale or multiplexed metabolite quantification.

[A human metabolic map of pharmacological perturbations reveals drug modes of action]

Schuhknecht and colleagues in Nature Biotechnology created a large-scale map of metabolic perturbations induced by 1,520 drugs, monitored by high-throughput non-targeted metabolomics in a human lung cancer cell line. They observed that most compounds cause discernible shifts in the metabolome, even when they do not strongly affect cell growth. By systematically linking these metabolic fingerprints to drug mechanisms of action, they identified new activities for approved drugs. These findings suggest that broad metabolomic profiling can advance both drug discovery and repurposing by clarifying how compounds reshape cellular metabolism.

Microbiome and Nutritional Interventions

The gut microbiome and diet-derived factors are crucial not only in digestion, immune function, and metabolic processes but also in child development. The following six studies explore how specific microbes, microbial metabolites, and targeted nutritional interventions can mitigate disorders ranging from bile-acid–driven diarrhea and celiac disease to age-related sarcopenia and alcohol-induced gastric injury, while also demonstrating how dietary modifications can recalibrate microbiomes in industrialized settings. Collectively, they underscore the intricate interplay among diet, microbiota composition, and host physiology in shaping health trajectories and guiding potential therapeutic or nutritional strategies.

Microbiota governs host chenodeoxycholic acid glucuronidation to ameliorate bile acid disorder induced diarrhea

Lin and colleagues in Microbiome found that a Lactobacillus reuteri–derived metabolite, indole-3-carbinol, controls chenodeoxycholic acid (CDCA) glucuronidation in the gut epithelium and thereby alleviates bile acid disorder-induced diarrhea. By downregulating the gene UGT1A4, their experiments showed reduced production of the problematic compound CDCA-3β-glucuronide. In mouse models, the authors observed that decreasing this metabolite promoted normal intestinal function and diminished diarrhea. This work highlights the gut microbe–host axis as a tractable target for ameliorating bile acid–related disorders.

Melatonin Ameliorates Age-Related Sarcopenia via the Gut-Muscle Axis Mediated by Serum Lipopolysaccharide and Metabolites

Zhou and colleagues in the Journal of Cachexia, Sarcopenia and Muscle demonstrated that melatonin protects aged mice from sarcopenia, partly by modulating gut microbiota and lowering serum lipopolysaccharide levels. By activating the Tnfrsf12a/caspase-8 pathway downstream of lipopolysaccharide, melatonin treatment reduced muscle apoptosis. The authors further showed that changes in gut-derived metabolites were linked to improved muscle mass and strength. These data reveal how a gut-muscle axis can be harnessed to combat age-related muscle degeneration.

Multi-omics analysis reveals the pre-protective mechanism of Dendrobium flexicaule polysaccharide against alcohol-induced gastric mucosal injury

Wang and colleagues in the International Journal of Biological Macromolecules reported that polysaccharides isolated from Dendrobium flexicaule conferred a protective effect against alcohol-induced gastric mucosal injury. Through multi-omics analyses, they showed that these polysaccharides modulate inflammatory mediators and upregulate key genes responsible for maintaining gastric barrier integrity. Specifically, the supplementation reduced proinflammatory cytokines while enhancing antioxidant defenses in animal models. These findings highlight a promising gastric-protective mechanism mediated by Dendrobium polysaccharides.

Serum metabolomics and lipoproteomics discriminate celiac disease and non-celiac gluten sensitivity patients

Vignoli and colleagues in Clinical Nutrition showed that serum metabolomics and lipoproteomics

can reliably distinguish between celiac disease, potential celiac disease, and non-celiac gluten sensitivity. By measuring lipid subclasses and small metabolites, they achieved robust cross-validated models with high area-under-the-curve values. Their data suggest that specific metabolite patterns linked to heavy regulation of immune and inflammatory pathways may underlie these gluten-related disorders. In turn, this metabolomic approach could help refine diagnoses and better characterize atypical or overlapping presentations.

Serum metabolome indicators of early childhood development in the Brazilian National Survey on Child Nutrition (ENANI-2019)

Padilha and colleagues in eLife found that circulating microbial- and diet-derived metabolites correlate with early childhood development. They performed untargeted metabolomics on serum samples from over 5,000 Brazilian children (ages 6–59 months) and assessed developmental milestones using the Survey of Well-being of Young Children questionnaire. Several metabolites, including cresol sulfate, hippuric acid, phenylacetylglutamine, and trimethylamine-N-oxide, were negatively linked to developmental quotient scores. Intriguingly, creatinine and methylhistidine had age-dependent associations, highlighting the complexity of metabolism across different developmental windows. The authors propose that these metabolic biomarkers could help identify children at risk for developmental delays and guide interventions to optimize early child development.

Cardiometabolic benefits of a non-industrialized-type diet are linked to gut microbiome modulation

Li and colleagues in Cell found that a diet mimicking non-industrialized eating patterns, combined with the administration of Limosilactobacillus reuteri, partially restored gut microbiome characteristics lost through industrialization. In a randomized controlled feeding trial, healthy Canadian adults displayed enhanced retention of a rural Papua New Guinean L. reuteri strain (PB-W1), alongside improvements in microbiome-associated plasma metabolites linked to chronic disease. Notably, favorable changes in cardiometabolic markers occurred even without the probiotic, underscoring the importance of dietary composition. Baseline microbiome features helped predict who would most benefit from the intervention, guiding future personalized diets. The authors propose that such a targeted "restore diet" could inform evidence-based strategies to reduce risk factors for chronic non-communicable diseases.

Integrated Metabolomics in Human Physiology and Disease

Multi-omics approaches that integrate metabolomics with genomics, transcriptomics, or proteomics are advancing our understanding of complex human disorders. From pinpointing mitochondrial cofactors to mapping immune responses, these studies illustrate how a broader systems-level view can reveal novel therapeutic targets and biomarkers across conditions such as anemia, aging, spinal cord injury, dry eye syndrome, and nephropathy.

SLC25A38 is required for mitochondrial pyridoxal 5'-phosphate (PLP) accumulation

Pena and colleagues in Nature Communications showed that the mitochondrial inner membrane protein SLC25A38 is essential for the accumulation of pyridoxal 5′-phosphate (PLP)—the active form of vitamin B6—inside mitochondria. Using genome-wide CRISPR interference and organellar metabolomics, they found that loss of SLC25A38 specifically disrupts mitochondrial PLP-dependent reactions, including serine-glycine interconversion and ornithine transamination. Notably, these deficits impair cellular proliferation under both normal and low vitamin B6 conditions. The findings clarify why SLC25A38 mutations might lead to sideroblastic anemia and highlight mitochondria-specific vitamin B6 transport as a critical node in cellular metabolism.

Assessing Metabolic Ageing via DNA Methylation Surrogate Markers: A Multicohort Study in Britain, Ireland and the USA

Xu and colleagues in Aging Cell evaluated a hybrid “DNAm-metabolic clock” derived from DNA methylation surrogates of over 100 metabolic markers. In multiple cohorts, their epigenetic-metabolite signature predicted chronological age and correlated with clinical risk factors such as heavy alcohol use, anxiety, and cardiometabolic diseases. When validated in the Health and Retirement Study, the clock also predicted mortality and frailty measures, suggesting a robust link between epigenetic regulation and metabolic health. This tool holds potential for early detection of metabolic-related aging processes and diseases.

Multi-omics uncovers immune-modulatory molecules in plasma contributing to resistance exercise-ameliorated locomotor disability after incomplete spinal cord injury

Zhou and colleagues in Genome Medicine used a multi-omics strategy (integrating plasma proteomics, PBMC transcriptomics, and metabolomics) to reveal immune-modulatory molecules underlying resistance-exercise benefits in individuals with incomplete spinal cord injury (SCI). Resistance training improved muscle function while altering humoral immune pathways and lipid metabolism in both human patients and a mouse SCI model. Intriguingly, plasma from exercised mice, when transferred intravenously, enhanced neuroprotection and improved locomotor outcomes in SCI recipients. The researchers propose immunoregulatory factors in plasma as key drivers of exercise-mediated recovery.

Identification of glutamine as a potential therapeutic target in dry eye disease

Chen and colleagues in Signal Transduction and Targeted Therapy identified glutamine metabolism as a critical factor in dry eye disease. By combining in situ metabolomics and gene-expression analyses, they observed that local glutamine levels increased in corneal tissues treated with a regenerative regimen. Experimental inhibition of glutamine reversed anti-inflammatory and anti-apoptotic effects, underscoring its importance in maintaining corneal homeostasis. These results highlight glutamine metabolism—and its upstream enzyme GLS1—as a promising therapeutic target for inflammation-driven ocular surface diseases.

MC16 promotes mitochondrial biogenesis and ameliorates acute and diabetic nephropathy

Thompson and colleagues in the British Journal of Pharmacology investigated a novel compound, MC16, that induces mitochondrial biogenesis and protects against both acute and diabetic kidney injuries. The authors demonstrated that MC16 activates the PI3K-AKT-eNOS-

FOXO1 axis, preserving mitochondrial oxidative phosphorylation and preventing renal tubular damage. In diabetic mouse models, MC16 improved mitochondrial function, restored renal metabolic profiles, and lessened interstitial fibrosis. These results underscore the therapeutic value of enhancing mitochondrial repair pathways to halt kidney disease progression.

Cancer Metabolism and Therapeutic Targets

Targeting tumor metabolism is a growing focus in oncology research, as malignant cells often rely on distinctive metabolic pathways. The following studies pinpoint essential metabolic vulnerabilities—including the glutamine–mTOR axis and de novo nucleotide synthesis—that could be leveraged to design more effective anticancer interventions

Baicalein induces apoptosis by inhibiting the glutamine-mTOR metabolic pathway in lung cancer

Li and colleagues in the Journal of Advanced Research found that the natural compound baicalein promotes apoptosis in non-small cell lung cancer cells by inhibiting glutamine-fueled mTOR signaling. The authors employed in vitro and metabolomic approaches to reveal that baicalein's anticancer effect arises through disruption of glutamine transporters and glutaminase, coupled with downstream mTOR inhibition. In both cell-based and animal models, baicalein reduced tumor growth by impairing glutamine-driven energy and biosynthetic processes. This study supports glutamine metabolism as a viable therapeutic target in lung cancer management.

Metabolic profiling of patient-derived organoids reveals nucleotide synthesis as a metabolic vulnerability in malignant rhabdoid tumors

Kes and colleagues in Cell Reports uncovered that malignant rhabdoid tumors (MRTs) are especially dependent on de novo nucleotide biosynthesis. Using patient-derived tumor organoids, they observed that inhibiting key enzymes in nucleotide pathways, such as dihydroorotate dehydrogenase (DHODH), suppressed MRT organoid viability. In vivo, targeting these enzymes slowed tumor progression. Their findings suggest that pharmacological disruption of nucleotide metabolism could selectively impede MRT cell growth.

Agriculture, Food, and Environmental Applications

From plant breeding and food-chain safety to fungal biotechnology, metabolomics is enabling more precise interventions in agriculture and related industries. These studies underscore how profiling metabolites at high resolution can guide improvements in plant traits, uncover functional polysaccharides for food or health applications, and enhance quality control across the food supply.

Spatial and Temporal Regulation of Flower Coloration in Cymbidium lowianum

Dong and colleagues in Plant Cell and Environment demonstrated that the red coloration in Cymbidium lowianum flowers is linked to elevated cyanidin-3-O-glucoside in the epichile region

of the lip. By integrating metabolomic and gene-expression data, they showed that F3′H drives anthocyanin biosynthesis, while other pigments like carotenoids and chlorophyll also shape petal coloration. Functional assays in transgenic plants further confirmed that MYB and PIF transcription factors coordinate pigment accumulation. This study enriches our understanding of flower pigmentation and guides future breeding of ornamental orchids.

Towards a safer food chain: Recent advances in multi-technology based lipidomics application to food quality and safety

Xue and colleagues in Trends in Food Science & Technology provided an overview of cutting-edge lipidomics approaches to ensure a safer food chain. They stressed that multi-technology integrations—combining advanced mass spectrometry, data analytics, and complementary chromatographic separations—can comprehensively profile lipids at high throughput. This strategy not only detects contaminants but also monitors nutrient quality, authenticity, and potential adulteration. Overall, the authors advocate that multi-platform lipidomics is indispensable for meeting modern food safety and quality demands.

Enhanced production of exopolysaccharide by Antrodia cinnamomea through batch feeding of tansglycocylated sugar mixture: Physicochemical properties, biotechnological application, and gut microbiota modulating potential

Shafiq and colleagues in the Chemical Engineering Journal reported a novel fermentation strategy using a transglycosylated sugar mixture to boost exopolysaccharide (EPS) production by Antrodia cinnamomea. Through multi-omics analyses, they found that key biosynthetic enzymes were upregulated, yielding EPS with enhanced antioxidant and emulsifying properties. Additionally, in vitro gut fermentation tests showed this EPS promoted beneficial short-chain fatty acid production and modulated microbial diversity in fish models. The study highlights new applications of fungal EPS in both nutraceuticals and aquaculture feed supplements.

Back to top

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

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.

Abstract Submission Deadline extended - **March 15, 2025**

Registration is 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.

Check for more details

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

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

Oral Abstract Submission Deadline - **March 6, 2025**
Poster Abstract Submission Deadline - **May 15, 2025**

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

Oral Abstract Submission Deadline - **March 6, 2025**
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

NIST SRM 1950 Beyond the Certificate of Analysis: mQACC Call to Provide Qualitative and Quantitative Data

Certified reference materials (CRM) values provide a known and standardized reference point against which the results of a metabolomic study can be compared. However, the certification of hundreds of individual metabolites is a cumbersome and time-consuming process. The Standard Reference Material (SRM) 1950, Metabolites in Frozen Human Plasma, is by far the most used reference material by the metabolomics community. NIST SRM 1950 provides certified and/or reference values for select metabolites and lipids such as fatty acids, electrolytes, vitamins, hormones, and amino acids. The metabolomics community would greatly benefit from consensus values and identification of metabolites and lipids in SRM 1950 that are not tied to a single analytical platform or method. This increases the accuracy, reliability, harmonization, and meaningful

comparisons of metabolomic studies utilizing the material. Additionally, having more values and information available for SRM 1950 metabolites and lipids would allow researchers to investigate a broader range of analytes in their studies, which in turn could lead to a better understanding of the underlying biology of the metabolic processes. To that end, the Reference and Test Materials Working Group of mQACC is actively collecting information on qualitative identifications and quantitative values of metabolites and lipids in NIST SRM 1950 beyond those listed on the NIST Certificate of Analysis. Any data from instrumental platforms with compound identification (LC-MS, GC-MS, NMR) are welcome to participate. The data was combined in order to produce a publicly available database of community-generated 1) consensus concentration values for quantified metabolites and lipids of critical interest within the community and 2) compounds identified but not quantified in SRM 1950.

More information and an example reporting form can be found at https://www.mqacc.org/srm1950

Back to top

Metabolomics Jobs

Metabolomics Jobs

If you have a job to post, please email the MetaboNews team at metabolomics.innovation@gmail.com

We may remove a listing after 6 months if we do not receive a confirmation that it is still necessary. However, if you would like us to repost it, please contact us.

Job Title	Employer	Location	Source
Chromatography and Mass Spectrometry Technologist	The James Hutton Institute	Dundee, Scotland, United Kingdom	The James Hutton Institute
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
Assistant/Associate Professor in Computational Metabolomics	Penn State University Park	PA, US	Metabolomics Society
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
Post-Doctoral Position in Stem Cell Metabolomics	Université Catholique de Louvain (UCL)	Brussels, Belgium	Metabolomics Society
Metabolomics Senior Research Associate	Berkeley Lab's (LBNL) Environmental Genomics and Systems Biology (EGSB) Division	Bay Area, California, United States	Berkeley Lab

Back to top

MetaboNews Feedback Form

Thank you for being a part of MetaboNews! Your input means a lot to us, and we're eager to hear your thoughts on how we can improve our newsletter. We've put together a brief, anonymous survey with just two mandatory questions that won't take more than a

minute of your time. Your feedback is invaluable, so please take a moment to share your opinions with us.

Fill Out Your Survey Here

If you have any questions, don't hesitate to contact us at metabolomics.innovation@gmail.com

Back to top


Our mailing address is:
metabolomics.innovation@gmail.com