MetaboNews

This month in metabolomics

May, 2025
Vol 15, Issue 5

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

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|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

We'll see you all very soon in Prague! Take a moment to review these important conference updates so you can maximize your participation at Metabolomics 2025!

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

Posters at the Conference

Thank you to everyone who submitted an abstract! Based on the high demand for poster presentations, we have modified the poster session format in order to accommodate as many presenters as possible.

In the new format, each poster will be displayed for 1.5 days during the conference, in 3 groups. We also host the online Poster Gallery, where presenters are welcome to upload a .pdf poster to the virtual gallery to display their work for 2 weeks prior to the conference through September.

Thank you for your enthusiasm and support! We can't wait to showcase the amazing research from our community!

Registration and Agenda

Do not forget to register! If you are presenting, you should already be registered. Please adhere to the registration deadlines for presenters if you want your abstract to appear in the digital abstract book.
Click here to register online.

Pro tip: receive an extra discount by renewing or becoming a member of the Metabolomics Society BEFORE registering for the conference.

The latest **online agenda** includes all parallel sessions and workshops, you don't want to miss this line-up. Look for the digital Session Schedule book to be posted on the website by the end of May.

Workshops – Save Your Spot

Select the workshops you want to attend on Sunday, June 22 and Monday, June 23. Several workshops have limited capacity, you must sign up to reserve your space. There is not a fee to attend the workshops, they are included in the full-access conference pass.

If you previously registered for the conference, log-in to your registration to sign up for workshops, it's easy to add. Instructions available on the website. You can also view the **PDF Workshop List** online.

We also have the BioHub in 2025 with scheduled sessions to discuss specific topics in a small, casual setting (approx. 20 people). When sessions are not active, feel free to use the

BioHub with your own small group to discuss ongoing problems or ideas in data processing, tool development, programming, etc. Details about the BioHub are available at the bottom of the **Workshop page**.

Attend a Sponsored Lunch Presentation

Our Platinum sponsors are planning interesting lunch presentations during the week, with invited speakers discussing the latest topics and trends. **Sign up** for the lunch presentations you would like to attend!

Members' Corner

Board of Directors

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

Dear Metabolomics Society Members and metabolomics friends,

It is May already and as I write this message there are 43 days to the start of Metabolomics 2025 in Prague. This will be my last message before the conference and so I would like to focus on the annual Society conference.

The first annual Society conference was held in Tsuruoka City, Japan in 2005 and so this year will be our 20th anniversary. The city of Prague will be a great location to celebrate! Having attended many of the conferences over the years, I have many great memories of the science presented and how this has evolved over time from technology development to real world applications and impact. Of course, the excitement of travelling somewhere new and exploring the history, culture and local experiences is also a significant positive. I have many stories to tell over a beer or meal. And finally, being able to meet old and new collaborators and friends and chat science and life is a must. The society conference is always the first in my calendar each year, even before annual leave.

This year's conference in Prague is going to be a week to remember. Sunday afternoon and Monday morning focus on workshops – remember to register for the workshops you want to attend though some are already fully booked. The science programme starts on Monday afternoon for us all to enjoy and includes five plenary speakers - Livia Eberlin, Erin Baker, Steffen Neumann, Peter Meikle and Clary Clish. There are a lot of events in the evenings also including the Metabolomics Society Town Hall meeting on Monday where the current standing and new initiatives of the society will be discussed and where we want

your feedback as members. The EMN also provide a great atmosphere and range of events including a career night roundtable on Sunday and EMN Reception on Tuesday – many thanks to Silvia and all of the EMN team for all of their hard work and commitment. We should not forget the conference dinner to help unwind and possibly check your vocal talent.

Record numbers of abstracts have been submitted for oral and poster presentations, and we hope the number of registrations will also be a record - we may break the 1000 attendees ceiling for the first time since 2019 in The Hague.

I would like to personally thank Natasa who has lead the conference committee for five years and through the difficulties of Covid to ensure the annual conference always operates successfully. Behind the scenes we have Leslie and her fantastic team at SnapIT, thank you. Tomas and David have lead the preparation for Prague as local organisers and leads of the scientific organising committee and again thank you (the beers are on me).

I look forward to seeing many of you in Prague and do not be shy, come and say hi.

All the very best,

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

Early-Career Members Network (EMN)

EMN Webinars

May Webinar

The EMN committee expresses its deepest appreciation to Dr. Farhana R. Pinu from The New Zealand Institute for Plant and Food Research, NZ, for the insightful webinar on 14th May 2025 entitled "Flavoromics - a new frontier in food and horticultural science". The webinar recording will soon be posted on the MetSoc website (https://metabolomicssociety.org/resources/multimedia/emn-webinars-2025/) and youtube channel (https://www.youtube.com/playlist?list=PLvyBs-HBY5R2o3FbAkGMeX8f4ZwXZ6iTw).
We thank Dr. Farhana for her time and exciting webinar!

EMN at Metabolomics 2025 in Prague

EMN Workshop – Monday, June 23

Registration is now open for the EMN Workshop – (W10, Monday, June 23)
MetaboMentors: Paving the way to successful mentorship!

The EMN organized a workshop to provide ECRs with a comprehensive understanding of mentoring and its crucial role in career development. The workshop will explore different aspects of mentoring and provide practical advice for identifying mentors and initiating/maintaining mentor-mentee relationships. A subsequent interactive session between the audience and invited panellists (Erin Baker, Evelina Charidemou, Biswapriya Misra, Álvaro Fernández Ochoa, Nicholas Rattray, and Lynn Vanhaecke) will offer an opportunity to share experiences of mentoring in academia and industry, and to discuss the integration of mentoring into diversity and inclusion initiatives. The EMN committee warmly thanks the invited panellists for their participation.

Career Night Roundtable Discussions

Sunday, June 22, 6:45 p.m. – 8:00 p.m.
Career Night provides an interactive roundtable event for participants to develop rapport and expand their networks to ready themselves for future employment. The session will run in three 20-minute discussion periods.

This roundtable event will feature discussion leaders, covering topics such as:

- Translating research into industry applications
- Career Transitions
- Careers in Industry
- International employment opportunities: Understanding visas, relocation, and cultural considerations
- Leadership and management in research teams
- How to be a good reviewer (tips and tricks for peer review)
- Obtaining a postdoctoral fellowship
- Grant Writing
- Science communication
- Diversity, Equity, and Inclusion

EMN Reception and Treasure Hunt
Tuesday, June 24, 6:45 p.m. – 8:15 p.m.
Are you a graduate student or within five years of completion of your highest degree? Then you are warmly invited to attend the Early-Career Members Network (EMN) annual reception! Join us for a spirited night where you learn more about the members and activities organized by the EMN committee. We will also host the award ceremony for the 2025 EMN Travel Bursary Award and MetaboART winners. Following the reception, light refreshments will be served, and participants are invited to join the EMN Treasure Hunt—a dynamic, team-based challenge. In groups of 4 to 6, you will navigate the venue, scanning QR codes to uncover and solve questions on a range of topics, including Prague, metabolomics, and more. Teams will have 40 minutes to complete as many challenges as possible. Strategy, speed, and teamwork will be key to success.

MetaboART
MetaboART 2025 is now open for submissions! This is a unique opportunity to transform your metabolomics research into visually striking artwork. This year's competition features two exciting categories: human-created and AI-generated. Submissions will close on May 31, 2025. Winners will be announced at the Metabolomics 2025 Early-career Members Network (EMN) Reception on June 24.

To learn how to apply, please read our information guide (https://acrobat.adobe.com/id/urn:aaid:sc:ap:7ab1f50d-0d73-4567-872f-9a121424d463). Submit your entries to: info.emn@metabolomicssociety.org

Task Groups Corner

Diversity, Equity and Inclusion Task Group

We're thrilled to announce the reactivation of the Diversity, Equity, and Inclusion (DEI) Task Group within the Metabolomics Society for 2025!

A warm welcome to our newly reformed team:

- Millena Barros Santos (Co-chair)
- Domenica Berardi (Co-chair)
- Candice Z. Ulmer Holland
- Laimdota Zizmare
- Sandi Azab
- Silvia Radenkovic
- Marvin Nathanael Iman
- Diana Pinto
- Breanna Dixon
- Thomas Dussarrat
- Marina Botana

We're excited to work toward a more diverse, inclusive and equitable metabolomics community.
As we relaunch, we want to hear from ***you***! Please take a moment to complete our survey and help shape our future initiatives:
https://docs.google.com/forms/d/e/1FAIpQLSdKrVc8xfYCSycYgr9fmEtCJNR63IzEKB2F-vRlROg-YO29YQ/viewform?usp=header

Your voice matters. Let's build a more diverse, equitable, and inclusive community—together.

International Affiliates' Corner

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

17th Scientific Days of RFMF in Paris
Join us from **June 10–13, 2025**, in the heart of Paris's historic Saint-Germain-des-Prés, for the 17th Scientific Days of the French-speaking Network of Metabolomics and Fluxomics (RFMF). This year marks the **20th anniversary** of the RFMF, promising an unforgettable celebration of science, innovation, and collaboration. https://17-js-rfmf-2025.sciencesconf.org/
Immerse yourself in a dynamic program for this French-speaking symposium and featuring:

- **5 plenary talks** by internationally renowned researchers (https://17-js-rfmf-2025.sciencesconf.org/resource/page/id/10)
- **Thematic sessions**, **oral presentations**, **flash communications**, and **poster**

sessions

- Dedicated slots for **junior researchers**
- Networking opportunities with **industrial partners**
- A warm welcome reception and a festive gala dinner

Don't miss this opportunity to showcase your work and connect with the French-speaking metabolomics and fluxomics community. Still some seats remaining!
Let's celebrate 20 years of "**Good Science, Good Food**" together in Paris!

RFMF thematic school on the annotation of plant metabolomes in Sète, France

Save the Date!
We are thrilled to announce the first edition of the Thematic School of the French-speaking Network for Metabolomics and Fluxomics (RFMF), focused on the annotation of plant metabolomes!
When? September 8–12, 2025
Where? Domaine du Lazaret, Sète, France
This thematic school is a unique opportunity for researchers — from PhD students to senior scientists — to deepen their skills in plant metabolomics annotation, a challenging yet essential aspect of our field.
Expect a rich week combining theoretical sessions, hands-on workshops, and invaluable discussions, all guided by leading international experts.

Please note: It is a French-speaking school but lectures and discussions can be held in English.

More than just a scientific event, this is a chance to connect, share, and build collaborations within the vibrant RFMF community.

More details & registration: https://1-et-rfmf.sciencesconf.org/

Follow the event with #ET1RFMF

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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 this month's Perspective, we're excited to feature Dr. Xianlin Han, who shares his views on the journey of Lipidomics

Prof. Han graduated from Zhejiang University, China, did his graduate/postdoctoral trainings in Dr. Richard Gross' lab, and became a tenured Associate Professor of Medicine in Washington University School of Medicine. He now is a chair Professor of Medicine and Barshop Institute, University of Texas Health San Antonio. Dr. Han has published >400 papers with nearly 45,000 citations and wrote the book "Lipidomics: Comprehensive Mass Spectrometry of Lipids". He is one of the pioneers in lipidomics; is the associate editor of JLR; received many awards

and served in NIH study sections; and has broad research interests in functional lipidomics.

From your perspective, why is Lipidomics important and how is it distinct/differ from metabolomics?

Lipidomics plays an essential role in defining the biochemical mechanisms underlying lipid-related disease processes through identification and quantification of alterations in cellular lipid signaling, metabolism, trafficking, and homeostasis, in addition to the applications for biomarker development (DOI: 10.1038/nrendo.2016.98).

Lipidomics falls under the larger umbrella of the general field of “metabolomics”. However, Lipids possess special physical and chemical characteristics in contrast to the most other water-soluble cellular metabolites which have been generally studying in metabolomics. These features include, but are not limited to, (1) lipids contain some hydrophobic region(s) and are extractable with some type of organic solvents to a certain degree, which makes the majority of lipids readily recovered and largely separated from other cellular metabolites; (2) there exist a large number of isomeric/isobaric lipid species in cellular lipidomes; and (3) the nature of amphiphilic structure of lipids makes them readily forming aggregates even in organic solvents.

Moreover, in the metabolic network, individual node represents one water-soluble cellular metabolite in general cases. The flux through the node can be determined by measuring the changes of its precursor and product or estimated from their statistical changes. However, for lipids, the node represents an entire lipid class which could contain thousands of individual molecular species. Thus, unlikely the metabolites in metabolomics, neither the content of individual lipid molecular species nor the mass of an entire lipid class can usually provide any information about the flux into and out of the node of metabolic network. Therefore, accurate quantification of individual lipid species becomes essential for determination of metabolic pathways and networks underlying lipid changes in the context of a metabolic condition.

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

It should always keep in mind that the amphiphilic structure of lipids makes them readily form aggregates even in organic solvents as the concentration of lipids increases and exceeds the ability of a given solvent to solubilize them as monomers. Thus, any solvent

systems which are favorable for metabolomic analysis could be problematic for lipid analysis due to the presence of aggregation under the conditions. This physical characteristic of lipids could lead to false annotation of the detected ion peaks which correspond to aggregates (DOI: 10.1016/j.jlr.2022.100201). This clearly makes quantification of intact individual lipid species difficult and inaccurate by mass spectrometry under certain conditions since different aggregates show very different ionization response factors. This type of artifact could represent one of the hindered factors for successful replication of metabolomics/lipidomics findings (DOI: 10.1016/j.trac.2024.117918). In fact, the occurrence of aggregation frequently happens when LC-MS is applied for lipid analysis, where the elusion of any lipid species from LC is a concentration-dependent process. Therefore, any newcomers should bear this special physical feature of lipids in mind and minimize the effects of aggregation on quantification in their method development and application for lipid analysis.

What are the largest barriers currently facing the field of Lipidomics? Are there particular limitations in how Lipidomics can be effectively integrated into metabolic research?

Metabolomics in general, lipidomics in particular, is an interdisciplinary research field. It requires the collaborative efforts from both analysts and biologists. Currently, the majority of the drivers in lipidomics are the analysts, particularly those in mass spectrometry. With the great advances in instrumentation and analytical technologies, it is the time to apply lipidomics methodology for biological, biomedical, and translational questions. The analysts should work together with biochemists to integrate the lipidomics into metabolic research. Specifically, we should move beyond the association studies to identify the molecular mechanism(s) underlying metabolic diseases-induced changes of cellular lipidomes at the levels of an organ, a species, or a subcellular organelle. We should uncover the consequences of the altered lipidomes in the context of the diseases. We should identify any potential drug target(s) toward to the altered lipidomes. In summary, the field of lipidomics should evolve to the functional lipidomics stage.

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

Recently, artificial intelligence (AI) including machine learning has emerged as a key component in biomedical data analyses including lipidomics research. AI clearly offers a promising initial response to lipidomics analysis by enabling reduced and informative data representation. To this end, a very recent study by transforming a serial two-dimensional

MALDI mass spectrometry imaging sections into a high-resolution three-dimensional spatial metabolome is a typical application of AI in lipidomics research (DOI: 10.1038/s42255-025-01242-9). However, to maximize AI's impact in the field, it is essential to overcome challenges related to data quality as aforementioned.

With your extensive experience in lipidomics, how do you envision the field evolving in the next 5–10 years?

In the near future, the focal points at the current lipidomics (such as deeply penetrating analysis of individual lipid species, accurate quantification and standardization, clinical lipidomics, functional lipidomics, lipidomics of organelles (including EVs), etc.) will inevitably evolve and be solved. Moreover, the following areas of research in lipidomics appear in high demand and should be well developed in the future. These include, but are not limited to, (i) further increases in the coverage of lipid classes and individual species (particularly for those very low abundance species) using an automated, quantitative, high throughput lipidomics in combination with instrumental advances and chemical breakthroughs; (ii) single cell lipidomics, as stimulated with the fruitful development and powerful applications of single cell genomics and demonstrated with limited studies, will likely become a rising star; (iii) MS imaging should evolve into more quantitative and multi-dimensional; (iv) more complex dynamic studies in metabolic flux to reveal the reaction rates in lipid metabolism to comprehensively determine lipid metabolism in the molecular levels and provide true understanding of the roles of lipids in biomedical sciences; and (v) integration of lipidomics with other omics considering the relationship with genes, transcripts, and enzyme data to perform metabolic pathway reconstruction and flux analyses is in high demand. Collectively, as an interdisciplinary field, lipidomics will continue its exponential growth and become fully integrated with the other omics technologies and phenotypic alterations. (Quoted from DOI: 10.1016/j.jlr.2021.100164)

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

In addition to working together with biologist to move toward to functional lipidomics and further developing advanced technologies as aforementioned, it is crucial for analysts to make efforts on standardization and harmonization of the lipidomics methodology. We all recognized from ring trial that huge variations are present in lipidomics analysis of identical samples by using different instruments and methods (DOI: 10.1194/jlr.M079012; DOI: 10.1038/s42255-019-0094-z.). In order to unify the community efforts to conquer this issue, the International Lipidomics Society has been founded. Numerous guidance covering preanalytical sample preparation to documentation of analytical conditions (e.g., DOI:

10.1038/s41467-021-24984-y; DOI: 10.1016/j.jlr.2021.100138; DOI: 10.1038/s42255-022-00628-3; DOI: 10.1016/j.jlr.2025.100817) has been extensively discussed and published from the Society. The Society is now working on in establishing reference lipid species of individual lipid classes (DOI: 10.1038/s41467-024-52087-x). I believe these community efforts should facilitate the further growth of the field.

Spotlight Article

Sponsored Content

MxP® Quant 1000 kit

The new standard of excellence in quantitative metabolomics

The MxP® Quant 1000 kit quantifies up to 1,881 pre-validated biomarkers per sample from only 40 µL, offering biocrates' most cost-effective solution to date. Validated for use with

human plasma and urine, the kit also delivers excellent performance with feces extracts.

For over 15 years, biocrates has led the field of standardized multiplexed metabolite quantification, developing targeted panels for metabolomics and lipidomics measurement with mass spectrometry. These highly standardized solutions have supported the growing use of metabolomics in all fields of biomedicine, from large population-based cohorts to fundamental and clinical research. With MxP® Quant 1000, biocrates sets a new standard of excellence and continues its mission to democratize metabolomics and transform medicine.

Making the difference

MxP® Quant 1000 takes biocrates' technology to a new level. Expanding the company's know-how to a brand-new set of small molecules multiplexed in a single product, the kit targets 327 small molecules and 906 lipids, enriched with up to 648 quantitative metabolism indicators.

Measuring metabolomics with biocrates means more than buying a set of reagents in a box. Our offering includes a patented combination of hardware and software tools that enables robustness, reproducibility and compatibility across laboratories and instruments (Figure 1).

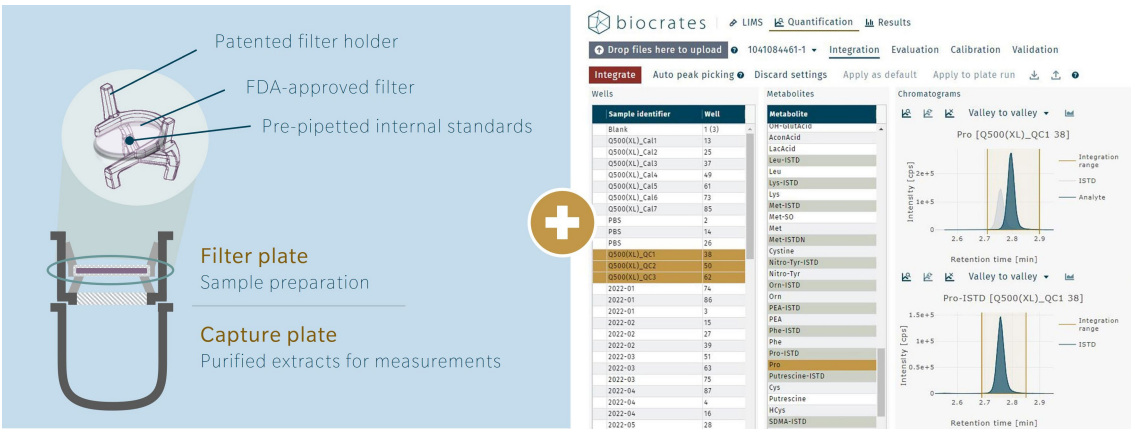

Figure 1: Hardware and software components combined patented technology for standardized metabolomics with the MxP® Quant 1000 kit and WebIDQ.

Hardware

The physical kit includes 96-well plates equipped with patented filter-holding technology and integrated internal standards to ensure efficient and reproducible sample extraction. It also contains batch-controlled calibration standards, quality controls test mixes, and analytical methods tailored to each of the supported triple quadrupole mass spectrometers – providing a comprehensive, ready-to-use solution for implementing standardized metabolomics in your laboratory.

MxP® Quant 1000 incorporates hundreds of carefully selected calibrators and internal standards, ensuring an unprecedented level of quantification precision. This high level of precision makes the kit ideal for biomarker discovery and validation, paving the way for translational research applications where metabolomics has the potential to transform medicine.

Each metabolite in the kit was selected for its relevance to complex chronic diseases, from neurodegenerative disease to cancer. Because our gut microbiome is a strong determinant of chronic disease, a large proportion of the small molecules are related to microbiome metabolism, including numerous tryptophan derivatives, and an expanded panel of bile acids compared to previous kits.

Software

WebIDQ is an all-in-one workflow manager from project management through metabolite quantification to statistical analysis (Figure 2). It guides kit users through the entire workflow, including sample registration and plate layout customization, automated metabolite quantification and validation data cleaning and statistical analysis in a single intuitive platform. In addition, the integrated MetaboINDICATOR tool automatically calculates predefined sums and ratios of metabolite concentrations for advanced biological interpretation.

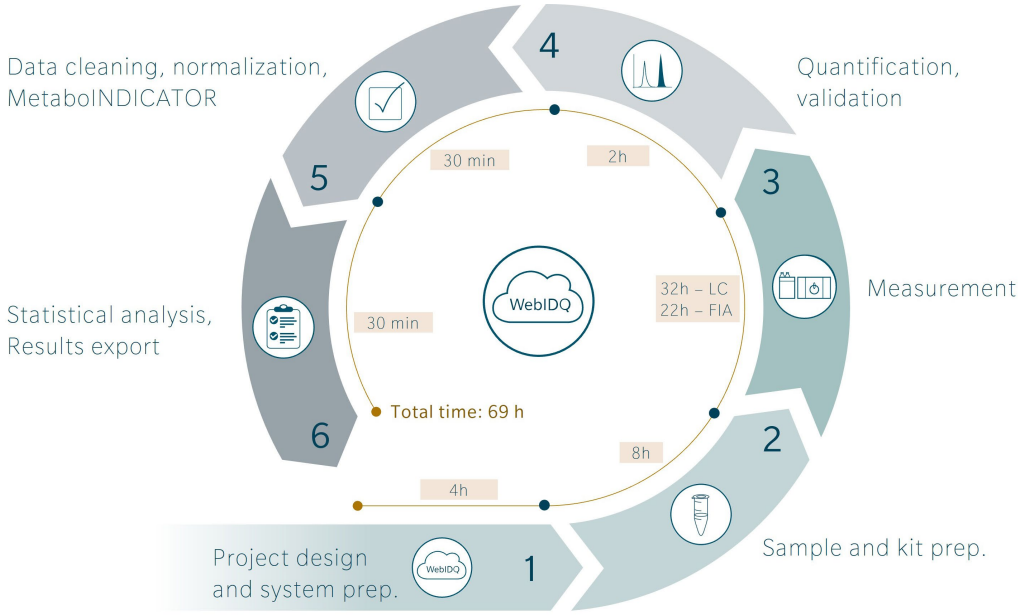

Figure 2: WebIDQ guides kit users through the entire workflow.

WebIDQ contributes greatly to the high quality and high reproducibility of measurements with MxP® Quant 1000. For example, AI-based automated peak picking (patent application filed) increases reproducibility in peak annotation and integration while dramatically

reducing data processing time. For this panel of 327 small molecules, manual peak picking and integration can take days, depending on the operator. With WebIDQ's AI-based automated peak picking, the task is reduced to 1 to 2 hours.

Transforming medicine with metabolomics

Omic technologies are set to transform medicine into 5P medicine. This concept addresses the limitations of traditional Western medicine, which typically focuses on reacting to illness or injury. Making use of five components – preventive, predictive, precision, participatory and population-based medicine – 5P medicine aims to shift the focus towards a more proactive and patient-centric practice.

MxP® Quant 1000 is a broad metabolomics solution offering a number of annotated metabolites comparable to untargeted approaches, while enabling quantitative and scalable metabolomics. It facilitates the way for 5P medicine in three key steps (Figure 3):

- Step 1 | Screen: cast a broad net to quantify metabolites relevant to health and disease
- Step 2 | Leverage: gain instant insights with automated analysis
- Step 3 | Translate: develop innovative solutions to your research questions

Read our blog series on the role of metabolomics in 5P medicine.

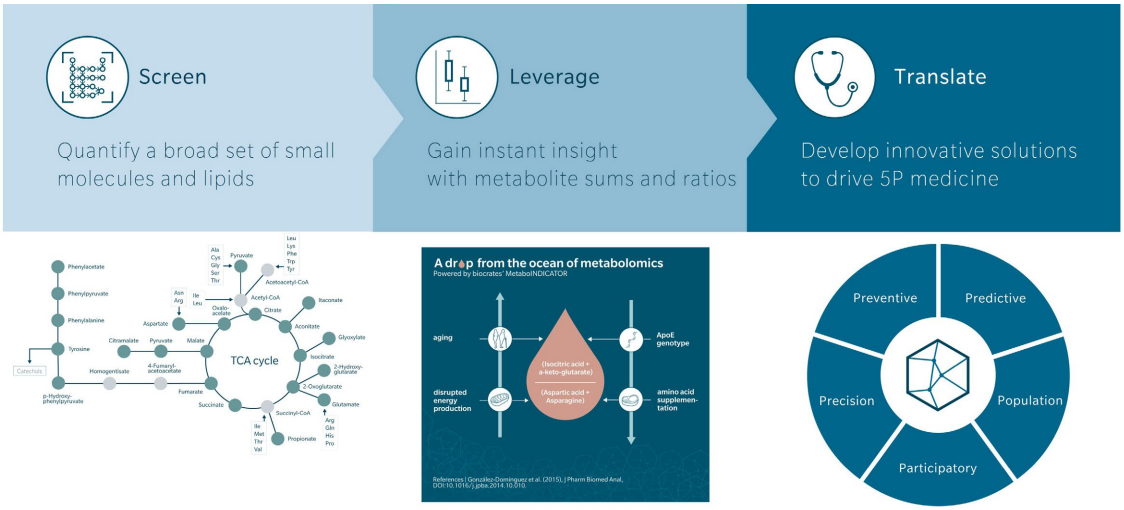

Figure 3: Three-step process to harness metabolomics and transform medicine with MxP® Quant 1000

Learn more about MxP® Quant 1000

MxP® Quant 1000 brings over 15 years of expertise in developing standardized targeted metabolomics and lipidomics workflows into a single solution. It is the ideal approach for researchers who want to broadly profile the metabolome using a reproducible and quality-controlled method, either through biocrates' services or by using the kit on their own

instrument.
To learn more about the kit, come and meet the biocrates team at:

- ASMS 2025, Baltimore | June 1-5, 2025 Breakfast seminar on June 2
- Metabolomics 2025, Prague | June 22-26, 2025 Session 10 on June 24

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MetaboReads

Metabolic checkpoints that shape immunity and oncogenesis

Tumours and immune cells compete for metabolic resources, and the resulting bottlenecks can dictate therapeutic outcomes. Recent studies reveal discrete metabolites, metabolic enzymes, and hormone-like factors that either blunt or enhance immune surveillance. They also demonstrate that metabolic interventions, from nutrient restriction to mitochondrial inhibition, can be deployed with sex-, microbiota-, or mutation-specific precision. Together these papers argue that future immunotherapies will need to account for the metabolic context of both cancer and host, rather than treating metabolism as an ancillary variable.

Tumour interstitial fluid-enriched phosphoethanolamine suppresses T cell function

Wang and colleagues in Nature Cell Biology showed that phosphoethanolamine accumulates in tumour interstitial fluid and restricts $CD8^+$ T-cell expansion by depleting diacylglycerol required for T-cell-receptor signalling. Using a chemically defined medium mimicking tumour fluid, they reproduced the dysfunctional phenotype in vitro. Genetic and pharmacological lowering of phosphoethanolamine in mouse tumours restored T-cell effector function. The work positions phosphoethanolamine as a dominant metabolic brake on antitumour immunity.

[Microbiota-derived bile acids antagonize the host androgen receptor and drive anti-tumor immunity]

Jin and colleagues in Cell found that a set of previously uncharacterised microbiota-derived bile acids antagonise the human androgen receptor and down-regulate androgen-responsive transcription. Metabolomic and microbial-genetic screens uncovered 56 new bile acids, many detectable in human samples. One antagonistic bile acid slowed tumour progression in mice and increased responsiveness to anti-PD-1 therapy. These results link microbiota metabolism to hormone signalling and immune checkpoint efficacy.

[Sex-specific effects of exogenous asparagine on colorectal tumor growth, 17(3-estradiol levels, and aromatase]

Aladelokun and colleagues in Pharmacological Research showed that exogenous asparagine suppresses colorectal-tumour growth in female but not male mice, coinciding with elevated serum oestradiol and increased aromatase-positive macrophages in females. Multi-omic profiling revealed sex-specific rewiring of amino-acid pools and macrophage abundance. In males, asparagine augmented tumour growth while reducing macrophage infiltration and oestradiol production. The study highlights a sex-dependent metabolic circuit involving asparagine, macrophages, and oestrogen biosynthesis.

[Malonate promotes CD8+ T cell memory formation via protein malonylation]

Duan and colleagues in Cellular & Molecular Immunology demonstrated that sodium malonate enhances lysine malonylation in $CD8^+$ T cells, promoting the formation of long-lived memory cells after bacterial infection. Proteomic mapping identified 77 malonylation sites, with modification of STAT6 at Lys374 alleviating repression of TCF1 and boosting memory programming. Metabolomic data confirmed broad shifts in central carbon metabolism following malonate treatment. The findings introduce protein malonylation as a tunable lever for adaptive immunity.

[Perturbing local steroidogenesis to improve breast cancer immunity]

Zhao and colleagues in Nature Communications showed that blocking local steroid hormone synthesis diminishes tumour-associated macrophages and invigorates dendritic- and T-cell responses in triple-negative breast cancer. Targeted metabolomics revealed glucocorticoid production by immune infiltrates, and genetic disruption of steroidogenesis reduced tumour growth. Pharmacological inhibition with posaconazole replicated these effects in a humanised mouse model. The study proposes steroidogenesis blockade as an immuno-metabolic strategy for breast cancer.

[Metformin reduces the competitive advantage of Dnmt3aR878H HSPCs]

Hosseini and colleagues in Nature reported that haematopoietic stem cells bearing the Dnmt3a^R878H mutation rely on elevated mitochondrial respiration for clonal advantage. The antidiabetic drug metformin curtailed this respiratory boost, reversed aberrant DNA and histone methylation signatures, and neutralised the mutant clone’s competitive edge. Prime-edited human stem cells carrying DNMT3A^R882H responded similarly to metformin. These data provide a metabolic rationale for repurposing metformin to prevent DNMT3A-driven clonal haematopoiesis.

Systemic metabolic modulation by drugs, diet, and genetic background

System-wide metabolic interventions often yield tissue-specific and sex-specific consequences that traditional endpoints fail to capture. The following studies dissect how glucose wasting, mitochondrial DNA haplotype, endothelial acetyl-CoA balance, and insulin resistance pathways influence bone, adiposity, neuroprotection, and pregnancy complications. They collectively emphasise the need for precision tailoring of metabolic therapies based on sex, organ, and genome.

Canagliflozin-Induced Adaptive Metabolism in Bone

Poudel and colleagues in Diabetes showed that six months of canagliflozin treatment triggers marked weight loss and suppression of cortical bone remodelling in male but not female UM-HET3 mice. Bone metabolomics uncovered enrichment of amino-acid transport and tryptophan catabolism signatures in males, whereas females displayed increased nucleic-acid metabolism. Integrated bone-tissue and marrow transcriptomics revealed down-regulation of oxidative stress and proliferation pathways in drug-treated males. The work indicates that SGLT2 inhibition affects skeletal integrity through sex-specific metabolic adaptation.

Multi-tissue metabolomics reveal mtDNA- and diet-specific metabolite profiles in a mouse model of cardiometabolic disease

Shastry and colleagues in Redox Biology found that mice harbouring C57BL/6 mitochondrial DNA gained more body fat and showed metabolomic signatures of oxidative stress when fed a high-fat diet, independent of nuclear background. Plasma and muscle analyses indicated altered glycerophospholipids and enriched beta-alanine pathways in C57 mtDNA carriers, while C3H mtDNA favoured branched-chain amino-acid metabolism. Metabolite co-expression pointed to heightened pentose-phosphate activity in C57 mtDNA strains. The study reveals mitochondrially encoded variation as a determinant of diet-induced metabolic risk.

Acetyl-CoA synthetase 2 alleviates brain injury following cardiac arrest by promoting autophagy in brain microvascular endothelial cells

Zhang and colleagues in Cellular and Molecular Life Sciences demonstrated that over-expression of acetyl-CoA synthetase 2 in brain microvascular endothelial cells replenishes acetyl-CoA pools, activates AMPKα–TFEB signalling, and enhances autophagy after cardiac arrest in mice. ACSS2 over-expression improved neurological scores and vascular sprouting, whereas endothelial-specific ACSS2 knockout worsened outcomes. In vitro oxygen–glucose deprivation confirmed that ACSS2 buffers energy stress and preserves endothelial integrity. These results position ACSS2 as a metabolic target for post-cardiac-arrest brain injury.

Metabolic pathways mediating insulin resistance and gestational diabetes mellitus discovered by high-dimensional systematic Mendelian randomization

Chen and colleagues in Cardiovascular Diabetology applied high-dimensional Mendelian randomisation to 566 pregnancies and confirmed a causal role for insulin resistance, measured by

HOMA-IR, in gestational diabetes. Two metabolic pathways, glyoxylate–dicarboxylate metabolism and lysine degradation, mediated 14.6 percent and 8.4 percent of this risk, respectively. Dietary intervention in an independent cohort modulated both pathways and improved metabolic markers. The work suggests that pathway-targeted nutrition could mitigate gestational diabetes development.

Environmental and microbial factors influencing metabolic and endocrine health

External exposures, from climate extremes to agricultural chemicals and gut-microbial metabolites, exert profound yet often overlooked metabolic pressures. These four studies illuminate how bile acids, herbicide by-products, acute heat, and phage–bacterium partnerships reshape host physiology and plant health. They argue for environmental stewardship that integrates omic-level insight.

Glycodeoxycholic acid alleviates central precocious puberty by modulating gut microbiota and metabolites in high-fat diet-fed female rats

Wu and colleagues in Cellular and Molecular Life Sciences showed that glycodeoxycholic acid and glycoursodeoxycholic acid levels are reduced in high-fat-diet female rats with central precocious puberty. Oral glycodeoxycholic acid delayed pubertal onset, coincided with shifts in gut Lachnospiraceae abundance, and altered oxidative-stress metabolites that modulate hypothalamic Sirt1. Mediation analysis implicated γ-glutamylcysteine and malonic acid in down-regulating Sirt1, while pregnenolone attenuated beneficial microbial effects. The study uncovers a bile-acid–microbiota axis in pubertal timing.

Dealkylation metabolites of Atrazine: A previously Neglected Contributor to soybean phytotoxicity within atrazine residue

Wang and colleagues in Environment International found that the atrazine metabolites DEA and DIA suppress soybean growth, inhibit photosynthesis, and disturb chloroplast ultrastructure. At environmentally relevant doses, DEA and DIA exhibited 74 percent and 34 percent of the toxicity index of atrazine, respectively, as determined by integrated biological response analysis. Molecular docking and metabolomics revealed that both metabolites target photosystem-II D1 and disrupt alpha-linolenic-acid metabolism, leading to reactive oxygen species accumulation. The findings highlight overlooked phytotoxic risks from herbicide dealkylation products.

Mechanistic insights into the cardiovascular effects of acute heat exposure: A multi-omics analysis based on a randomized crossover trial

Zhu and colleagues in Environment International conducted a randomised crossover trial exposing healthy adults to 32 °C for two hours and observed significant increases in arterial stiffness indices and blood-pressure wave reflections. Multi-omic profiling identified coordinated changes in inflammatory cytokines, oxidative-stress markers, coagulation proteins, and lipid metabolites. Pathway enrichment pointed to accelerated atherosclerotic processes and plaque instability. The results provide mechanistic evidence linking acute heat exposure to cardiovascular risk.

[Enhanced Phytopathogen Biofilm Control in the Soybean Phyllosphere by the Phoresy of Bacteriophages Hitchhiking on Biocontrol Bacteria]

Zhang and colleagues in Environmental Science & Technology showed that bacteriophages hitchhiking on carrier biocontrol bacteria reduce soybean-leaf pathogen biofilms by 82 percent compared to controls. Transcriptomics indicated enhanced flagellar and pili genes in carriers and diminished defence genes in pathogens, while metabolomics revealed increased flavonoid and alkaloid secretion that strengthens plant stress responses. Bliss independence analysis confirmed a synergistic interaction between phages and carriers. The phoresy approach offers a novel strategy for sustainable crop protection.

Molecular adaptations to ageing, mechanical cues, and inflammation

Ageing trajectories and stress responses are encoded in dynamic protein modifications, epigenetic clocks, and mechano-sensitive metabolic circuits. The next four papers dissect these levels of control, connecting amino-acid acetylation, epigenetic age acceleration, extracellular-matrix stiffness, and inflammatory sensitisation to functional outcomes. They show that lifespan and pain perception are not passive processes but modifiable biochemical programs.

[The mammalian longevity associated acetylome]

Feldman-Trabelsi and colleagues in Nature Communications mapped the protein acetylomes of 107 mammalian species and discovered 695 human and 482 mouse lysine residues whose acetylation status correlates with species lifespan. Long-lived mammals often replace reversible lysine acetylation with fixed glutamine or arginine at key sites, whereas short-lived species show the opposite substitution pattern. Pathway analysis implicated mitochondrial translation, fatty-acid oxidation, transsulfuration, and DNA repair in lifespan extension. Functional assays demonstrated that introducing long-lived-type arginine at Lys386 in mouse cystathionine-β-synthase increased its pro-longevity activity.

[Multi-Omic Associations of Epigenetic Age Acceleration Are Heterogeneously Shaped by Genetic and Environmental Influences]

Drouard and colleagues in Aging Cell assessed proteomic, metabolomic, and exposomic correlates of epigenetic age acceleration in twin cohorts aged 22 and 62 years. Forty multi-omic factors associated with accelerated epigenetic age in young twins, but within-pair analysis showed that only six remained significant after accounting for shared genetics. These included histidine, lactate, several complement proteins, and neighbourhood longevity metrics. Partial replication in older twins suggested that environmental rather than genetic influences dominate select ageing-related biomarkers.

[Extracellular Matrix Microstructures Modulate Hepatic Methionine Cycle and Methylations]

Terrell and colleagues in Biomacromolecules demonstrated that hepatocytes cultured on flat,

fibrosis-mimicking substrates up-regulate methionine-cycle enzymes and DNA, RNA, and protein methylation through integrin β1 signalling. Inhibiting integrin activation with an RGD peptide normalised enzyme expression and metabolite levels, indicating that extracellular-matrix geometry can steer methyl-donor availability. The study proposes the methionine cycle as a mechanosensitive metabolic node with relevance to fibrosis therapy.

Altered aminoacid and lipid metabolism in a rat orofacial inflammation model determined by omics approach: potential role in trigeminal sensitisation

Takacs-Lovasz and colleagues in Journal of Headache and Pain used multi-omic profiling to investigate a rat model of orofacial inflammation. Plasma metabolomics showed elevated carnosine and serotonin but reduced tryptophan, kynurenine, and several lipids at peak allodynia. Trigeminal-ganglion RNA sequencing revealed up-regulation of Cxcr3 and down-regulation of Gnrhr, pointing to neuroinflammatory signalling pathways. Joint pathway analysis linked altered amino-acid metabolism and fatty-acid β-oxidation to trigeminal sensitisation.

Methodological frontiers for large-scale and high-resolution metabolomics

Extracting biological insight from ever-larger metabolomics datasets requires both conceptual and computational innovation. One paper surveys how integrative omics, real-time imaging, and artificial intelligence can sharpen cellular immunotherapy, while another introduces an image-based algorithm that streamlines cohort-scale mass-spectrometry data processing. Together they illustrate the next wave of analytical infrastructure for precision biomedicine.

From Multi-Omics to Visualization and Beyond: Bridging Micro and Macro Insights in CAR-T Cell Therapy

Gong and colleagues in Advanced Science reviewed recent advances in integrating genomics, epigenomics, transcriptomics, proteomics, metabolomics, and microbiomics to refine chimeric antigen-receptor T-cell therapy. The authors highlighted single-cell and spatial omics for resolving intratumoral heterogeneity, and discussed emerging imaging modalities that enable 3D tracking of CAR-T cells in vivo. They argued that artificial-intelligence methods are essential for navigating the resulting high-dimensional data landscape. The review provides a roadmap for uniting omic profiling and live imaging to optimise cellular immunotherapies.

MetCohort: Precise Feature Detection and Correspondence for Untargeted Metabolomics in Large-Scale Cohort Studies

Yang and colleagues in Analytical Chemistry presented MetCohort, a computational pipeline that aligns chromatographic retention times across hundreds of liquid-chromatography high-resolution mass-spectrometry files by constructing a two-dimensional region-of-interest matrix. The matrix resembles an image, allowing application of computer-vision techniques for holistic peak detection. Benchmarking showed reduced false-positive rates and improved quantification of low-abundance metabolites compared with conventional software. MetCohort therefore offers a scalable solution for untargeted metabolomics in population studies.

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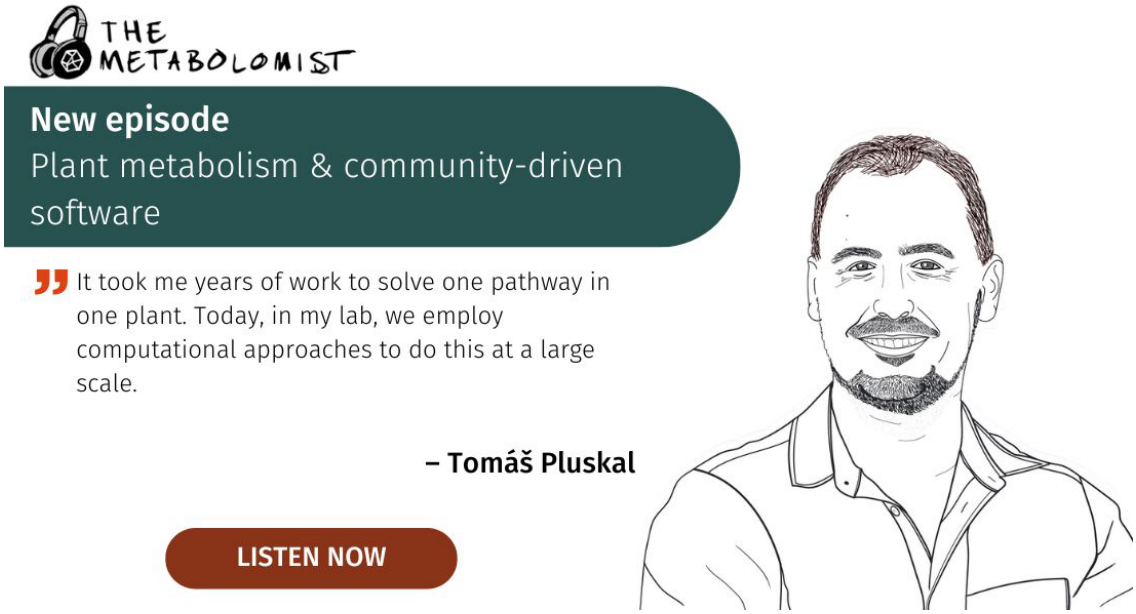
The Metabolomist Podcast



Metabolomics Events

|MC:SUBJECT|

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.

Check for more details

MANA SODAMeet

June 10, 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

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

Check for more details

7th Annual Metabolomics Society of North America (MANA) Conference

September 2-5, 2025

Venue: Banff, Canada

The 7th Annual Conference of the Metabolomics Association of North America (MANA) will be hosted Dr. Ian Lewis, and the
organizers have developed an engaging program. Check out the website for program information, speakers, events, registration, awards, and more.

Oral submissions deadline: **May 30, 2025**
Poster submissions deadline: **June 9, 2025**
Early registration deadline: **June 30, 2025**

Check for more details

Bits & Bites #5: Bayesian Statistics for Metabolomics

September 11, 2025

Venue: Online

The short course is taught by Dr. Christopher Brydges. This introductory-level session requires JASP (version will be announced before the course) and assumes only basic knowledge of statistics (for example, you know what a t-test and a correlation are); no coding experience is needed.

Short description of the course:
Bayesian statistics are a useful method for estimating effect sizes and testing the strength of

evidence in favor of one hypothesis over another - things that p-values and traditional statistics can't do. However, they are under-utilized in metabolomics research. This short course will provide a brief refresher on traditional statistics, teach the basic principles behind Bayesian statistics, learn how to conduct basic Bayesian analysis in JASP, and learn how to report the results in the style of a journal article.

Check for more details

DG5th Annual Metabolomics Society of North America (MANA) Conference

October 1 - 2, 2025

Venue: Hanover, Germany

The DGMet Annual Meeting 2025 will take place at the Fraunhofer Institute for Toxicology and Experimental Medicine Fraunhofer ITEM in Hanover.

Key Topics:
Metabolomics and Nutrition
Exercise & Muscle Metabolism
Computational Metabolomics
Plant Metabolomics
Metabolomics and Lipidomics in Health and Disease

Visit the website for more details

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2025 World Critical Care and Anesthesiology Conference

October 10 - 11, 2025

Venue: Singapore/Hybrid Online

The 9th World Critical Care & Anesthesiology Congress (2025 WCAC) will take place in Singapore, offering both physical and virtual participation options. Speakers and delegates will have the chance to meet international faculty members, enjoy extensive networking sessions and explore the city's landmarks. The congress invites submission of speaker proposals as well as oral and poster presentations on the latest topics in critical care and emergency medicine, anesthesiology

and pain medicine, trauma, pediatrics, neurocritical and cardiac critical care, COVID-19 and related subjects.

Standard registration deadline: **July 15, 2025**

Click here to view more details

Frontiers in Metabolomics & Metabolomic Imaging in Medicine: Challenges & Opportunities

October 16 - 18, 2025

Venue: Italy

This inaugural Metabolomics and Metabolomic Imaging (MMI) workshop is designed for scientists, clinicians, and trainees from academia, healthcare, and industry, who seek to learn and discuss the frontiers of metabolomics in medicine. The central focus of this workshop is medical metabolomics and metabolomic imaging, a burgeoning field with enormous potential for medical applications, particularly in the context of malignant and neurodegenerative diseases, which can present heterogenous systematic metabolic alterations that can only be collectively evaluated by metabolomics.

Learning Outcomes

- Identify technologies used in metabolomics and metabolomic imaging
- Understand the challenges and potential of metabolomics and metabolomic imaging for malignant and neurodegenerative disease studies
- Become familiar with advanced metabolomic data analysis using AI and machine learning
- Expand collaborative networks with metabolomic experts from multiple domains

Click here to view more details

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Job Title	Employer	Location	Source
Assistant Professor, Cell Metabolism	University of Saskatchewan	Saskatoon, SK, Canada	University of Saskatchewan
Senior Principal Scientist / Associate Director – Lipidomics & Metabolomics	Novartis	Cambridge, MA, USA	Novartis
Technician in Mass Spectrometry – DeMarco Lab	University of British Columbia	Vancouver, BC, Canada	University of British Columbia
Manager, Quantitative Metabolite Analysis Center	University of California, San Francisco	San Francisco, CA, USA	UC San Francisco
Research Scientist I/II - Mass Spectrometry, Metabolomics - Bioinformatics	Georgia Institute of Technology	Atlanta, Georgia, USA	Georgia Institute of Technology
Ovarian Cancer Metabolomics and Proteomics Postdoctoral Fellow Gordon Lab	Emory University	Atlanta, USA	Metabolomics Society
Postdoctoral Scholar - Metabolomics	Lund University	Lund, Sweden	Lund University

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