MetaboNews

This month in metabolomics

April, 2025
Vol 15, Issue 4

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

This Months Features:
Spotlight Article
GIGA Kit Launch

Conference Report
Canadian Metabolomics Conference 2025

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

METABOLOMICS
SOCIETY

METABOLOMICS SOCIETY
EARLY- CAREER MEMBERS NETWORK

Conference Corner

We hope to see you in Prague this June – please read the below for an **IMPORTANT update regarding poster abstracts**. The conference is on track to be one of the highest attended in several years!

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

Poster Abstracts - IMPORTANT

We're thrilled by the overwhelming interest in the Prague conference!
Due to the high volume of submissions, we will likely need to close abstract submission earlier than the announced deadline, as we're quickly approaching capacity for poster presentations.

If you're planning to submit, we strongly encourage you to do so as soon as possible to ensure your work is considered. Once we have reached the capacity limit, we will close the submission portal, very likely before May 15. Submit here.

If you submitted an abstract in the "Oral or Poster" category you should have received notification of your acceptance/decline between April 18 – 23. If you did not receive, contact us at info@metabolomicssociety.org

Registration – Don't Delay

This week is a **great time to register**, since we have opened sign-up for workshops and sponsored lunch sessions. If you previously registered for the conference, log-in to your registration to sign up for workshops, it's easy to add, no additional fee!

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.

Workshops – Save Your Spot

You can select workshops 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.

Last Call for 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.

Attend a Sponsored Lunch Presentation

A few sponsorship packages are still available. Visit the website to **view the brochure**.

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!

Thank you to the following PLATINUM sponsors for your partnership:

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Members' Corner

Board of Directors

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

Dear Metabolomics Society Members and metabolomics friends,

It is April already and I have started counting down the days to Metabolomics 2025 in Prague (55 and counting). Record numbers of abstracts have been submitted for oral presentations (submission deadline has passed) and for poster presentations, to the point where we are quickly reaching capacity for posters. **To make sure you can present your work, submit your poster as soon as possible, as the portal may close early.** We hope the number of registrations will also be a record and we may break the 1000 attendees ceiling for the first time since 2019 in The Hague. The workshops are posted online with a diverse and great line up of topics, sign up is available.

I would like to take this opportunity to thank all the companies who have already sponsored the conference (see https://www.metabolomics2025.org/sponsor-list). This sponsorship is important for both parties; it allows the Society to provide reduced registration costs and a high-quality venue, and it allows the sponsors the opportunity to engage with the metabolomics community. Different sponsorship packages are available (see https://www.metabolomics2025.org/sponsor-information) and do consider whether you would like to sponsor the conference.

On a separate note, and both from a metabolomics community member and a researcher, the ability to understand methods applied, data acquired and their reporting in peer-reviewed publications and data repositories is hugely important to allow interpretation of data quality and biological mechanisms and to enable integration or meta-analysis across studies. The use of defined reporting standards to provide recommended minimal levels of information by all is hugely important. As an example, last week I found 23 different names for a single acyl carnitine in data repositories with the ability to match across studies for only 9 of the entries using chemical structure or database identifiers. The Metabolomics Society along with other societies and organisations applying small molecule analysis including the International Lipidomics Society, mQACC and BP4NTA have started working together to discuss, agree on and promote the common use of reporting standards. Watch this space.

All the very best,

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

Early-Career Members Network (EMN)

EMN Committee News
Due to special circumstances, EMN is happy to welcome two new EMN committee members, Ellen De Paepe (Ghent University) and Juan José Oropeza Valdez (National Autonomous University of Mexico). Applications for the EMN 2025-2026 committee will open in Summer 2025 per usual.

EMN Webinars - May
The next EMN webinar will occur on Wednesday, 14th May 2025, 21:00 UTC (22:00 CET and 9:00 NZST on 15th May) featuring **Dr. Farhana Pinu** from the Biological Chemistry and Bioactives Group, The New Zealand Institute for Plant and Food Research, New Zealand. The EMN committee is delighted to invite you for the talk about "*Flavoromics- a new frontier in food and horticultural science*", focusing on flavoromics.

Registration is available at this Zoom link: https://zoom.us/webinar/register/WN_i9RfBdoWSkWRz3lPa-4o5g

EMN Networking Event
The EMN-MetSoc, in collaboration with Metabolomics South Africa, organized an online networking event focused on “Career Paths and Transitions” for Early Career Researchers (ECRs) to be held on April 10. Herna de Wit (OmniSci Consulting, SA), Fabien Jourdan (MetaboHUB, France), Olli Kärkkäinen (Afekta Technologies Ltd. & University of Eastern Finland), and Efficient Nsikayezwe Ncube (Tshwane University of Technology, SA), shared their experiences and advice on career opportunities in academia, industry, government/clinical settings, and alternative careers. More info on our social media accounts. We thank the panellists and Metabolomics South Africa once again for their time!

MetaboART Competition
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.
Submit your entries to: info.emn@metabolomicssociety.org

Task Groups Corner

Lipidomics Task Group (LipidMet)

The next LipidMet meeting will be on Monday, June 2nd, at 17:00 UTC.

Theme: Studying the chemical exposome and its impact on lipid metabolism – analytical and biological considerations

- 17:00 (UTC). Introduction and LipidMet updates.
- 17:05. Impact of chemical exposome on human lipidome. Tuulia Hyötyläinen (Örebro University)
- 17:20. Network for Exposomics in the U.S. (NEXUS): ChemBio Analytical Sciences Hub. Tom Metz (Pacific Northwest National Laboratory) and Krystal Pollitt (Yale University). See info about NEXUS below the meeting link.
- 17:45. Q&A and general discussion on the topic

Meeting link: https://oru-se.zoom.us/j/64241518228?pwd=zwjv1OAMmsSHbAb1bpecTOycG7bpxj.1
Meeting ID: 642 4151 8228
Passcode: 932230

Find your local number: https://oru-se.zoom.us/u/cP3INgGzt

About NEXUS

Dear All,

We are writing on behalf of Drs. Chirag Patel (Harvard University), Rima Habre (USC), and Gary Miller (Columbia University) who are Multi-PIs of NEXUS (Network of EXposomics in the United States), a Center for Exposome Research Coordination (CERC), which was recently funded by NIEHS.

The goal of NEXUS is to form a large national consortium that will develop harmonized approaches for exposomics profiling that integrates digital, biological, and geospatial markers to make exposome-wide association studies a reality for studies of all human disease. The center will include hubs focused on chemical and biological analytical sciences led by Drs. Krystal Pollitt (Yale) and Tom Metz (Pacific Northwest National Laboratory), geospatial sciences headed by Drs. Habre and Arcot Rajasekar (UNC), data sciences directed by Drs. Patel (Harvard) and Marina Sirota (UCSF). A strong international research advisory board, including Roel Vermeulen, Jana Klanova, Martine Vrihjied, Robert Barouki, Emma Schymanski, David Wishart, Jeff Xia, and Francesca Dominici, will oversee the center together with industry advisors.

As part of the ChemBio Analytical Sciences Hub, Krystal Pollitt and Tom Metz are planning a collaborative, community-based exposome ring trial to assess the chemical space covered by current and emerging technologies in biological and environmental matrices. The goal is to aggregate data across a wide range of laboratories to facilitate knowledge exchange on the exposomic coverage of current and emerging technologies and identify streamlined, scalable, and harmonized analytical and computational infrastructures needed to systematically characterize the exposome. As a first step, they are requesting the community's input via a survey on methods and tools used to measure molecular features of the exposome. The survey results will be used in part to design the exposome ring trial. Ultimately, they hope that the results of this survey and the ring trial will inform the development of a harmonized method for measuring the exposome.

We invite you to become a NEXUS collaborator and provide your critical expertise as input to the survey by **May 1, 2025**.

The survey may be accessed here: https://yalesurvey.ca1.qualtrics.com/jfe/form/SV_2fXBCW7RRHvkRkq.

Note, the survey is a bit long to be comprehensive, but it is possible to begin it and return to it to pick up where you left off.

International Affiliates' Corner

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ASSOCIATION OF
NORTH AMERICA

Metabolomics Association of North America (MANA)

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

It's time to start planning participation in the 7th Annual Metabolomics Association of North America (MANA) Conference that will take place September 2-5, 2025, at the Banff Centre for Arts and Creativity, Alberta, Canada! Please check the **MANA 2025 website** for the latest details, including information on conference registration, abstract submissions, and travel to the Banff Centre.

In addition, here are several other reminders:

- Remember to renew your membership or become a new member **here!**
- MANA Virtual Symposium: “From Metabolomics to Mechanism”. May 8th, 2025 - Save the Date! **Click here** for registration.
- Remember to visit the MANA website **here** for the latest information on MANA. Be sure to check out our Events page and new Job Board!

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Nordic Metabolomics Society

Visit www.nordicmetsoc.org

Nordic Metabolomics Society Webinar
AI in Metabolomics

June 12, 2025, 13-15 CEST (Stockholm)

Program

- 13:00 *Introduction*. Matej Oresic (Örebro University, Sweden, and University of Turku, Finland)
- 13:05 *How to cheat with your data analysis*. Rasmus Bro (University of Copenhagen, Denmark)
- 13:35 *Machine learning for structural elucidation of LC-MS/MS data*. Juho Rousu (Aalto University, Finland)
- 14:05 Q&A and Discussion

Meeting link: https://oru-se.zoom.us/j/69402041796?pwd=mN4dRFmbf9CUdRkwfrEguCGuIGxGJA.1

Meeting ID: 694 0204 1796
Passcode: 895167

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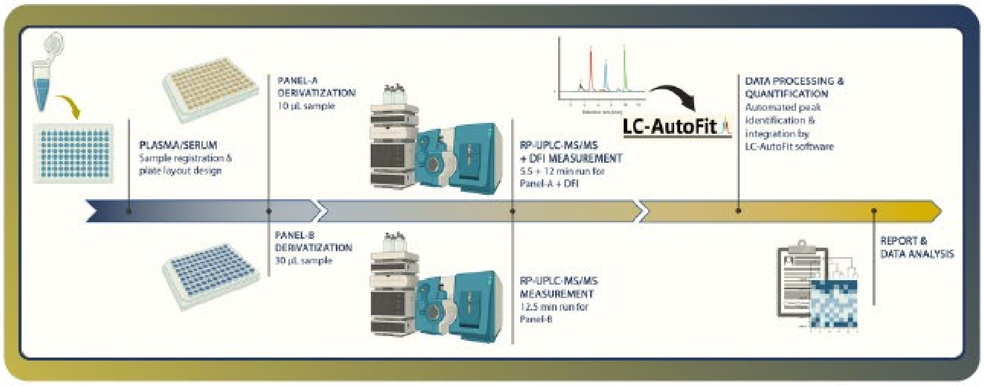
Spotlight Article

The GIGA metabolomics kit brings the world's most comprehensive quantitative metabolomics assay directly into your lab. This low-cost, ready-to-use kit has all the reagents, directions and software to allow you to absolutely quantify up to 1,780 metabolites in a single 40 µL sample. This includes 378 small molecules and 1402 lipids across 38 chemical families. The GIGA kit has been fully validated and tailored for serum/plasma (versions for urine and fecal samples are forthcoming) and works on several popular LC-MS platforms (QQQs, Qtraps and Orbitraps).

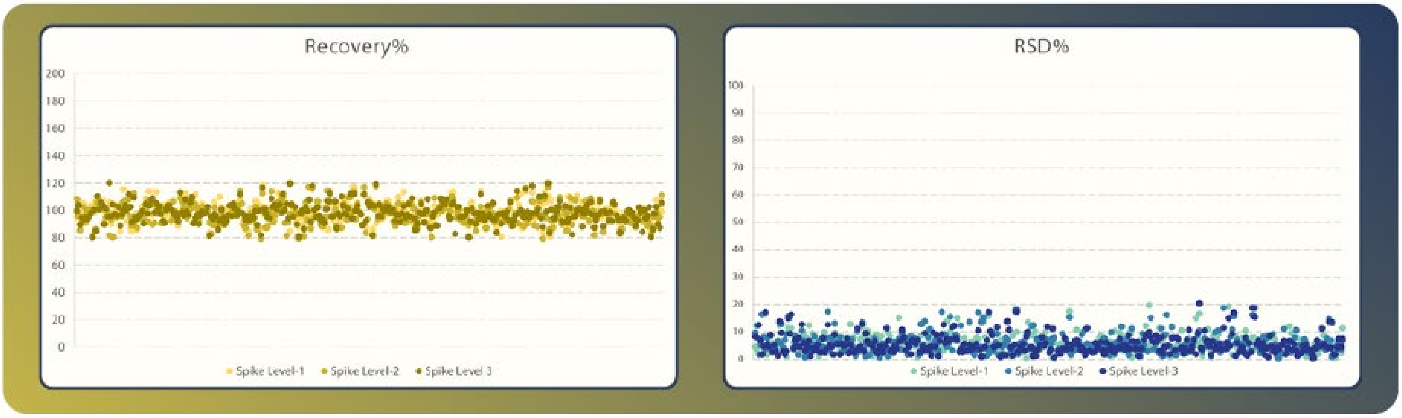
GIGA is the successor to MetabolomiX's popular MEGA metabolomics kit. Like the MEGA, the GIGA kit is designed to work in a 96-well plate format. This allows for efficient sample processing, high-throughput analysis and facile automation. The GIGA kit uses MetabolomiX's new LC-AutoFit software, a web-based application which provides ultra-fast, user-friendly data processing. It takes <1 hr to identify and quantify up to 150,000 metabolites on a single 96-well plate! LC-AutoFit also provides normal reference ranges for most metabolites and calculates >400 metabolite sums and ratios, bringing the total number of useful metabolite measurements possible with the GIGA kit to >2200.

Assay Overview



The GIGA kit measures both exogenous (exposome) and endogenous compounds. By integrating the measurement of both types of molecules, the GIGA Kit offers unique insights into the complex interactions between internal metabolic states and external environmental influences. Exogenous compounds, such as those derived from diet, pharmaceuticals, environmental contaminants, and microbial co-metabolism, offer critical markers of exposure and lifestyle. Profiling these compounds is crucial for understanding how dietary habits, pharmacological treatments, and environmental factors shape human biology.

Assay Performance

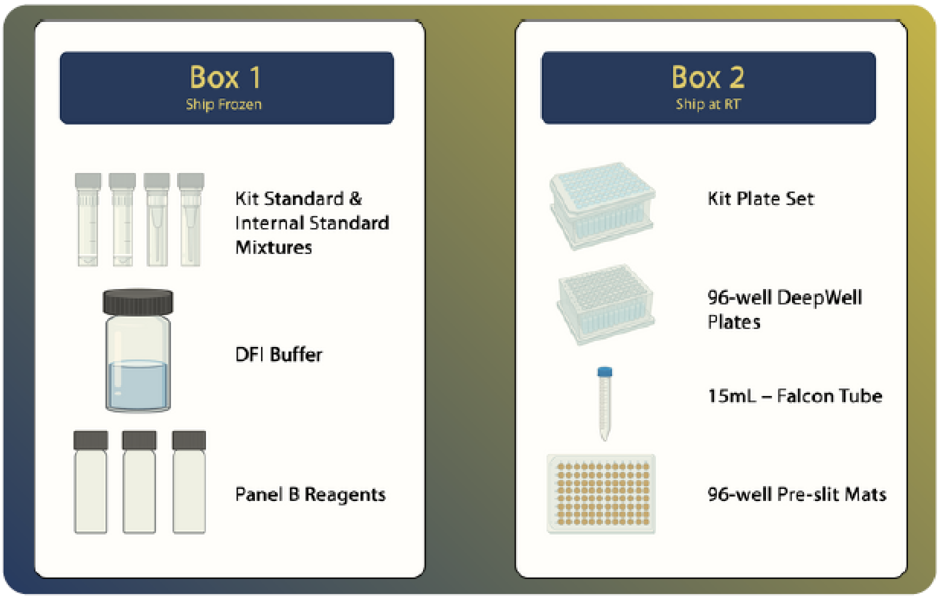


Inter-day Recovery% = 98.0 ± 7.41

RSD% of Inter-day Recovery= 5.78 ± 3.49

Endogenous metabolites reflect the body’s intrinsic biochemical processes, providing important information on metabolic health, immune response, inflammation, and cardiovascular risk. Incorporating lipidomics further enhances the GIGA Kit’s value, measuring key lipid species that are involved in energy storage, membrane structure, and signal transduction, among other processes. These lipids serve as biomarkers for metabolic health and disease, making the GIGA Kit an indispensable asset in studies involved in personalized nutrition, early disease detection, and biomarker discovery.

What's in the Box



Curious to learn more? Don't miss our upcoming webinar!

LIVE WEBINAR

May, 27th 10:00 AM MDT

[Email for more details]

www.metabolomix.ca

+1 (780) 492-4005

info@metabolomix.ca

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Conference Report

The 6th Annual Canadian Metabolomics Conference Recap

April 24–25, 2025 · New Residence Hall, Montreal, QC

The 6th Annual Canadian Metabolomics Conference (CanMetCon 2025), hosted at The New Residence Hall (McGill University), brought together experts, clinicians, early-career researchers, and industry partners for two days of research, collaboration, and innovation. Organized by **The Metabolomics Innovation Centre (TMIC)**, the conference highlighted key advances in metabolomics and its growing role in human health, environmental science, and precision medicine.

Day one kicked off with inspiring talks from plenary speakers Gary Siuzdak and Erin Baker, along with engaging presentations from all TMIC PIs. The presentations covered a range of topics in clinical metabolomics including:

- From Data to Decisions: Computational Methods in Metabolomics
- Enabling the Clinical Revolution in Metabolomics
- Metabolic Health Assessments: Microbiota, Nutrition, and Clinical Insights
- Multi-Omic Signatures in Exposure, Treatment and Infection

Day 2 of our Conference featured our final plenary speaker Mary-Ellen Harper and invited speakers Stéphane Bayen, Michael Chen, Lorraine Brennan, Tom Metz, Matej Oresic, Lekha Sleno and Ines Thiele. Lectures covered a range of topics including:

- Predictive Tools and Multi-Omic Integrations
- Metabolites to medical Insights
- Metabolomics at the Intersection of Diet, Health and Disease
- Multi-Omic Signatures in Exposure, Treatment and Infection.

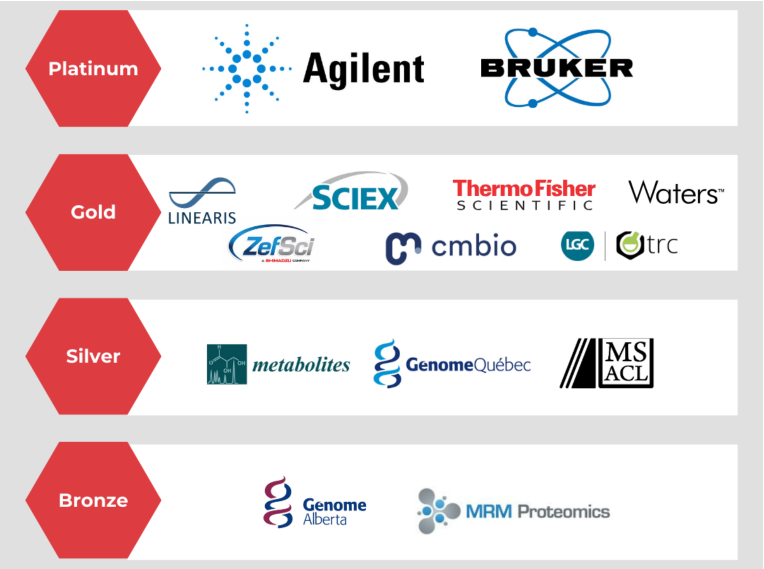
Congratulations Winners

The conference featured oral and poster presentations from selected abstracts, showcasing emerging talent and their research in metabolomics.

Left to Right: Zachary Kroezen (Best Oral Presentation), Ana Stanciu (1st Place Poster Presentation), Michael Atser (2nd Place Poster Presentation), Nathan Ghafari, Devanshi Pandit, & Linda Nartey (3rd Place Poster Presentation)

Thank you Sponsors

The success of CanMetCon 2025 would not have been possible without the support of our sponsors. We extend our sincere thanks to:



CanMetCon 2026

TMIC is excited to announce that the 7th Canadian Metabolomics Conference will be taking place in Toronto, Ontario next year. Follow TMIC for more details.

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MetaboReads

Microbiome & Metabolites in Therapy, Toxicity and Extreme Habitats

A converging body of work demonstrates that the structure and chemistry of microbial communities can determine drug safety, pathogen resistance, pollutant detoxification and even the environmental health of spacecraft. By pairing metagenomics with untargeted metabolomics, each study pinpoints small molecules that either mediate or mark these effects, turning descriptive ecology into actionable insight. The papers also show that microbiome-centred interventions—whether probiotic, metabolic or engineering—scale from individual animals to closed orbital habitats. Finally, they underscore a common principle: when host or habitat is stressed, beneficial outcomes usually arise from restoring metabolic balance rather than simply shifting taxonomic composition.

Microbiota-indole-3-propionic acid-heart axis mediates the protection of leflunomide against alphaPD1-induced cardiotoxicity in mice.

Huang et al. in Nature Communications showed that leflunomide reshapes the gut microbiota of melanoma-bearing mice treated with anti-PD-1 antibodies, markedly enriching indole-3-propionic acid (IPA). IPA binds the aryl-hydrocarbon receptor, activates PI3K and shields the heart from immune-mediated damage without compromising tumour control. Faecal transfer and IPA gavage reproduced protection, defining a microbiota-IPA-heart axis that could be pharmacologically exploited to curb checkpoint-inhibitor cardiotoxicity.

Interplay between gut microbial communities and metabolites modulates pan-cancer immunotherapy responses.

Zhu et al. in Cell Metabolism found that multi-omics profiling of 165 patients uncovered five faecal enterotypes whose joint bacterial–metabolite signatures predicted response to PD-1/PD-L1 blockade. A model trained on these features retained high accuracy in 706 external cases, and phenyl-acetyl-glutamine was shown experimentally to blunt anti-PD-1 efficacy. Integrated microbial and metabolic markers therefore promise more reliable immunotherapy stratification than taxonomic profiles alone.

Rhodobacter sphaeroides reduces Pb accumulation by reshaping the intestinal microenvironment and improving liver oxidant resistance in common carp (Cyprinus carpio L.).

Zhou et al. in Journal of Hazardous Materials showed that dietary Rhodobacter sphaeroides colonises carp intestine under lead stress, boosts denitrifying and heavy-metal-tolerant taxa and reverses pro-inflammatory gene expression. Metabolomics revealed enhanced antioxidant status, and probiotic feeding lowered Pb residues in gut, liver, kidney and blood. Microbiome engineering thus emerges as a feasible countermeasure to heavy-metal toxicity in aquaculture.

Investigation of the mechanisms of liver injury induced by emamectin benzoate exposure at environmental concentrations in zebrafish: A multi-omics approach to explore the role of the gut-liver axis

Gu et al. in Journal of Hazardous Materials demonstrated that chronic emamectin-benzoate exposure disrupts zebrafish gut microbiota and intestinal integrity and drives hepatic glycerophospholipid accumulation that culminates in steatotic injury. Increases in Plesiomonas and Cetobacterium correlated positively with harmful liver lipids, whereas protective taxa declined. The work flags the gut–liver axis as a critical but overlooked target in pesticide-risk assessment.

Gut microbiota contributes to protection against porcine deltacoronavirus infection in piglets by modulating intestinal barrier and microbiome

Zhang et al. in Microbiome showed that transplanting adult-pig microbiota into neonatal piglets mitigates deltacoronavirus diarrhoea, restores microbial diversity and tight-junction proteins and up-regulates intestinal arginine biosynthesis. The treated piglets exhibit reduced inflammation and better weight gain, linking specific metabolite pathways to viral resilience. Microbiota transplantation could therefore become a practical prophylaxis against enteric coronaviruses in livestock.

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

Salido et al. in Cell mapped 803 samples across nine International Space Station modules, revealing that crew activity sculpts distinct microbiological and chemical niches. Relative to Earth habitats, the ISS lies at the extreme end of an “industrialisation axis,” illustrating how closed environments select for unique microbiomes. The study validates culture-independent sequencing as an operational health-monitoring tool for long-duration missions.

Cancer Metabolism & Diagnostic Chemistry

These six papers demonstrate that tumours hijack metabolic circuits to fuel growth, resist therapy or cloak themselves from immunity, and that metabolites themselves can serve as highly sensitive diagnostic cues. Collectively they argue for metabolic intervention at three levels: blocking nutrient-sensing pathways that drive anabolism, reprogramming antioxidant defences that foster drug resistance and exploiting unconventional biofluids to catch disease earlier. They also underscore a translational loop in which mechanistic insight feeds directly into biomarker discovery—most clearly in the supersulfide study, where the metabolic alteration is both driver and marker. This expanding toolkit of metabolic targets and read-outs could unlock more precise, less invasive cancer management.

Taurine and proline promote lung tumour growth by co-regulating Azgp1/mTOR signalling pathway

Liang et al. in NPJ Precision Oncology found that taurine and proline accumulate in lung tumours and down-regulate AZGP1, thereby unleashing mTOR-mediated lipid synthesis to accelerate tumour growth. Forced AZGP1 expression reduced mTOR activity, curtailed lipid build-up and slowed disease in mouse models. The taurine/proline–AZGP1–mTOR axis thus represents a tangible metabolic vulnerability.

PHGDH activation fuels glioblastoma progression and radioresistance via serine synthesis pathway

Liu et al. in Journal of Experimental & Clinical Cancer Research showed that glioblastoma stem-like cells overexpress PHGDH, diverting glycolytic carbon into serine synthesis to sustain redox buffering, one-carbon metabolism and DNA repair. MYC drives PHGDH transcription, and genetic or pharmacological blockade of PHGDH suppressed tumour growth and reinstated radiosensitivity in orthotopic xenografts. Targeting serine-synthesis enzymes could therefore enhance radiotherapy in glioblastoma.

Circadian Rhythm Disruption in Triple-Negative Breast Cancer: Molecular Insights and Treatment Strategies

He et al. in Journal of Pineal Research reported that triple-negative breast cancers exhibit compressed peaks of rhythmic gene expression, widespread clock disruption and a metabolic shift toward tryptophan catabolism. High CRDscore tumours showed fewer infiltrating immune cells, more exhausted $CD8^+$ T cells and inferior relapse-free survival. Restoring circadian regulation or inhibiting tryptophan breakdown may thus boost immunotherapy efficacy.

Tobacco smoke exposure is a driver of altered oxidative stress response and immunity in head and neck cancer

Li et al. in Journal of Translational Medicine demonstrated that cigarette-smoke exposure persistently activates NRF2 antioxidant genes in head-and-neck cancer, rewires metabolism for oxidative-stress adaptation and elevates PD-L1 while down-regulating antigen-presentation genes in myeloid cells. This NRF2-driven programme confers cisplatin cross-resistance and immune evasion. Dual targeting of NRF2 signalling and metabolic outputs could resensitise smoke-associated tumours.

Supersulfide metabolome of exhaled breath condensate applied as diagnostic biomarkers for esophageal cancer.

Asamitsu et al. in Cancer Science showed that cysteine and homocysteine supersulfides rise sharply in plasma and exhaled-breath condensate of patients with esophageal cancer. Plasma HomoCysSSH discriminated cases from controls with an AUC of 0.93, while breath CysSSH achieved non-invasive detection with 96 % specificity. Supersulfide profiling thus offers a painless screening alternative to endoscopy and expands the repertoire of breath-based cancer diagnostics.

Metabolite-Guided Countermeasures to Drug Resistance & Nanotoxicity

By leveraging metabolomics, these studies identify natural or nutritional molecules that disarm antibiotic resistance or temper nanoparticle stress, illustrating how small-molecule ecology can be turned to therapeutic or environmental advantage. Together they champion a paradigm in which “helper” metabolites restore the efficacy of existing interventions rather than replacing them outright. They also highlight the value of mechanistic depth: knowing exactly how a metabolite interacts with membranes, energy metabolism or redox state speeds translation to in-vivo proof-of-concept. Finally, each paper offers a template for One-Health research that bridges laboratory biochemistry and real-world applications.

Inosine monophosphate overcomes the coexisting resistance of mcr-1 and blaNDM-1 in Escherichia coli

Zhao et al. in Journal of Advanced Research showed that inosine monophosphate exploits purine-pathway perturbations in E. coli harbouring mcr-1 and blaNDM-1, increasing membrane permeability, collapsing ATP synthesis and triggering oxidative damage. IMP treatment improved survival in a mouse sepsis model and outperformed colistin alone. The data position a ubiquitous purine metabolite as a lead compound against dual colistin–carbapenem resistance.

Vitamin B6 resensitizes mcr-carrying Gram-negative bacteria to colistin

Xu et al. in Communications Biology found that mcr-positive Gram-negative bacteria are depleted in pyridoxal-5′-phosphate (PLP); supplementing PLP restores proton motive force, enhances colistin binding and triggers iron-driven lipid peroxidation. PLP combined with colistin eradicated resistant strains in vitro and is likely safe as a dietary adjuvant. Metabolic supplementation could therefore resurrect last-line antibiotics without synthetic drugs.

Functional Modification of Ferroferric Oxide Nanoparticle Regulates the Uptake, Oxidative Stress, Tissue Damage, and Metabolic Profiles in Eisenia fetida

Tao et al. in Environmental Science & Technology demonstrated that earthworms exposed to citric-acid- or PVP-coated Fe_3O_4 nanoparticles accumulate more particles yet suffer less oxidative stress and tissue injury than with bare NPs. Metabolomics revealed adaptive shifts in amino-acid and energy pathways that support detoxification. The work guides safer nano-agrochemical design through surface functionalisation.

Multi-Omic Biomarkers for Diagnosis & Treatment

These studies use metabolomics integrated with transcriptomics, proteomics or lipidomics to uncover biomarkers that refine diagnosis, stage disease or map basic physiology. They exemplify the power of multi-layer data to reveal patterns invisible to single-omic snapshots. Each paper also illustrates a crucial translational arc: discovery in small cohorts leads rapidly to predictive models that can be validated in independent sets or paired-sample designs. Finally, they remind us that metabolic signatures often illuminate underlying biology, such as altered mitochondrial pathways in lipedema or triacylglycerol uptake in ageing brains, thereby guiding both diagnostics and therapy.

Defining lipedema's molecular hallmarks by multi-omics approach for disease prediction in women

Straub et al. in Metabolism showed that lipedema adipose tissue down-regulates inflammatory genes yet up-regulates mitochondrial oxidative-phosphorylation transcripts, while serum sphingolipids and glutathione are perturbed. A machine-learning model using circulating factors accurately staged disease across early and late cohorts. Objective biochemical staging could streamline diagnosis and monitor response to future therapies.

Metabolomic profiles in serum uncover novel biomarkers in children with Williams-Beuren syndrome

Bai et al. in Scientific Reports found that children with Williams–Beuren syndrome exhibit 169 serum metabolites at altered abundance, enriching cholesterol, arginine and tryptophan pathways. A serotonin-to-kynurenine shift hints at neuro-immune dysregulation consistent with clinical features. Such biomarkers may aid longitudinal monitoring and point to metabolic adjuncts for supportive care.

Altered metabolic profiles in colon and rectal cancer

Wu et al. in Scientific Reports reported that a six-metabolite dried-blood-spot panel (Glu, C0, C8, C20, Gly/Ala and C10:1) distinguishes rectal from colon cancer with high accuracy in cross-validation and an independent cohort. Location-specific metabolic signatures could guide screening and personalised surgery or chemoradiation strategies. Prospective trials are the next step toward clinical adoption.

Comprehensive characterization of metabolic consumption and production by the human brain.

Wang et al. in Neuron characterised paired arterial and cerebral-venous blood from 41 individuals, profiling 1,365 metabolites and 140 lipids. The brain consumes glucose, taurine, hypoxanthine and triacylglycerols while releasing glutamine and pyruvate; ageing and venous-sinus pathology amplify glycolytic by-product release. These flux maps establish a quantitative baseline for cerebral metabolic health and potential diagnostic read-outs.

Treatment response variations to a single large bolus of enteral cholecalciferol in vitamin D deficient critically Ill children: Metabolomic insights for precision nutrition

Helmeczi and colleagues in Molecular and Cellular Endocrinology showed that administering a single enteral bolus of 10 000 IU kg^{-1} cholecalciferol to vitamin-D-deficient, critically ill children produced a 128-fold spike in serum vitamin D_3 within 24 h and a 4.7-fold rise in 25-OH-D_3 by day 3, whereas placebo patients given ≤1 000 IU day^{-1} showed no such changes. Targeted and untargeted assays revealed a 24-fold surge in 3-epi-25-OH-D_3 and the first documented appearance of circulating 3-epi-D_3, whose abundance was tightly coupled to vitamin D_3 uptake ($r = 0.898$), pointing to C3-epimerase activity as a key driver of inter-patient response without inducing hypercalcaemia. By day 7, children who achieved vitamin-D sufficiency (>75 nmol L^{-1}) exhibited lower plasma 3-methyl-histidine, cystine, S-methyl-cysteine, uric acid and two lysophosphatidylcholines, a metabolic signature consistent with reduced oxidative stress, dampened inflammation and slower muscle-protein catabolism. These results position epimer-specific vitamin-D metabolites and ancillary small-molecule markers as practical read-outs for precision-nutrition interventions in paediatric intensive-care settings.

Analytical Frontiers for Forensics, Sample Prep & Beyond

Progress in metabolomics often hinges on better separations, smarter extraction workflows and rigorous chemometrics. The two studies here broaden the reach of the field by tackling long-standing practical hurdles: species-level wood identification for enforcement and one-pot extraction of chemically diverse metabolites for high-throughput analysis. They illustrate how methodological creativity—whether two-dimensional chromatography or successive electromembrane extraction—translates directly into real-world impact. They also emphasise validation: both methods were benchmarked on challenging matrices and achieved detection limits or classification accuracies that meet professional standards. As instrumentation spreads and costs fall, such advances will give regulators, clinicians and researchers sharper metabolomic lenses.

Classification of wood species in trade using metabolomic profiling by GC×GC-TOFMS

Dias et al. in Wood Science and Technology showed that GC×GC-TOF-MS fingerprints combined with PCA and PLS-DA classify Quercus, Acer and Picea woods at species level with up to 100 % accuracy from sapwood, heartwood or branch material. The model performed well on external validation sets and can operate on field-collected cores. Metabolite fingerprinting thus emerges as a robust forensic tool against illegal logging.

Successive electromembrane extraction: A new insight in simultaneous extraction of polar and non-polar metabolic molecules from biological samples

Chen et al. in Analytica Chimica Acta introduced successive electromembrane extraction that uses twin organic membranes and pH switching to co-extract polar carnitine and non-polar acylcarnitines from the same bio-sample. Recoveries reached 47–119 % with sub-ng mL^{-1} detection limits in blood and urine, and LC-MS/MS validation confirmed quantitative accuracy. A single micro-extraction step can therefore replace multiple sample-prep workflows in clinical or forensic metabolomics.

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The Metabolomist Podcast

THE METABOLOMIST

New episode

Dietary intervention & precision medicine

"What we know is that supplements work to increase the levels of unsaturated fatty acids in lipids

– Cristina Legido-Quigley

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Metabolomics Events

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

Bits & Bites #4: Quality Control and Quality Assurance (mQACC) from sample preparation to reporting

May 8, 2025

Venue: Online

The new course is taught by Dr. Oliver Fiehn from UC Davis. This introductory course is designed for participants with no prior knowledge and no software required.

Short description of the course: For several years, an independent consortium of more than 100 metabolomic scientists has discussed and published best practice documents in metabolomics, from sample preparation and data acquisition (LC-MS, GC-MS, and NMR) to data processing and reporting, including for the use of reference materials and quality control samples. In this course, participants will review the major conclusions of all mQACC reports and discuss strategies to utilize this information for data and manuscript submissions that require detailed descriptions of methods used in metabolomics studies. The course will also examine whether best-practice documents are clear enough for implementing strategies into standardized lab workflows, and identify where the community reports do not clearly distinguish quality differences between different strategies.

Check for more details

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

June 9 - 13, 2025

Venue: In person, London Hammersmith

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

Early Bird registration - May 9, 2025

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

Poster Abstract Submission Deadline - **might close before May 15, 2025 due to the high volume of submissions.**

Check for more details

DGMet Annual Meeting

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

2025 World Critical Care and Anesthesiology Conference

October 10 - 11, 2025

Venue: Singapore

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

Click here to view more details

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Metabolomics Jobs

Metabolomics Jobs

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
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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