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MetaboNews

This month in metabolomics

June, 2025
Vol 15, Issue 6

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

In This Issue

This Months Features:

Spotlight Article
NIST

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

International Affiliates' Corner

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

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

Réseau Francophone de Métabolomique et Fluxomique

THEMATIC SCHOOL 1

Annotation of Plant Metabolomes

*The thematic school is designed **for researchers** looking to deepen their expertise in this field.*

Sept. 8–12, 2025

Domaine du Lazaret, Sète (France)

Organized by P. Petriacq and 19 experts

Theoretical Courses and Hands-on Workshop

Day 1 **Introduction to MS & fundamental principles**
- Overview of plant metabolomes
- Acquisition strategies (GC/LC-MS)
- Identification/annotation principles

Day 2 **Pre-processing tools for untargeted data**
- Introduction to data processing tools
- Importance of in-house libraries (FragHUB)
- Hands-on training

Guest: Guillaume Marti

Day 3 **MS annotation tools and chemotaxonomy**
- Introduction to SIRIUS & CANOPUS
- Metabolic networks: annotation propagation
- Hands-on training (SIRIUS & MetGem)
- Annotation by analog search (MS^2Query)

Guest: David Touboul

Day 4 **Contextualization of metabolic markers**
- Practical introduction to TimaR
- Biological interpretation
- Introduction to GCxGC-TOFMS

Guests: Jean-Chrisologue Totozafy & Ludovic Cottret & LECO

Day 5 **Complementarity of techniques and Conclusion**
- Benefits and opportunities of spatial data
- Complementarity of NMR
- Concluding remarks

Guests: Dimitri Heintz & Patricia Homobono

Registration open until June 15

Academics 1,300 €
Industry 2,000 €
Visit our site web for more informations and registration :
https://1-et-rfmf.sciencesconf.org/

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#ET1RFMF

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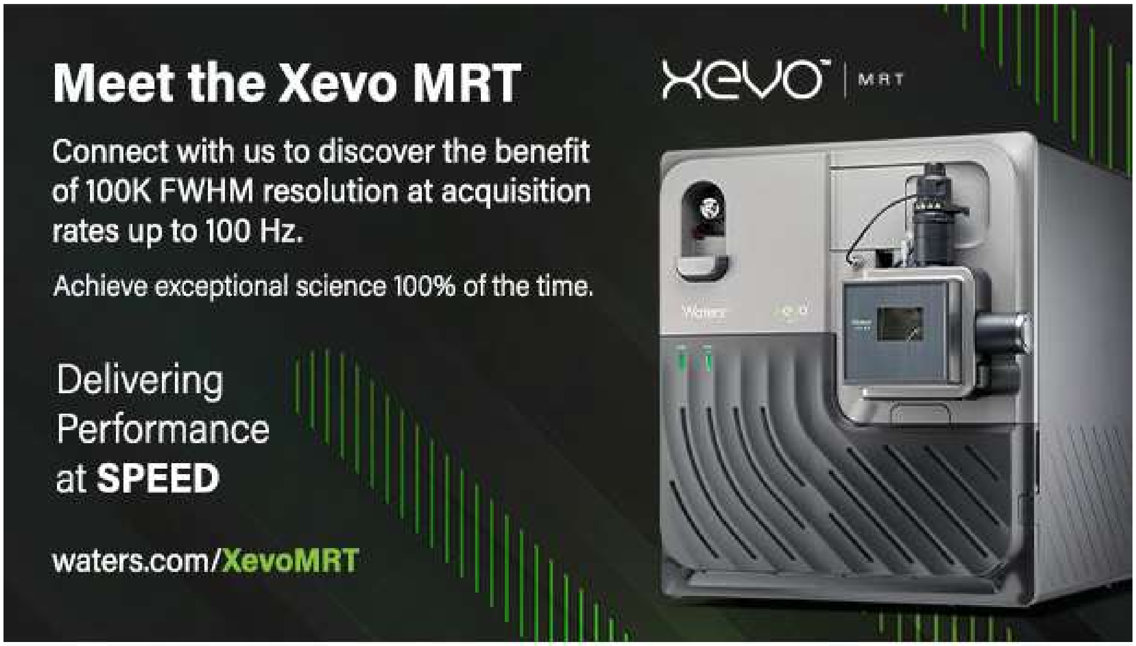

[Spotlight Article](#)

Sponsored Content

NIST Metabolomics and Microbiome Reference Materials Now Available!

Confidence in Data Quality

The National Institute of Standards and Technology (NIST) has launched two new reference material (RM) suites for the metabolomics communities to facilitate high quality measurements, promote reproducibility and reliability of results, and encourage data harmonization and comparability.

RM 8231 - Frozen Human Plasma Suite for Metabolomics

RM 8231 was created as a suite of three phenotypically distinct human plasma. Pooled Plasma 1, Diabetic Plasma: designed to represent a Type 2 diabetic plasma material with glucose >126 mg/dL and low/normal triglyceride (<150 mg/dL). Pooled Plasma 2, Hypertriglyceridemic Plasma: designed as a hypertriglyceridemic plasma material with glucose <100 mg/dL and triacylglycerols >300 mg/dL. Pooled Plasma 3, African-

American Plasma: created as a young (ages 20-25 years of age), African American plasma material. A unit of RM 8231 consists of two vials each of the three phenotypes.

RM 8048 – Human Fecal Material

RM8048 was designed to assist scientists in improving the reproducibility of their data and advancing diagnostics and clinical tools that focus on the gut microbiome. The RM 8048 unit includes four vials from vegetarian cohorts and four vials from omnivores. This material has identified over 150 metabolites and more than 150 genetic signatures.

Requesting community input!
RGTM 10212 – Fecal Calibrant Solution

NIST is developing a fecal metabolite calibrant solution as a research grade test material (RGTM) designed specifically to evaluate the performance and precision of microbiome metabolomics measurements. This solution contains 70 compounds at biologically relevant concentrations, representing a diverse range of chemical classes found within the gut microbiome including short-chain fatty acids (SCFAs), amino acids, phenols, and pyrimidines. We are offering **a unit free of charge** for community evaluation that will aid in assessing suitability for microbiome metabolomics and the data will provide NIST important feedback in the evolution of the RGTM to a reference material.

Materials can be acquired at the NIST Storefront!

Confidence in your data! Confidence in published results! Confidence in deposited data!

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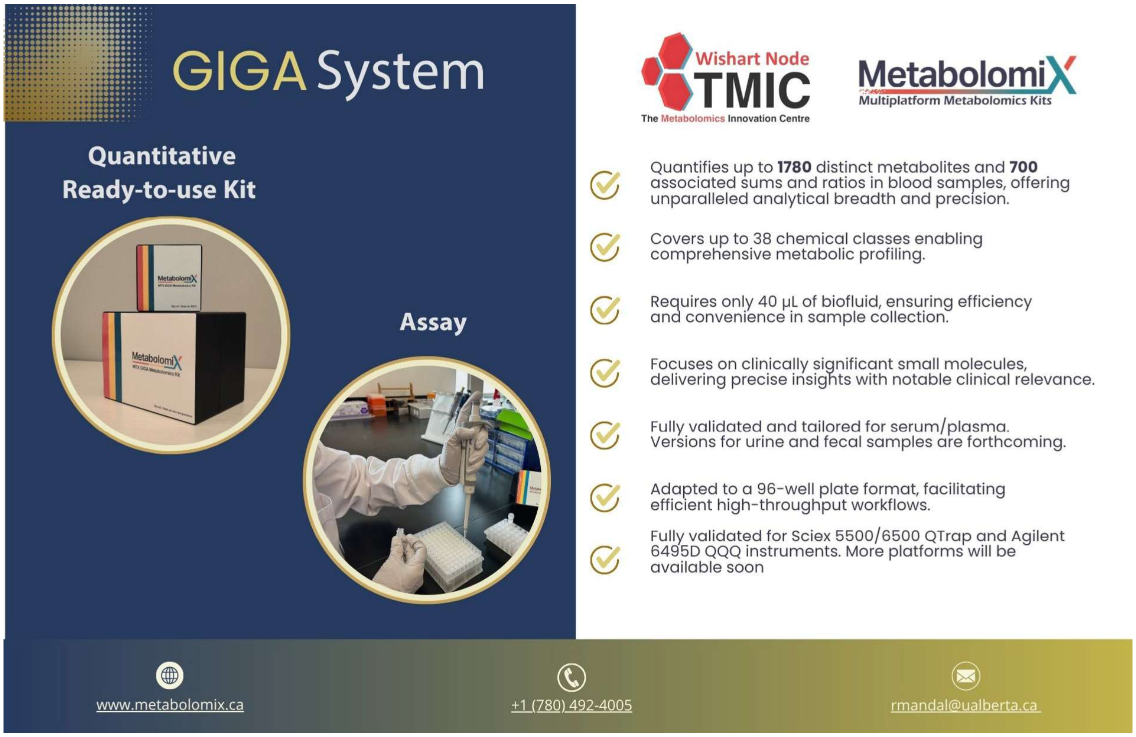
GIGA SYSTEM



GIGA System

Wishart Node TMIC
The Metabolomics Innovation Centre

MetabolomiX
Multiplatform Metabolomics Kits

Quantitative Ready-to-use Kit

Assay

- ✓ Quantifies up to **1780** distinct metabolites and **700** associated sums and ratios in blood samples, offering unparalleled analytical breadth and precision.
- ✓ Covers up to 38 chemical classes enabling comprehensive metabolic profiling.
- ✓ Requires only 40 µL of biofluid, ensuring efficiency and convenience in sample collection.
- ✓ Focuses on clinically significant small molecules, delivering precise insights with notable clinical relevance.
- ✓ Fully validated and tailored for serum/plasma. Versions for urine and fecal samples are forthcoming.
- ✓ Adapted to a 96-well plate format, facilitating efficient high-throughput workflows.
- ✓ Fully validated for Sciex 5500/6500 QTrap and Agilent 6495D QQQ instruments. More platforms will be available soon

www.metabolomix.ca
+1 (780) 492-4005
rmandal@ualberta.ca

Click on video to learn more about The GIGA System - Next Gen Metabolomics

MetaboReads

Gut Microbiota and Host Metabolic-Immune Crosstalk

Recent work highlights how specific bacterial taxa, transferable metabolites, and dietary components modify host glucose control, epithelial integrity, and immune priming. Across five independent models, investigators link microbial shifts to defined molecular pathways, showing that targeted manipulation of the gut ecosystem can either aggravate or alleviate metabolic and inflammatory disease trajectories.

Characterization of POP mixture redistribution and identification of their molecular signature in xenografted fat mice

Jamay and colleagues in Environmental Pollution showed that xenografting persistent-organic-pollutant–laden adipose tissue into mice caused POP redistribution to liver and brain, with adipose retaining the highest load. Multi-omics profiling revealed broad suppression of mitochondrial programs and induction of xenobiotic and inflammatory pathways in liver and fat. Per- and polyfluoroalkyl substances accumulated chiefly in liver, diverging from other POP classes. The authors conclude that mixed POP exposure produces a systemic metabolic disturbance consistent with obesity and diabetes pathogenesis.

Vitamin D3 ameliorates hyperglycemia by modulating gut microbiota and metabolites in prediabetic KKay mice

Zhang and colleagues in Food Research International found that intraperitoneal vitamin D_3 restored glucose tolerance in pre-diabetic KKay mice fed a high-fat diet. Treatment tightened colonic junctions, reduced endotoxemia, and tempered TLR4–NF-κB signaling while reactivating PI3K-AKT insulin pathways. 16S rRNA sequencing showed enrichment of beneficial gut taxa and shifts in carbohydrate-metabolism modules. Fecal transplantation from vitamin D_3 donors reproduced the metabolic benefits in naïve recipients, confirming a microbiota-mediated mechanism.

Bacterial microcompartments and energy metabolism drive gut colonization by Bilophila wadsworthia

Sayavedra and colleagues in Nature Communications demonstrated that Bilophila wadsworthia exploits a 34-gene microcompartment and a flavin-linked dehydrogenase complex to use taurine and isethionate in high-fat-diet mice. Metabolite production of H_2S, acetate, and ethanol enhanced gut permeability and modest hepatic inflammation when B. wadsworthia co-colonised with a defined consortium. The bacterium displayed flexible electron-donor usage, including formate, which supported higher in vivo abundance. These findings explain how dietary lipids select for sulfidogenic pathobionts with multifaceted host impact.

Psyllium husk powder enhances the management of type 2 diabetes by modulating gut microbiota and their metabolic products

Wang and colleagues in Food Research International reported that psyllium-husk dietary fibre improved hyperglycaemia and insulin resistance in high-fat + streptozotocin diabetic mice. Metagenomics showed a lower Firmicutes:Bacteroidota ratio and enrichment of Muribaculaceae and Parabacteroides. Short-chain-fatty-acid production and alpha-linolenic-acid and PPAR signaling pathways were elevated, correlating with reduced systemic inflammation. Higher psyllium doses produced the most pronounced metabolic rescue.

Live bacteria in gut microbiome dictate asthma onset triggered by environmental particles via

modulation of DNA methylation in dendritic cells

Ramar and colleagues in Cell Reports found that gut microbiota from particle-exposed pregnant mice transferred asthma susceptibility to germ-free recipients. Gamma sterilisation or antibiotics abolished this effect, proving that live bacteria were essential mediators. Metabolomics linked the pro-asthma microbiome to diminished butyrate synthesis. Methylome analysis revealed altered dendritic-cell DNA modifications that heightened allergen presentation, which could be normalised by an epigenetic drug.

Chemical Exposures, Redox Balance, and Vascular-Endocrine Health

These studies examine how endogenous or exogenous chemicals perturb antioxidant defences, vascular integrity, and hormone signaling. Integrative omics pinpoint glutathione, arachidonic-acid, and lysosome-dependent pathways as critical nodes that can be modulated for therapeutic benefit.

Lysine Carboxymethyl Cysteinate, as a Topical Glutathione Precursor, Protects Against Oxidative Stress and UVB Radiation-Induced Skin Damage

Gao and colleagues in Antioxidants showed that topical lysine carboxymethyl cysteinate permeated the stratum corneum, boosted keratinocyte glutathione pools, and elevated metabolites involved in GSH biosynthesis. The compound shielded reconstructed skin from blue-light oxidative stress, prevented UVB-induced barrier disruption, and suppressed inflammatory cytokines. Histological analysis confirmed reduced pigmentation and preserved epidermal structure. These results position the molecule as a multifunctional skin protectant.

Endogenous acrolein accumulation in akr7a3 mutants causes microvascular dysfunction due to increased arachidonic acid metabolism

Zhang and colleagues in Redox Biology found that akr7a3 mutant zebrafish accumulated endogenous acrolein, leading to enlargement of retinal and renal microvessels. Transcriptomics and metabolomics implicated up-regulated arachidonic-acid and leukotriene pathways in the vascular defects. Pharmacological inhibition of leukotriene synthesis mitigated the phenotype, confirming pathway causality. The study establishes acrolein as a driver of microvascular inflammation and remodeling.

Estrogenic activity of E2-conjugated GLP-1 is mediated by intracellular endolysosomal acidification and estrone metabolism

Coupland and colleagues in Molecular Metabolism reported that an estradiol-conjugated GLP-1 analogue entered GLP-1-receptor-positive cells without altering receptor trafficking. Lysosomal acidification liberated an E2-3-ether intermediate that was converted to estrone-3-sulfate and then active estradiol. Co-administration of a V-ATPase activator amplified estrogenic signaling, supporting a pH-dependent release mechanism. The work clarifies intracellular events governing GLP-1–small-molecule conjugate activity.

Metabolomic Pathways of Inflammation and Mitochondrial Dysfunction Are Related to Worsening Healthy Aging Index and Mortality

Yao and colleagues in The Journals of Gerontology A identified 42 plasma metabolites, mainly lipids, whose concentrations correlated with baseline Healthy-Aging-Index scores, ten-year decline, and mortality in 2,015 older adults. Lipid species associated with poor aging overlapped mitochondrial and oxidative-stress pathways. Adjustment for C-reactive protein and IL-6 weakened most associations, suggesting inflammation as an intermediary. A metabolite-based score predicted both functional deterioration and death beyond standard risk factors.

Associations between seminal plasma metal mixture and semen quality: A metabolome-mediated case-control study

Zhao and colleagues in Ecotoxicology and Environmental Safety showed that combined seminal exposure to copper, iron, and selenium shaped semen quality in 522 men. Regression and mixture-model analyses linked higher copper with abnormal parameters, whereas iron and selenium were protective. Untargeted metabolomics identified 74 differential metabolites, with 16-glucuronide-estriol and trans-cinnamate mediating metal effects on fertility endpoints. The study proposes candidate biomarkers for metal-related male infertility.

Multi-Omics for Sustainable Crops, Fermentation, and Animal Feed

These papers apply metabolomics and microbiome profiling to optimise plant productivity, fermented-food flavour, and livestock nutrition. The data reveal that community composition and specialised metabolites can be engineered to improve yield, stress tolerance, and sensory qualities while reducing environmental burdens.

Flavor characteristics and metabolomics of sweet rice wine fermented with different non-Saccharomyces yeasts

Deng and colleagues in Food Research International found that inoculation of sweet-rice-wine fermentations with five non-Saccharomyces yeasts altered physicochemical traits, antioxidant activity, and amino-acid profiles. Hanseniaspora uvarum produced the most desirable volatile organic compounds and lowest bitter amino-acids, increasing sensory acceptance. Volatile analysis pinpointed ethyl decanoate as a dominant flavour driver, whereas metabolomics highlighted the TCA cycle and pyruvate pathways as key nodes. The work recommends H. uvarum for premium sweet-rice-wine production.

Intercropping improves plant biochemistry and soil microecology to realize healthy and sustainable production of Platycodon grandiflorus

Mei and colleagues in Journal of Cleaner Production showed that intercropping Platycodon grandiflorus with Allium fistulosum raised tuber yield by 56–59 percent and enriched bioactive metabolites linked to stress resistance and quality. Rhizosphere profiling revealed higher levels of sulfurous allelochemicals and increased abundance of beneficial bacteria such as Actinomycetes and Pseudomonas, while pathogenic fungi declined. Correlation analyses indicated reciprocal feedback between altered root exudates and microbial community shifts. The study provides a blueprint for ecological intensification of medicinal crops.

Rhizosphere metabolomics reveals benzoxazinoid-mediated interspecific root interactions that promote N and Fe uptake in intercropped plants

Luo and colleagues in Soil Biology & Biochemistry demonstrated that wheat–fava-bean intercropping stimulated wheat root secretion of benzoxazinoids that migrated into the fava rhizosphere. Metabolomic comparisons identified more than 600 differential compounds including flavonoids and monoterpenes associated with improved nitrogen and iron acquisition. Positive correlations between 6-methoxy-2-benzoxazolinone and nutrient-mobilising metabolites suggested a coordinated chemical dialogue. The findings reveal specialised metabolites as mediators of interspecific nutrient facilitation.

Multi-omics analysis reveals insights into hypoxia-tolerant rice growth and identifies the 1-Cys peroxiredoxin B-like protease

Chen and colleagues in International Journal of Biological Macromolecules investigated a hypoxia-tolerant rice line and showed elevated antioxidant enzymes, salicylic- and indole-acetic-acid levels, and higher alpha-amylase activity under flooded germination. Integrated transcriptomics, proteomics, and metabolomics uncovered 8,096 genes, 1,886 proteins, and 588 metabolites differing from a sensitive variety, with enrichment in glutathione and sucrose metabolism. External salicylic acid rescued the sensitive line, confirming its role in adaptation. These data clarify mechanisms that support direct-seeded rice under waterlogging.

Feeding probiotics-fermented distiller's grains diets increases rumen enzyme activities and glycerophospholipid levels in finishing cattle by modulating rumen microbiota

Zhang and colleagues in Microbiome found that finishing cattle fed 20 percent probiotics-fermented distillers grains showed higher rumen cellulolytic enzyme activities and increased Prevotella 1, Bifidobacterium, and Candida. Lipidomics revealed elevated glycerophospholipids, and metabolite profiling indicated enrichment in neuroactive-ligand and taste-transduction pathways. Correlations linked specific microbial genera to enzyme activities and lipid levels, explaining improved feed utilisation. The authors recommend 20 percent inclusion of fermented distillers grains for optimal performance.

Multiomics-Driven Biomarkers and Mechanistic Insights in Disease

Several investigations combine metabolomics, proteomics, genomics, and advanced analytics to refine disease prediction, reveal therapeutic targets, and expand basic metabolic maps. The studies illustrate how integrated omics can both validate and challenge clinical assumptions.

Predicting Placenta Accreta Spectrum Disorder Through Machine Learning Using Metabolomic and Lipidomic Profiling and Clinical Characteristics

Miller and colleagues in Obstetrics and Gynecology showed that untargeted metabolomics and targeted lipidomics of third-trimester plasma from 54 placenta-previa pregnancies did not outperform nine clinical variables for predicting placenta-accreta spectrum. Elastic-net models achieved area-under-curve values near 0.70 for either data type alone, and combining omics with clinical metrics did not improve classification. Univariate analyses flagged 31 lipids and 214 metabolites before correction, but none survived false-discovery adjustment. The study concludes that circulating metabolite profiles add limited value over conventional risk factors in this cohort.

Unveiling the biological effects of DNA G-quadruplex ligands through multi-omics data integration

Romano and colleagues in International Journal of Biological Macromolecules found that the G-quadruplex ligand pyridostatin produced coordinated transcriptomic, proteomic, and metabolomic suppression of energy metabolism in HeLa cells, reducing precursors for lipid and nucleotide synthesis and lowering redox cofactors. RHPS4 selectively impaired mitochondrial activity, whereas berberine showed negligible effects. Pathway integration suggested that mitochondrial G-quadruplex stabilisation underlies RHPS4 specificity. These insights inform rational design of anticancer G-quadruplex drugs.

An integrative systems-biology approach defines mechanisms of Alzheimer's disease neurodegeneration

Leventhal and colleagues in Nature Communications integrated a Drosophila forward-genetic screen with multi-omic datasets and human eQTLs to map Alzheimer’s-relevant pathways. They predicted and validated that HNRNPA2B1 and MEPCE enhance tau toxicity, while CSNK2A1 and NOTCH1 influence DNA damage in fly and human neural progenitors. Proteomic and phosphoproteomic layers converged on RNA processing and chromatin regulation. The systems-biology approach nominates new therapeutic targets for neurodegeneration.

A metabolome-driven deep exploration into Moringa's medicinal efficacy

Cai and colleagues in Food Research International developed a signature metabolome of Moringa oleifera that predicted hepatoprotective activity in a rat model of alcoholic fatty-liver disease. Quantitative validation identified the lipid pair FA 18:3/FA 20:2 as an early disease biomarker responsive to treatment. The integrated workflow provides a template for evidence-based evaluation of botanical medicines. The findings support Moringa as a candidate for metabolic-liver disorders.

Charting unknown metabolic reactions by mass spectrometry-resolved stable-isotope tracing metabolomics

Gao and colleagues in Nature Communications applied IsoNet, an isotopologue-similarity networking strategy, to stable-isotope tracing data and discovered about 300 previously unannotated reactions in cells and mice. Detailed analysis of glutathione metabolism revealed a trans-sulfuration reaction forming γ-glutamyl-seryl-glycine directly from glutathione, establishing glutathione as a sulfur donor. Functional assays showed that these new reactions influence cellular redox and amino-acid pools. The work greatly expands known metabolic connectivity and offers new research avenues.

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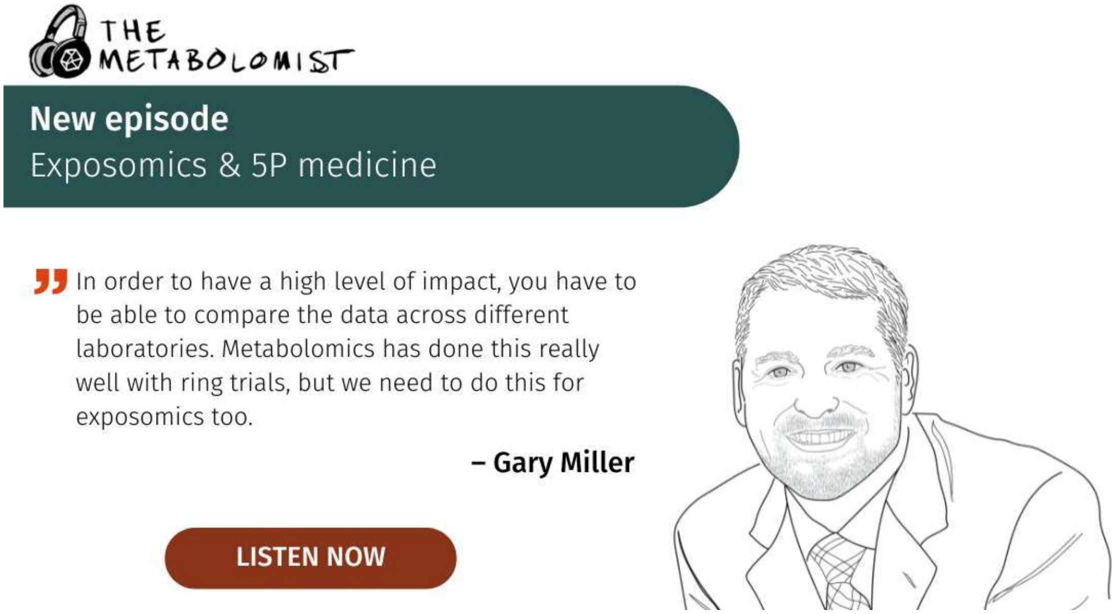
The Metabolomist Podcast



THE METABOLOMIST

New episode
Exposomics & 5P medicine

> In order to have a high level of impact, you have to be able to compare the data across different laboratories. Metabolomics has done this really well with ring trials, but we need to do this for exposomics too.
>
> **– Gary Miller**

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Metabolomics Events

MANA SODAMeet

August 12, 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

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. This year's conference will be hosted in the heart of the Rocky Mountains. Check out the website for program information, speakers, events, registration, awards, and more.

Early registration deadline: **June 30, 2025**

Register today

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

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
Research Fellow in Computational Metabolomics - School of Biosciences	University of Birmingham	Birmingham, England, United Kingdom	University of Birmingham
Metabolomics Specialist I	Memorial Sloan Kettering Cancer Center	New York, NY, USA	Memorial Sloan Kettering Cancer Center
Senior Research Scholar - Mass Spectrometry Metabolomics	North Carolina State University	Raleigh, NC, USA	North Carolina State University
Applications Scientist - Liquid Chromatography and Mass Spectrometry -	Thermo Fisher Scientific	Montreal, QC, Canada	Thermo Fisher Scientific

Proteomics			
Research Associate Principal	Berkeley Lab	Berkeley, CA, USA	[Lawrence Berkeley National Laboratory]()
Metabolomics Associate Director	Botany and Plant Pathology Department at Purdue University	West Lafayette, IN, USA	[Botany and Plant Pathology Department at Purdue University]()
Post Doctoral Fellow Research - American Elderberry Metabolomics (Dr. Lloyd Sumner's Lab)	University of Missouri-Columbia	Columbia, MO, USA	[University of Missouri-Columbia]()
Assistant Professor, Cell Metabolism	University of Saskatchewan	Saskatoon, SK, Canada	[University of Saskatchewan]()
Manager, Quantitative Metabolite Analysis Center	University of California, San Francisco	San Francisco, CA, USA	[UC San Francisco]()

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Your input means a lot to us, and we're eager to hear your thoughts on how we can improve our newsletter. Please take a moment to share your opinions with us at metabolomics.innovation@gmail.com

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