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MetaboNews

This month in metabolomics

September, 2026

Vol 16, Issue 8

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



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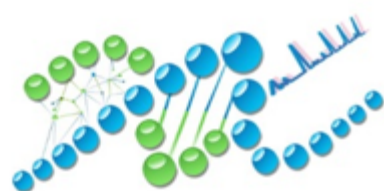
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METABOLOMICS SOCIETY
EARLY- CAREER MEMBERS NETWORK

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

Members Corner

Board of Directors

Message from Warwick (Rick) Dunn, President

Dear Metabolomics Society Members and metabolomics friends,

I am writing this with a saddened heart as this will be my last MetaboNews message as President of the Metabolomics Society. The society has been something close to my heart for two decades, starting with a great conference (and some baseball) in Boston in 2006. Sorry but I still follow the Red Sox when I can (and what a summer they are having). The society will continue to be close to my heart and it has been a huge honour to be your President for the last two years.

I have enjoyed my time as President and have relished being able to shape the society and its operations. From day one I wanted to demonstrate that the society is global in its operations and reach. I have been able to do this in two ways, (1) ensuring global distribution of our Directors now and in the future and (2) holding Metabolomics 2026 in South America (the first time the conference had been hosted in South America).

I would like to thank all of the Directors during my tenure, the society is operated by all 14 Directors and not just the President with each Director having a maximum of four

years to contribute. I would also like to send huge thanks to Candice (Treasurer), Maria (Secretary) and Aurelia (Conference committee chair). There has been a lot to do in the last two years and nothing would have been completed without these three marvellous women. I will miss our monthly meetings ladies. Finally, I would like to thank Leslie (and the team at Snap) for all of her work behind the scenes in supporting the society in its operations.

I know the society is being passed in to good hands. Aurelia Williams was elected as our President for the next two years and Nik Rattray was elected as our new Secretary (to replace Maria). Candice will remain as Treasurer for one more year. Liz Want, Nik and Aurelia were all voted on to the board for their second terms. I would also like to welcome four new Directors for their first terms - Ian Castro-Gamboa (São Paulo State University, Brazil), Facundo Fernandez (Georgia Institute of Technology, USA), Nicola Gray (Murdoch University, Australia) and Huiru Tang (Fudan University, China).

I pass to all of the Officers and Directors my support to continue strengthening and expanding the society for all of our members.

All the very best,
Warwick (Rick) Dunn, University of Liverpool, UK
President, Metabolomics Society

Early-career Members Network (EMN)

EMN Chair Election

We are pleased to announce that Carolina D'Almeida has been elected as the new chair for the EMN 2026-2027 committee. We extend our gratitude towards our outgoing EMN committee members Ellen De Paepe, Jayden Lee Roberts, Juan José Oropeza, Ambrin Farizah Babu, Silvia Radenkovic, Thomas Dussarrat, and Marina Tonetti Botana, and wish them all the best in their next endeavours! We are currently finalizing the new committee members who will be joining us from October, and are excited to announce them next month!

EMN & Affiliates Virtual Symposium - REGISTER NOW!

The EMN-MetSoc, in collaboration with the Polish Metabolomics Society, Spanish Metabolomics Society, Australian and New Zealand Metabolomics Society, and Metabolomics Association of North America, is pleased to announce the EMN & Affiliates Virtual Symposium. The symposium will feature keynote and ECR presentations and will take place virtually on **Tuesday, 3 November**, with regional

sessions for **Europe/Africa (14:00–16:30 CET)** and **Asia/Oceania (14:00–16:30 AEDT)**.

Register here:

Europe/Africa: https://zoom.us/webinar/register/WN_gfStOhKdRdqObgpGFm3G0A

Asia/Oceania: https://zoom.us/webinar/register/WN_91_r-TpeQEykBvWeqXnt0A#/registration

EMN Webinars

August EMN Webinar - Thank you!

The EMN Committee extends its gratitude to **Prof. Osbaldo Resendis-Antonio**, Full Professor at the Universidad Nacional Autónoma de México (UNAM) and the National Institute of Genomic Medicine (INMEGEN), Mexico, and **Samaria Johana Gutiérrez Félix**, a Ph.D. student in Biochemical Sciences at UNAM, for the August webinar entitled 'Digital microbiota: from associations to mechanisms in the era of AI and Genome-scale metabolic modeling'. The webinar recording is available on the MetSoc website: <https://metabolomicssociety.org/resources/multimedia/emn-webinars-2026/>.

September/October EMN Webinar - REGISTER NOW!

The EMN Committee is pleased to welcome **Dr Zoe Hall**, Associate Professor, and **Dr Aleksandra Gruevska**, postdoctoral researcher at Imperial College London (UK). Together, they will present the September/October webinar entitled 'Spatial metabolomics to explore metabolic microenvironments in liver disease and cancer' and 'Integrating spatial lipidomics with imaging mass cytometry for metabolic profiling of liver fibrosis'. The webinar will take place on Friday, 2 October at 14:00 BST/13:00 UTC/15:00 CEST.

Register here: https://zoom.us/webinar/register/WN_x95_dbd6SVyADyOps2RZaw

International Affiliates Corner



Mexican Proteomics Society (SMP)

Visit <https://www.smp.org.mx/>

The Mexican Society of Proteomics (SMP) is pleased to present the 10th Symposium of the SMP, our biennial MS-based Omics meeting. This edition will cover "Multi-Omics & Integrative Biology: advances and applications", bringing experts in proteomics, metabolomics, systems biology, genomics, and transcriptomics with an MS-based focus. Additionally, we offer five workshops and an Industrial forum where you can connect with national and international researchers, improve your skills, and explore new horizons for applying your knowledge.

Early registration is still open until September 30th.

See you in Mexico City, at IPN-ESIQIE, November 9 - 13th, 2026

Please visit for details: <https://www.smp.org.mx/xsymposium/>



Thailand Metabolomics Society (TMS)

Visit <https://thailand-metabolomics.org/>

Chulalongkorn University Hosts International Conference on Precision Health, Omics, Drug Design and Personalized Nutrition

The Department of Food and Pharmaceutical Chemistry, Faculty of Pharmaceutical Sciences, Chulalongkorn University, successfully organized the 2nd Annual International Conference 2026, under the theme “Advancing Precision Health through Omics, Drug Design and Personalized Nutrition,” on September 2–3, 2026, in Bangkok, Thailand.

The two-day event brought together researchers, clinicians, academics, and industry experts working across metabolomics, proteomics, mass spectrometry, drug discovery, and personalized nutrition. The conference aimed to promote interdisciplinary exchange and highlight how advanced analytical technologies and omics approaches can contribute to translational research and improved health outcomes.

The program began on September 2 with a Pre-Conference Short Course at Chulalongkorn University. The course provided participants with practical and conceptual perspectives on modern chromatographic and mass spectrometric techniques for metabolomics research. Sessions covered the principles and applications of gas chromatography and liquid chromatography, followed by hands-on and application-oriented discussions of GC-TOF-MS for metabolomics and LC-TIMS-QTOF-MS for 4D metabolomics. Experts from Chulalongkorn University, LECO Instruments (Thailand), and Bruker (Thailand) contributed to the training program, providing participants with insight into both fundamental analytical concepts and current technological developments.

The main conference was held on September 3 at the Pathumwan Princess Hotel in Bangkok. The scientific program featured invited speakers from Thailand and abroad, with presentations spanning a wide range of topics related to precision health, omics, drug design, and personalized nutrition. Highlights included rapid lipidomics profiling for infectious disease applications, AI-guided design and targeted nanodelivery of natural bioactives, precision immune engineering, biologic drug discovery and development, proteomics, metabolomics, PFAS exposure, spatial systems biology, mass spectrometry imaging, gut microbiome profiling, personalized nutrition, phytonutrients, and functional health claims.

Several presentations emphasized the growing role of multi-omics, artificial intelligence, computational approaches, and spatially resolved analytical technologies in understanding complex biological systems. AI was highlighted as an increasingly important tool for integrating complex datasets, supporting molecular and drug design,

identifying biologically relevant patterns, and accelerating the translation of omics data into actionable insights. Applications presented during the meeting ranged from biomarker discovery and biologic development to environmental exposure assessment, natural-product research, and individualized nutritional strategies. The conference also demonstrated how advances in mass spectrometry, ion mobility, data integration, and AI-assisted analysis are expanding the capabilities of metabolomics and related omics disciplines.

The conference provided an important platform for scientific exchange among researchers from universities, research institutes, healthcare organizations, and industry. It also created opportunities for networking and future collaboration in areas where metabolomics intersects with pharmaceutical sciences, medicine, nutrition, artificial intelligence, and translational research.

Through this annual international event, Chulalongkorn University continues to support the advancement of omics research and its translation into practical applications in precision health, drug discovery, and personalized nutrition.

The 2nd Annual International Conference 2026
Advancing Precision Health through Omics, Drug Design and Personalized Nutrition
 September 2, 2026 • Bangkok, Thailand

Pre-Conference Short Course

GC-MS
 High-Throughput Gas Chromatography
 Time of Flight Mass Spectrometry
 LECO Pegasus[®] BT GC-MS/TOF

LC-MS
 4D-Metabolomics™
 4D-Lipidomics™
 Trapped Ion Mobility Chromatography
 Quadrupole Time-of-Flight Mass Spectrometry
 BRUKER timsTOF[®] LC-TIMS-QTOF-MS/MS

Event Venue
 Meeting Room, 13th Floor, Sabbasatavicaya (Multidisciplinary Research) Building,
 Chulalongkorn University (near SIAMSCAPE, Siam Square & BTS Siam)

PROGRAM SCHEDULE

08:30 - 09:45	Registration
09:45 - 10:00	Opening Remarks Asst. Prof. Dr. Assaree Tanasart Head, Department of Food and Pharmaceutical Chemistry, Faculty of Pharmaceutical Sciences, Chulalongkorn University (CU)
10:00 - 10:05	Keynote: Principles and Applications Asst. Prof. Dr. Chaitin Kulasing Department of Chemistry, Faculty of Science, CU
10:05 - 12:00	Supervising 90,120-40 for metabolomics applications Dr. Ranyisa Janta / Dr. Ranyisa Rattanasakulapong LECO instruments (Thailand) LTD
12:00 - 12:05	Lunch
12:05 - 14:00	Liquid Chromatography: Principles and Applications Dr. Jeeprad Srangthongse / Asst. Prof. Dr. Patsornchai Limkittakul Department of Food and Pharmaceutical Chemistry, Faculty of Pharmaceutical Sciences, CU
14:00 - 16:00	Introducing timsTOF™: The next-generation research engine for 4D-Metabolomics Dr. Janta Janta / Dr. Janta Janta Bruker (Thailand) LTD

Organized by
 Department of Food and Pharmaceutical Chemistry
CPE 4 credits
 Code: 1001-2-000-090-09-2569

More Information
<http://www.ce.pharm.chula.ac.th/>
 email: foodchem.ph@pharm.chula.ac.th
 Tel: 085-360-3693, 081-594-1179

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 Selected applicants
 will be contacted
 by our staff

The 2nd Annual International Conference 2026
Advancing Precision Health through Omics, Drug Design and Personalized Nutrition
 September 3, 2026 • Pathumwan Princess Hotel, Bangkok, Thailand

International Invited Speakers

Michael Chan The University of British Columbia Canada	Anne Bendi National University of Singapore Singapore	Yilin Song Shenyang Pharmaceutical University China
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National Invited Speakers

Tarav Pathan Faculty of Medicine, CU	Worrap Vassanaphan Srinakharinwirot Srinakharinwirot	Wanida Rungtassan Srinakharinwirot Srinakharinwirot	Sakda Khomkum Srinakharinwirot Srinakharinwirot	Piti Chanasakote Faculty of Pharmacy, CU
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Poster Sessions

Rosarin Tanasart Asst. & Prof. Chien	Rodin Tanasart Asst. & Prof. Chien	Pattana Srirattanasak Asst. & Prof. Chien	Rutana Mahasarak Asst. & Prof. Chien
Jeeprad Srangthongse Asst. & Prof. Chien	Patsornchai Limkittakul Asst. & Prof. Chien	Teevan Srirattanasak Asst. & Prof. Chien	

Organized by
 Department of Food and Pharmaceutical Chemistry, Faculty of Pharmaceutical Sciences, Chulalongkorn University

HYBRID MEETING: ONLINE & ONLINE
 Lectures and activities at this conference will be conducted primarily in English.
 Conference code: 1001-2-000-090-09-2569 **CPE 5.5 credits**

More Information
<http://www.ce.pharm.chula.ac.th/>
 email: foodchem.ph@pharm.chula.ac.th
 Tel: 085-360-3693, 081-594-1179

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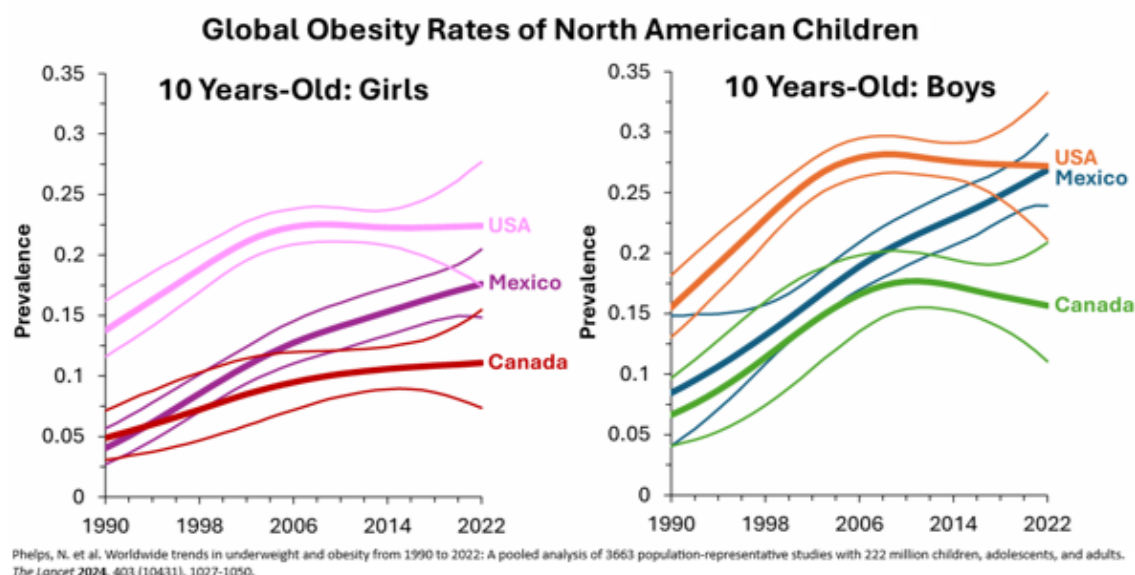
Zachery Kroezen



Zach obtained his Honours B.Sc. in Chemistry at McMaster University in 2019. From 2019 until 2025 he worked alongside Dr. Philip Britz-McKibbin and Dr. Meera Shanmuganathan at the McMaster University node within TMIC as a research assistant. Here Zach was involved in collaborative works with colleagues from McMaster, other academic institutions and industry partners, performing metabolomic analyses on diverse biological samples ranging from urine, serum, plasma, cord blood, intestinal fluid, tissue, stool, cecum, saliva, dried blood spots, and cell extracts. Since 2019, Zach has co-authored 20 peer-reviewed publications and analyzed over 25,000 biological samples using high-throughput multisegment injection-capillary electrophoresis-mass spectrometry technology. In January 2025, Zach started his PhD studies within the Britz-McKibbin laboratory and based on his research contributions as a young scientist was awarded the prestigious NSERC Vanier Canada Graduate Scholarship.

What inspired you to pursue this area of research within Metabolomics?

I have been working in the Britz-McKibbin TMIC node since 2019. In 2025 I took the plunge to return as a full-time PhD student. During my tenure as research assistant, after graduating in 2019, colleagues from Mexico approached our group to explore the possibility of a research collaboration involving metabolomics and biomarker discovery. This collaboration morphed into the work I presented at the Canadian Metabolomics Conference in 2026. For context, this research project is using plasma metabolomics to better understand the early impact of childhood obesity on health outcomes. Specifically, we are using metabolomics to identify biomarkers associated with metabolic syndrome, which includes a cluster of comorbid conditions linked to excessive central adiposity in Mexican children. Since Mexico has some of the highest rates of childhood obesity worldwide, coinciding with high consumption of sugar-sweetened beverages, there is a growing need to understand how dietary patterns impact cardiometabolic health in children. Although childhood obesity rates remain high in all North America, its prevalence is stabilizing in Canada and the USA, unlike in Mexico.



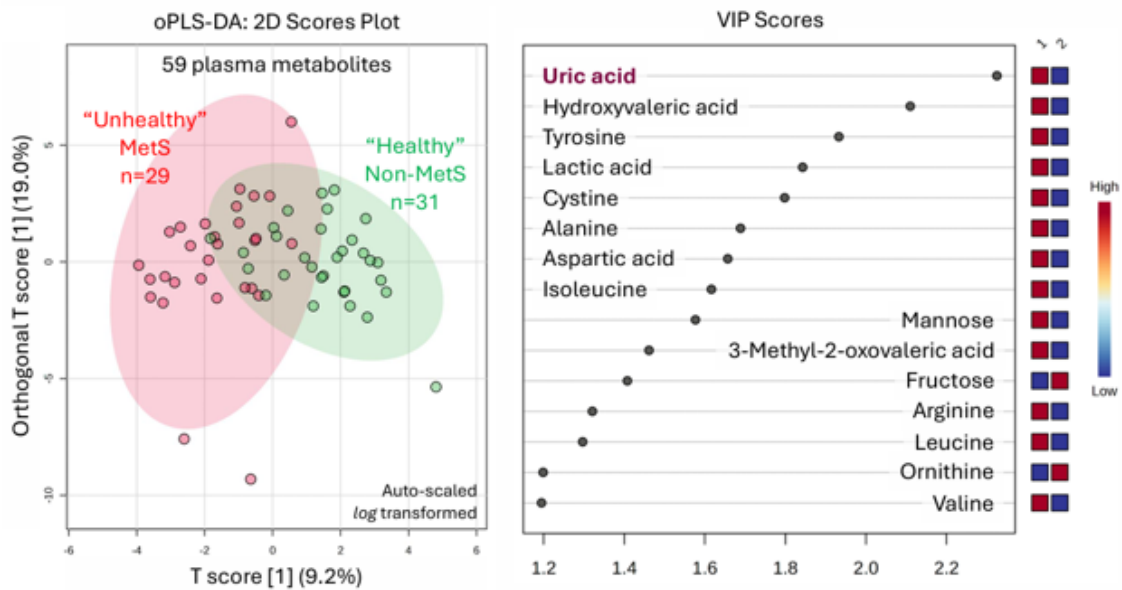
Has working in Metabolomics changed the way you think about biology, health, or disease?

Of course it has! If anything, metabolomics has demonstrated how integrated biological processes truly are to human health. As scientists, it is sometimes easier to classify research into discrete categories. For years genomics, proteomics and metabolomics were studied as distinct fields within biology. Today, however, we recognize these layers are all interconnected! While the central dogma of molecular biology describes the flow of genetic information from DNA to RNA to proteins to metabolites, this flow isn't always unidirectional. In fact, many bioactive metabolites can influence upstream processes, such as inhibitors of enzyme activity and various environmental exposures (mostly comprised of small molecules) that functions as epigenetic factors regulating gene expression. Why this matters is that fully understanding human health often requires a more holistic view of biology. Since aberrant metabolic processes are closely associated with clinical outcomes, metabolomics offers an exciting opportunity to gain important insights into the mechanisms of disease.

Was there a specific finding or result from your research that surprised you the most?

Our most interesting finding was the positive association between circulating uric acid levels and pediatric metabolic syndrome risk. Historically, uric acid has been a classic clinical biomarker of gout, a painful inflammatory condition caused by the build up of uric acid crystals in joints. So, it was somewhat unexpected when this metabolite became our lead candidate differentiating children with and without metabolic syndrome.

Although this research study is still in progress, the literature supports a possible link between excessive fructose intake and elevated uric acid. Given that individuals with metabolic syndrome are more likely to be overweight or obese, greater habitual fructose consumption due to excessive soda consumption by Mexican children, may be a modifiable risk factor. Specifically, following a large fructose load, uric acid can be produced through increased purine catabolism resulting from rapid ATP depletion. Although uric acid is a potent extracellular antioxidant, intracellular uric acid can promote mitochondrial oxidative stress, which in turn impairs fatty acid oxidation thereby promoting *de novo* lipogenesis.



What is one discovery or advancement in Metabolomics that you think deserves more attention?

Although unrelated to my research work, in my opinion one of the most important advancements in metabolomics has been the creation of the Metabolomics Standards Initiative. I hope researchers would be familiar with these important recommendations in minimum reporting standards, but for those new to the metabolomics community, this initiative was created to develop consensus approaches for how metabolomic experiments should be performed and how metabolites should be identified. Whether through the stringent quality assurance and quality control guidelines applied to our experiments or the rigorous criteria used to unambiguously identify unknown metabolic features of clinical significance, the work from this community-led initiative has played an important role in advancing the quality, reproducibility, and trustworthiness of published metabolomics data.

What is one thing you wish more people understood about researchers or scientific work?

I wish colleagues would understand (but also appreciate) that the best scientists always follow the data. We do not become scientists because we want to be popular, we become scientists so we can objectively pursue answers to the questions we seek to better understand. Of course, there will always be a few bad apples among us who only seek to prove their own opinions and theories. However, most scientists are guided by evidence and are willing to revise their findings as new data emerges. Sometimes this means challenging previous consensus and cherished opinions. This doesn't represent a failure of science, rather, it demonstrates that science is working as intended.

How do you think your research could translate into real-world applications?

Although metabolic syndrome is well classified in adults, there remains a lack of consensus when classifying pediatric metabolic syndrome. Metabolic syndrome is defined as a cluster of comorbid conditions including (1) abdominal adiposity, (2) low HDL cholesterol, and elevated (3) blood glucose, (4) triglycerides and (5) blood pressure. Adults with at least three of these comorbid conditions meet the criteria for metabolic syndrome, but there is no established threshold for determining metabolic syndrome in children. In many ways, metabolic syndrome is a better determination of one's health than relying on BMI or weight alone. This is even demonstrated in the work I presented at CanMetCon 2026 where we identified overweight children that were otherwise metabolically healthy. It is important to identify children most at-risk of developing metabolic syndrome, so that interventions can be tailored to these individuals. Specifically, childhood intervention is critical since poor nutrition and growth in early life have the most impact on future health outcomes. Therefore, by identifying high-risk metabolic phenotypes and addressing these needs in early life, the long-term health benefits should be amplified into adulthood. Considering the major challenges faced by our healthcare systems given the growing burden of obesity-related and age-related conditions, urgent reforms are needed to promote disease prevention that can be achieved by optimal dietary and lifestyle modifications.

If you could expand your project without any limitations, what would you explore next?

Our sample size (n=60) was somewhat limited in this pilot study, so being able to reproduce these results in a larger study is important for biomarker validation. It would

also be great to capture greater regional variability since all our samples were collected from children in Mexico City. In fact, our colleagues recently provided additional samples from Mexico City and the state, Chiapas, which may help us perform several of these follow-up experiments. Extending this work to Chiapas is ideal since this region is the leading consumer of sugar-sweetened beverages globally and has the highest prevalence of childhood obesity in Mexico. The consumption of sugar-sweetened beverages is staggering in Chiapas where it is estimated that individuals consume over 600L (or 4 bathtubs full) of soda annually!

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MetaboReads

Metabolic Control Points in Cancer and Immune-Mediated Disease

Tumors and inflamed tissues rarely fail metabolically in a general way; they depend on particular enzymes and particular metabolites, and the work collected here is aimed at finding those dependencies and testing whether removing them changes how the disease behaves. Two of the studies nominate a catabolic enzyme, carbamoyl-phosphate synthase 1 in IDH-mutant glioma and spermine oxidase in inflamed islets, as the node that keeps a damaging metabolic state running. A third moves in the opposite direction, starting from a circulating microbial metabolite and tracing its effect onto natural killer cell activation in liver disease. The fourth carries the question into a randomized trial built around a cellular biomarker of hyperprogression, with metabolomic and microbiome profiling written into the protocol rather than added afterwards. Isotope tracing, organoid models and enzyme inhibition carry most of the weight across this group, which is a sign of how far the field has moved from descriptive profiling. What connects the four is the working assumption that a pathway is worth naming only if interrupting it does something.

[Metabolic checkpoint CPS1 sustains TCA anaplerosis via urea cycle in IDH-mutant gliomas](#)

Xu and colleagues in *Cancer Letters* demonstrated that IDH-mutant gliomas keep the tricarboxylic acid cycle running by routing carbon and nitrogen through a truncated urea cycle. Metabolomic profiling of two clinical cohorts found urea cycle intermediates consistently elevated in IDH-mutant tumors, and stable isotope tracing with labeled aspartate, ammonium and glutamate placed carbamoyl-phosphate synthase 1 at the head of the route running from ammonia to arginine. Blocking CPS1 cut fumarate anaplerosis, lowered 2-hydroxyglutarate both in vitro and in vivo, impaired mitochondrial respiration and suppressed growth in patient-derived organoids. The result reframes 2-HG accumulation as a state the tumor must actively support rather than a passive consequence of the mutation, and it names an enzyme whose

inhibition lowers the oncometabolite and the tumor burden at once.

[Spermine oxidase promotes oxidative stress during islet inflammation](#)

Checkcinco and colleagues in the *Journal of Biological Chemistry* reported that spermine oxidase is the polyamine enzyme responsible for generating reactive oxygen species during islet inflammation. Proinflammatory cytokines induced Smox but not Paox in mouse and human islets, and in a zebrafish model with beta-cell-specific ROS induction, smox knockdown lowered intra-islet ROS and reduced macrophage recruitment. Metabolomics of the knockdown embryos showed no change in spermine or spermidine but an accumulation of acetylated polyamines, consistent with flux rerouted through acetylation rather than oxidation. Transcriptional profiling separated the baseline consequences of Smox loss, which fell on cell cycle and RNA processing, from its effects during injury, which reached stress, translational and immune programs. Polyamine catabolism therefore looks modifiable in beta-cell injury without the confound of depleting the polyamine pool itself.

[Hippuric acid contributes to NK-cell activation with dependence on TLR2 in chronic hepatitis B complicated by MASLD](#)

Zhang and colleagues in *iScience* found that hippuric acid, enriched in the plasma of patients with chronic hepatitis B and metabolic dysfunction-associated steatotic liver disease, contributes to natural killer cell activation through TLR2. Patients with the combined condition carried higher peripheral NK cell frequencies and inflammatory effector gene signatures, and the proportion of TLR2-expressing NK cells tracked with metabolic parameters and liver stiffness. Metabolic-stress modeling in vitro raised TLR2 expression and increased NK cell cytokine output, while hippuric acid itself promoted activation in a manner partly reversed by TLR2 blockade. Co-culture of hippuric acid-stimulated NK cells with LX-2 cells raised activation readouts that were again attenuated when TLR2 was blocked. The study puts forward a specific metabolite as the link between metabolic dysfunction and the accelerated fibrosis seen when steatotic liver disease is superimposed on hepatitis B.

[Hyperprogression Upon Cemiplimab Alone or With Short Course Chemotherapy in PD-L1 \$\geq\$ 50% Non-small Cell Lung Cancer: A Biomarker Guided Multicenter International Phase 2 Trial-HYPERBOLIC Study](#)

Mollica and colleagues in *Clinical Lung Cancer* reported that HYPERBOLIC, a randomized phase 2 trial selecting patients by a cellular biomarker, will test whether three cycles of platinum chemotherapy added to first-line cemiplimab prevent hyperprogression. Enrollment is restricted to stage IV non-small cell lung cancer with PD-L1 at or above 50 percent and circulating CD10-low-density neutrophils at or above 30.5 percent, the threshold previously associated with hyperprogressive disease. The primary endpoint combines hyperprogression, defined by tumor growth rate at the week 7 scan, with early death occurring before any radiological assessment. A translational platform runs alongside the clinical endpoints and includes spatial transcriptomics, single-cell sequencing of PBMCs, circulating free DNA and plasma factors, and longitudinal saliva and stool microbiome genomics and metabolomics. Trials that pre-specify metabolic and microbial readouts at this depth remain uncommon, and

the design is a useful template for testing whether treatment escalation can be assigned by biomarker instead of after failure.

Microbial Communities and Host Metabolic Phenotypes

Microbial communities are easy to correlate with host physiology and hard to pin to a mechanism, and the papers in this section differ mainly in how far past correlation they manage to push. The settings run from a mouse model of circadian disruption to a broiler feeding trial, a cohort of young adults with periodontitis and a birth cohort followed to two years, but the analytical shape is constant: sequence the community, profile the metabolites, look for the compound carrying the effect. Bile acids, short branched-chain fatty acids and indole derivatives keep surfacing as the currency, which reflects their biological reach and also the practical fact that they survive sample handling well enough to be measured reliably. The strongest of these studies name a metabolite and then perturb it, as with chenodeoxycholic acid supplementation canceling the benefit of exercise. The others end at a list of differential features and a correlation matrix, a limitation the authors of the human studies state plainly. Read together they mark where this field currently sits, with mechanistic claims available in animal models and mediation analysis standing in for causality in human cohorts.

Efficacy of Physical Exercise in Ameliorating Circadian Rhythm Disruption-Related Intestinal Inflammation: A Benefit Correlated with Reduced Chenodeoxycholic Acid

Du and colleagues in *Cells* showed that the anti-inflammatory benefit of exercise in circadian-disrupted mice tracks with a fall in chenodeoxycholic acid. Two-sample bidirectional Mendelian randomization first supported a route from physical activity through gut microbiota to intestinal inflammation, after which the prediction was tested in mice subjected to circadian rhythm disruption. Exercising animals showed less intestinal injury and inflammation, and oral chenodeoxycholic acid was sufficient to blunt that protection. Transcriptomic, 16S rRNA and fecal metabolome analyses linked the effect to restored intestinal clock gene expression and to the genus *Prevotella*. The supplementation arm is what lifts this above the familiar correlative exercise study, since it places a named bile acid in the causal path rather than alongside it.

Replacement of soybean meal with water-soluble corn protein improves early growth performance of broilers via regulating intestinal microbiota and metabolites

Guo and colleagues in *Poultry Science* reported that replacing five percent of dietary soybean meal with water-soluble corn protein improves early broiler growth, while the same substitution with cottonseed protein does the opposite. Birds on the corn protein diet were heavier at day 14, had better duodenal villus morphology and lower digesta pH and kept barrier function intact, whereas cottonseed protein suppressed growth and reduced goblet cell density. Cecal sequencing found no shift in alpha diversity but a restructured community, with *Clostridium*, *Romboutsia* and *Anaerofilum* enriched and *Anaerobutyricum* reduced. Metabolomics identified protein digestion and absorption as the enriched pathway, with isovaleric acid accumulating and harmful indole metabolites falling, and isovaleric acid correlating with villus height, body weight and average daily gain. Running two alternative protein sources in the same trial is what makes the result interpretable, since it separates the effect of removing soybean meal

from the effect of whatever replaces it.

Periodontitis in a Large Cohort of Young Chinese Adults: Associated Factors and Salivary Microbiome-Metabolome Profiles

Huang and colleagues in the *International Dental Journal* found that periodontitis affected 25 percent of 2888 Chinese adults aged 18 to 35, with salivary microbial and metabolic differences accompanying the clinical diagnosis. Logistic regression associated the condition with marital status, suboptimal health, adverse childhood experiences, smoking and alcohol use, while longer brushing duration was negatively correlated. Salivary community richness and composition differed between groups, with Fusobacteriota enriched in cases. Untargeted metabolomics returned 267 differential metabolites, mainly lipids and amino acids, with nucleotide metabolism among the enriched pathways and Fusobacteriota inversely correlated with 5-phosphoribosyl-4-carboxy-5-aminoimidazole. The authors flag that the omics work was performed on a small matched subgroup from a single center, the right caveat for a study whose epidemiological arm is far better powered than its molecular one.

Antibiotic mixture exposure in meconium affects child neurodevelopment via altering early-life gut microbiome and metabolome

Zhou and colleagues in *Environmental Pollution* reported that antibiotic burden measured directly in meconium is associated with lower neurodevelopmental scores through the first two years of life. Working with 300 mother-infant pairs from the Shanghai Maternal-Child Pairs Cohort, the group quantified 18 antibiotics by HPLC and found chlortetracycline, penicillin and chloramphenicol to dominate exposure. Each interquartile range increase in burden corresponded to a lower total Ages and Stages score at six months across all five developmental domains, and to greater odds of falling into the low-scoring trajectory group. High-dimensional mediation analysis of six-month fecal samples nominated *Lactobacillus* and 2-(14,15-epoxyeicosatrienoyl) glycerol as candidate intermediates. Measuring internal fetal exposure rather than relying on prescription records is the methodological advance here, and it moves a well-worn association onto firmer ground even while the mediation results stay hypothesis-generating.

Bioactive Compounds and Mechanism-Led Pharmacology

Natural product research has a recurring problem: the material works in a model, and the account of why tends to arrive as a list of enriched pathways rather than an argument. The four studies gathered here confront that problem with much the same toolkit, pairing network pharmacology or transcriptomics with untargeted metabolomics and then attempting to close the loop with a direct assay. Their subjects have little in common, a multi-herb Chinese formula for colitis, a single flavonoid applied to diabetic fibroblasts, a freeze-dried leech preparation for hyperlipidemia and a terpene tested against a soil-borne crop pathogen, yet the reasoning is shared. Where they succeed it is because a named protein or a named metabolic step is measured after the intervention rather than inferred from enrichment statistics. Where they remain provisional the framing is candid, with the diabetic wound study presenting its target assignment as a hypothesis rather than a conclusion. This methodological convergence is

worth watching, since it is becoming the default template for mechanism claims in the literature and its weaknesses travel as widely as its strengths.

[Multi-omics-driven network pharmacology and experimental validation elucidate the therapeutic mechanism Bupi Yichang Pill in ulcerative colitis via the PI3K/Akt/IKK/NF- \$\kappa\$ B signaling pathway](#)

Zou and colleagues in the *Journal of Ethnopharmacology* demonstrated that Bupi Yichang Pill protects against dextran sulfate sodium colitis by suppressing PI3K/Akt/IKK/NF- κ B signaling. UHPLC-HRMS identified 115 constituents, of which kaempferol, liquiritin, quercetin, berberine, paeoniflorin, cryptopine, perlolyrine and glabrone were prioritized by network pharmacology and docking against IL6, TNF, AKT1 and PTGS2. Treated mice lost less weight and retained colon length, with lower TNF- α , IL-1 β and IL-6 and higher IL-10, while 16S sequencing, untargeted metabolomics and RNA-seq together showed restored microbial composition and improved bile acid and amino acid metabolism. Western blotting and immunofluorescence confirmed reduced phosphorylation of PI3K, Akt, IKK and NF- κ B p65 in colonic tissue and in LPS-stimulated RAW264.7 macrophages. The value of the work lies less in the pathway, which is well traveled in colitis research, than in tying a defined constituent set to it within a single experimental series.

[Integrated bioinformatics and experimental validation reveal Luteolin targets the PI3K/AKT/NRF2 Axis in diabetic wound healing](#)

Pandey and colleagues in *International Immunopharmacology* proposed that luteolin acts on diabetic wound healing through PIK3R1. Differential expression analysis across three public diabetic wound datasets yielded 520 shared genes, and target prediction with network construction and 200 ns molecular dynamics converged on PIK3R1, which bound at -9.62 kcal/mol against weaker affinities for mTOR and AKT1. In HS27 dermal fibroblasts, luteolin at 25 μ g/mL raised viability to 130 percent, cut intracellular ROS and closed scratch wounds roughly 40 percent faster, with blots showing higher p-PI3K, AKT, NRF2 and Bcl-2 alongside lower GSK-3 β and Bax. LC-MS/MS metabolomics identified responsive metabolites including L-leucine and sphingomyelin species already tied to PI3K/AKT signaling. The authors present the target assignment as a hypothesis supported by computational, cellular and metabolomic evidence rather than as settled, which is the appropriate reading given that PIK3R1 itself was never genetically manipulated.

[Freeze-Dried *Poecilobdella manillensis* Powder Regulates Cholesterol Homeostasis to Alleviate Hyperlipidemia](#)

Yang and colleagues in *Biomolecules* showed that freeze-dried *Poecilobdella manillensis* powder lowers lipids in high-fat-fed ApoE-null mice by acting on both arms of cholesterol handling. Eight weeks of daily oral administration reduced triglycerides, total cholesterol and LDL cholesterol while raising HDL cholesterol, limited histopathological damage in liver, kidney and heart and restored antioxidant enzyme activity. Untargeted metabolomics placed the response in choline, glycerophospholipid and arachidonic acid metabolism. The mechanism proved to be coordinated rather than single-ended, with CYP7A1 upregulated to push

cholesterol into bile acids and HMGCR and HMGCS1 downregulated to slow synthesis. The same preparation suppressed foam cell formation and lipid accumulation in ox-LDL-treated RAW264.7 macrophages, which supports a direct cellular effect alongside the systemic lipid changes.

[The antifungal activity and mechanism of action of limonene against tobacco-isolated *Fusarium oxysporum* causing tobacco root rot](#)

Yang and colleagues in *Frontiers in Plant Science* reported that limonene attacks the *Fusarium oxysporum* isolate responsible for tobacco root rot on several fronts at once. The terpene inhibited mycelial growth with an EC₅₀ of 201.2 µg/mL, repelled the fungus chemotactically at concentrations as low as 25 µg/mL and compromised membrane integrity and permeability at 100 µg/mL. Transcriptomics returned 3871 differentially expressed genes enriched in ribosome, proteasome, ER protein processing, autophagy and glyoxylate metabolism, with eight representatives verified by RT-qPCR. Metabolomics found 626 differentially accumulated metabolites, among them ortho-hydroxyphenylacetic acid, 4-methylphenol and lenticin, with enrichment in starch and sucrose, riboflavin, folate and tyrosine metabolism. The multi-target picture that emerges, spanning membrane damage, chemotaxis blockage and metabolic disturbance, argues for limonene as a botanical fungicide and is also a reminder that compounds acting this broadly are harder to optimize than single-target chemistry.

Metabolic Signatures of Cellular Injury

Metabolomics is often the first readout available when a tissue is injured by something with no obvious receptor or target, and both studies in this short section take that position. One exposes human endothelial cells to silica nanoparticles that acquire a biomolecular corona in serum, the other irradiates mouse brain and examines the hippocampus afterwards. Neither insult acts through a defined pathway, so the metabolite profile becomes the instrument for generating one, and in both cases the profile converges on oxidative stress, disturbed energy metabolism and depleted reducing capacity. That convergence is informative and also a caution, since a similar signature follows most forms of cellular damage and does not by itself separate mechanism from consequence. Both groups say directly that their conclusions require functional follow-up, which is the correct posture for work of this design. Read side by side, the two exposures share little except the shape of the metabolic response they produce.

[Dose- and time-dependent endothelial metabolic reprogramming induced by biomolecular corona-forming silica nanoparticle agglomerates](#)

Vivas and colleagues in *Toxicology in Vitro* reported that silica nanoparticle agglomerates carrying a biomolecular corona drive dose- and time-dependent metabolic reprogramming in human endothelial cells. Proton NMR metabolomics showed rising glucose consumption with extracellular accumulation of succinate and glycolytic end products, a profile consistent with greater glycolytic reliance and altered TCA-associated metabolism. Depletion of NADP⁺ and glutathione precursors alongside increased extracellular pyroglutamate pointed to disturbed redox handling and glutathione turnover, supported by direct measurement of reactive oxygen species. Falling phosphocholine metabolites, UDP-GlcNAc and creatine-phosphocreatine

indicated changes in membrane remodeling, protein glycosylation and energy homeostasis, and fluorescence microscopy showed cytoskeletal disorganization, cell shrinkage and apoptotic-like features. Using the agglomerated, corona-bearing form rather than pristine particles is the more realistic exposure scenario, and it matters for how these results should be read against the existing nanotoxicology literature.

Identification of new targets for the protection against radiation-induced brain injury through integrated dual-omics analysis

Li and colleagues in *Experimental Neurology* found that pairing transcriptomics with metabolomics in irradiated mouse hippocampus yields tractable candidate targets for radiation-induced brain injury. After 15 Gy of whole-brain X-ray exposure, behavioral testing and histopathology confirmed cognitive dysfunction and neuronal damage. Transcriptomics returned 29 differentially expressed genes, with the neuroinflammatory Pcsk9 and Ifi213 upregulated and the neuroprotective Tlx3, Irx1 and Irx5 suppressed. Metabolomics found 63 altered metabolites, including elevated markers of DNA oxidative damage and depleted branched-chain amino acids, a combination pointing toward mitochondrial dysfunction. The proposed interventions, inhibiting Pcsk9, supporting DNA repair or supplementing BCAAs, rest on correlative evidence the authors acknowledge requires functional validation, though the BCAA arm is the most directly testable of the three.

Environmental Gradients and Organismal Metabolism

Environmental applications ask metabolomics to work without the controls laboratory biology takes for granted, and these three papers show both what that buys and what it costs. A moss exposed to graded cesium concentrations, a soil bacterium degrading TNT with and without biochar, and migrating fish sampled at two points along the Yangtze span biomonitoring, remediation engineering and ecophysiology. In each the metabolite profile serves as a sensor, reporting either how much stress an organism is under or what it is doing to a contaminant. The cesium and TNT studies retain dose control and can therefore make concentration-dependent claims, while the fish study inherits the confounding that comes with sampling wild animals along a gradient where salinity, migration distance and population structure vary together. The authors of that study say as much and offer their results as a baseline rather than a finding, a restraint not universal in ecological metabolomics. Taken together the three make the case that environmental work is most convincing when the exposure itself can be quantified.

Biochar-assisted biotransformation of 2,4,6-trinitrotoluene by *Pseudomonas* sp. CMR5c T22: synergistic mechanisms and metabolic reprogramming

Dong and colleagues in *Environmental Research* showed that wood-derived biochar roughly doubles the efficiency with which a *Pseudomonas* strain transforms TNT. After screening four biochars from different waste feedstocks, the best performer raised removal from 46.2 to 88.7 percent over 48 hours at 100 mg/L and tripled the first-order rate constant. Biochar lowered aqueous TNT concentrations, relieved growth inhibition of the strain and stimulated extracellular polymeric substance secretion. Untargeted metabolomics found 330 upregulated

metabolites in the amended system, with nitrotoluene degradation and cofactor biosynthesis pathways activated, and the authors attribute the synergy to weakened exposure, stronger antioxidant metabolism, activated transformation routes and better basal metabolic supply. Complete mineralization and soil-scale validation fall outside the study, so the work stands as mechanistic groundwork for biochar-microbe remediation rather than a demonstration of field performance.

[Multi-Level Physiological and Metabolomic Responses of *Hypnum plumaeforme* Reveal Oxidative Imbalance, Photosynthetic Disruption and Metabolic Reprogramming Under Cesium Stress](#)

Sun and colleagues in *Plants* found that the moss *Hypnum plumaeforme* responds to cesium in a sharply concentration-dependent manner. Exposure at 5 mg/L produced early oxidative signaling with slight stimulation of photosynthesis, moderate stress triggered superoxide production and antioxidant activation, and 500 mg/L caused cellular deformation, photosystem II disruption, hydroxyl radical accumulation and collapse of the coordinated antioxidant and osmotic regulatory network. Untargeted LC-MS metabolomics under severe stress showed carbon metabolism inhibited, tryptophan metabolism enriched and defensive secondary metabolites accumulating, a shift of resources from growth toward defense. Oxidative biomarkers and chlorophyll fluorescence parameters both tracked the exposure gradient closely. That sensitivity is what supports the proposal of this species as a bioindicator for cesium contamination, an application with clear relevance wherever radiocesium monitoring is required.

[Tissue-specific lipidomic and metabolomic divergence in mature anadromous *Coilia nasus* along the Yangtze River migration corridor](#)

Guo and colleagues in *Comparative Biochemistry and Physiology Part D* found that muscle, not ovary, carries the clearest lipidomic signal of migratory position in mature female *Coilia nasus*. Twelve fish with anadromy confirmed by otolith Sr/Ca were sampled at an estuarine site and a freshwater mainstem site, with targeted lipids profiled in muscle, liver and ovary and untargeted metabolites in muscle. Muscle alone showed significant global differentiation, with 40 of 41 phosphatidylcholine species higher at the estuarine end and 43 of 47 acylcarnitines higher upstream, the latter pattern echoed in liver and in untargeted features. Ovary showed no detectable global divergence despite balanced ovarian stage composition and matched body size and gonadosomatic index, which suggests reproductive tissue is buffered against the recent energetic history muscle records. With twelve animals and covarying salinity, distance and population structure, the authors present this as a hypothesis-generating baseline, and the tissue contrast is the part most likely to hold.

Fermentation, Storage and Flavor Chemistry

Food metabolomics answers to a constraint the rest of the field does not share, since its endpoint is what a person tastes or how long a product lasts. The three studies here work at different stages of that chain: a nine-day solid-state fermentation of two Andean crops, three years of ambient storage of a dark tea, and a single postharvest treatment applied to

pineapple. Each connects a compositional measurement to a property that can be perceived or sold, whether texture and protein hydrolysis, aroma shifting from sweet toward woody, or delayed browning and softening. The tea work is the most direct about this, running molecular sensory analysis and metabolomics on the same samples so that the compounds and the perceived change are reported as one result. What makes the area productive at present is that the outcome variable is unambiguous, which pushes the analytical work toward prediction rather than description. The practical consequence is that storage and processing conditions become adjustable parameters rather than inherited tradition.

[Tempeh-type fermentation kinetics of tarwi \(*Lupinus mutabilis*\) and red quinoa \(*Chenopodium quinoa*\) with *Rhizopus oligosporus*: effects on texture, metabolite profile and nutritional potential](#)

Alarcon and colleagues in *Frontiers in Nutrition* reported that substrate composition rather than the fungus determines how tempeh-type fermentation proceeds in two Andean crops. *Rhizopus oligosporus* growth on tarwi and red quinoa over nine days followed Gompertz kinetics, with enzyme production fitting the Luedeking-Piret model and behaving as growth-associated. Tarwi gave the better fit to both models and stronger proteolytic activity, quinoa was predominantly amylolytic, and texture measurements put the optimum for both substrates between 48 and 72 hours. Metabolomics identified 448 compounds that clustered by substrate, with quinoa tempeh characterized by carbohydrate metabolism, nucleotide turnover and nucleoside derivatives, and tarwi tempeh by amino acid-related compounds consistent with intensified proteolysis. For groups working on underused legumes and pseudocereals the kinetic parameters are the transferable part, since they set the fermentation window without the metabolomics having to be repeated.

[Effects of storage environments on flavor formation in Ancha tea](#)

Yang and colleagues in *LWT - Food Science and Technology* showed that three years of storage in Beijing, Shanghai or Foshan produces three distinguishable flavor profiles in Ancha dark tea. As temperature and humidity rose across the three sites, aroma moved from sweet and roasted toward stale and woody, a shift traced to changing proportions among 13 key aroma compounds. Bitterness and astringency fell under warmer and more humid storage, following declines in catechin-3-O-gallate, epigallocatechin gallate, dihydroquercetin, epicatechin and epigallocatechin. Combining molecular sensory analysis with metabolomics on the same material is what allows the sensory shift and the underlying chemistry to be reported as a single result. The finding gives producers a basis for selecting storage conditions deliberately instead of treating natural aging as one uncontrolled process.

[The impact of ultraviolet-C and ozone treatment on the pineapple fruit quality and the critical regulating factors identification through transcriptome analysis](#)

Qiu and colleagues in *Food Research International* found that a 16-minute combined UV-C and ozone treatment delays pineapple senescence and browning without the chilling injury or residue risk of conventional approaches. The treatment suppressed hydrogen peroxide, superoxide and malondialdehyde accumulation while raising superoxide dismutase and

catalase activity, ascorbic acid and total antioxidant capacity. It also inhibited the browning enzymes peroxidase and polyphenol oxidase along with polygalacturonase and pectate lyase, preserving cell wall integrity and slowing softening. Metabolomics showed reshaped polyphenol accumulation, with dihydrobenzoic acid pentose, pelargonidin-3-O-(6-O-malonyl) glucoside and other phenolics elevated, while transcriptomics implicated plant-pathogen interaction, MAPK signaling and starch and sucrose metabolism. Weighted gene co-expression network analysis identified WRKY and bHLH transcription factors as hub regulators, which gives the hormetic response a plausible coordinating layer instead of leaving it as a set of enzyme measurements.

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Metabolomist Podcast



New episode

Standards for biomarker development and translational tools

” On what success means for the metabolomics community: “At the end of the day, I would love to hear a non-metabolomics person say ‘Metabolomic data? Sure, I’ll integrate it into my pipeline. It’s pretty streamlined now’. That is true success.”

– Ewy Mathé

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[Metabolomics Events](#)

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MSACL 2026

16th Annual Conference & Exhibits

October 4 - 9, 2026

Venue: Montreal, Canada

MSACL's mission is to support the community in translating pre-clinical research to clinical patient care. The conference is focused on providing a forum of interaction for participants in all stages of the development, advancement and use of analytical tools, including data analytics, in the clinic to improve patient care. Although the group primarily focuses on mass spectrometry, presentations and discussion on other platforms are welcome.

There were 628 attendees for MSACL 2025. 600-700 attendees are expected for MSACL 2026.

[Check for more details](#)

MANA SODAMeet

October 13, 2026

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](#)

Australian Lipid Meeting 7 & 5th International Lipidomics Society Conference

October 18 - 21, 2026

Venue: Perth, Western Australia

This special event unites two major gatherings in lipid research, bringing together researchers, scientists, clinicians and industry leaders from around the world to share discoveries, promote collaborations and shape the future of lipidomics.

Participants can expect a diverse range of topics, spanning:

- Microbial & Plant Lipids in Health and Biotechnology
- Lipid Imaging & Single-Cell Lipidomics
- AI, Computational Tools & Data Standards for Lipidomics
- Lipids in Health and Disease
- Advancements in Lipidomic Technologies
- Translational and Precision Lipidomics
- Clinical Lipidomics: From Pre-analytics to Cohort Studies
- Lipid Particles and Delivery Systems

Whether you are a biochemist, clinician, analytical chemist, nutritionist or cell biologist, this conference will provide a forum to engage with the global lipid research community.

[Visit website for more details](#)

Introduction to Applying LC-MS in Untargeted Metabolomics

October 26 - 28, 2026

Venue: Liverpool, United Kingdom

The course introduces attendees to the metabolomics workflow and applying LC-MS in metabolomics. It is designed to develop knowledge, skills and experience in small group session with hands-on experience in sample preparation, LC-MS data acquisition (MS and MS/MS), data analysis and metabolite annotation and identification. The course is aimed at individuals with minimal knowledge of LC-MS based metabolomics and only a small number of attendees are accepted on each course to maximise opportunities for laboratory experience and interaction with instructors.

[Registration and additional event details](#)

X Symposium of the Mexican Proteomics Society

November 09 - 13, 2026

Venue: Mexico City

The Mexican Proteomics Society brings together national and international experts in Omics Sciences at the X symposium, “MultiOmics and Integrative Biology: Advances and Applications” hosted at Instituto Politécnico Nacional – ESIQIE, in Mexico City. The symposium includes workshops in proteomics (AlphaDIA, IA & MS), metabolomics (LC-MS), transcriptomics, and spatial MS, as well as the Industrial forum “Omics beyond academia: entrepreneurship and professional fields”. Check out the program website for workshops, offers, awards, speakers, and more.

[Visit website for more details](#)

Introduction to Applying GC-MS in Untargeted Metabolomics

February 2 - 4, 2027

Venue: Liverpool, England, United Kingdom

The course provides an introduction to metabolomics, experimental design and the application of GC-MS in untargeted metabolomics, sample preparation, hands-on data acquisition using the LECO Pegasus BT 4D GC x GC-ToF MS, data processing and analysis. The course is delivered using a combination of lectures, laboratory sessions and computer workshops to develop your knowledge, skills and confidence to apply GC-MS in your own research. The course is aimed at individuals with minimal knowledge of GC-MS based metabolomics, and only a small number of attendees are accepted on each course to maximise opportunities for laboratory experience and interaction with instructors.

[Registration and event details](#)

2027 Metabolomics and Human Health Gordon

Research Conference and Gordon Research Seminar

February 27 - March 5, 2027

Venue: Liverpool, United Kingdom

The 2027 Metabolomics and Human Health Gordon Research Conference and affiliated Gordon Research Seminar will bring together scientists across metabolomics, exposomics, One Health, nutrition, environmental health, and human disease. The GRS is organized by and for early-career researchers, including students and postdoctoral fellows, while the GRC provides opportunities to engage with world leaders in metabolic research and build collaborations across disciplines. The 2027 GRC theme is “One Health, the Exposome, and Lifecourse Health and Disease,” and the GRS theme is “Decoding Metabolism at the Health-Disease-Environment Interface Through Emerging Technologies.”

Gordon Research Conference

Gordon Research Seminar

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Postdoctoral Associate in Microbial Metabolomics	Yale School of Public Health	New Haven, CT, US	MANA
ARISE2 Fellowship program	ARISE Career Accelerator for Research Infrastructure Scientists	Six EMBL sites	European Molecular Biology Laboratory (EMBL)

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