|MC:SUBJECT|

MetaboNews

This month in metabolomics

December, 2024
Vol 14, Issue 12

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

In This Issue

This Months Spotlight Article:

A Comprehensive LC–MS Metabolomics Assay for Quantitative Analysis of Serum and Plasma

|MC:SUBJECT|

Metabolomics Society News

The Metabolomics Society is an independent, non-profit organization dedicated to promoting the growth, use, and understanding of metabolomics in the life sciences.

General Enquiries

info@metabolomicssociety.org

Conference Corner

The Metabolomics Society along with the Scientific Organizing Committee are delighted to extend this invitation to you to attend Metabolomics 2025, the 21st Annual Conference of the Metabolomics Society, in Prague, Czech Republic. The conference will be held June 22-26, 2025 at the Prague Congress Centre.

Metabolomics 2025
Prague Congress Centre

June 22 - 26
www.metabolomics2025.org

The website will be continually updated, check back often for updates.
Follow **@MetabolomicsSoc** on X to stay current and meet new peers before the event!

Open Call for Workshop Proposals – Deadline Extended!

The conference workshops provide a terrific venue to discuss a wide range of important topics and practical aspects of metabolomics and may include hands-on learning opportunities.

You can submit your workshop application online. The deadline for workshop proposals has been extended to January 10.

Abstract Submission

Get ready to submit your abstract in the new year! Abstract submission will open in January, with a deadline of **March 6 for oral abstracts** and May 15 for poster abstracts.

Conference registration will also be available in January. Stay tuned for announcements.

Calling all Sponsors!

The Sponsorship Brochure is available for Metabolomics 2025.

As we approach the conference, we look forward to partnering with your organization to continue the success of bringing together all the major international organizations involved in human, plant, microbial, animal, and environmental metabolomics.

We have a variety of packages available to position your brand and product at the forefront of the scientific community. Opportunities are limited and available on a first-come first-served basis.

Your support is extremely important to the success of the meeting, helping to keep registration costs down, which allows more of our younger scientists to attend. We look forward to partnering with you for Metabolomics 2025!

Members' Corner

Board of Directors

Message from Warwick (Rick) Dunn, President

Dear Metabolomics Society Members and metabolomics friends,

It is that time of year for some of us when we have the urge for mince pies, enjoy time with the family and hopefully some exercise to burn off the excessive Christmas dinner. For many of us in the Northern hemisphere all of this can be indoors, but I am always reminded by friends in Australia that Christmas Day is spent on the beach. Of course, for some of us it is just time for a break from work and to spend precious time with family and friends.

At the end of every calendar year, we start to reflect on the past and future. 2024 has been a fantastic year for the Society with a successful conference in Osaka with great science being discussed in the lecture halls, poster sessions and beyond. Some other developments which I hope all of you will agree with and applaud are ready for announcement in 2025, so watch this space. Personally, I am looking forward to Metabolomics 2025 in Prague in June 2025, again for the great science but also to see old and new friends and to revisit this great city which is one of my favourites in Europe (a walk over Charles Bridge is a must for the to do list). Planning is well under way for the conference with all plenary and keynote speakers now being finalized and as I write this as the deadline for workshops is closing. I have already seen a small number of the workshop proposals which I am involved with and they always inspire me – the conference starts on Sunday lunchtime.

As a Board of Directors we are driving new ideas forward to help support the metabolomics community and ensure we work for equality and diversity. We will be announcing a new award in 2025 and are looking at diversity across the society. More to follow.

Whatever you are doing in late December and early January, enjoy the time you have with family and friends, relax and recharge your batteries … and start thinking of your abstract for Metabolomics 2025.

All the very best,

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

Call for Nominations! Society Honorary Fellows and Career Medals

2025 Honorary Fellows of the Metabolomics Society

An Honorary Fellowship is a significant lifetime award granted by the Metabolomics

Society to exceptional members of our community. Commissioned in 2012, and with up to two awards each year, the Board of Directors welcomes nominations from Members for these Fellowships, with a closing date of January 31, 2025.

See https://metabolomicssociety.org/awards/honorary-fellowships/ for further details. The Board will consider only complete nomination packages, and these consist of the four items mentioned on the web page.

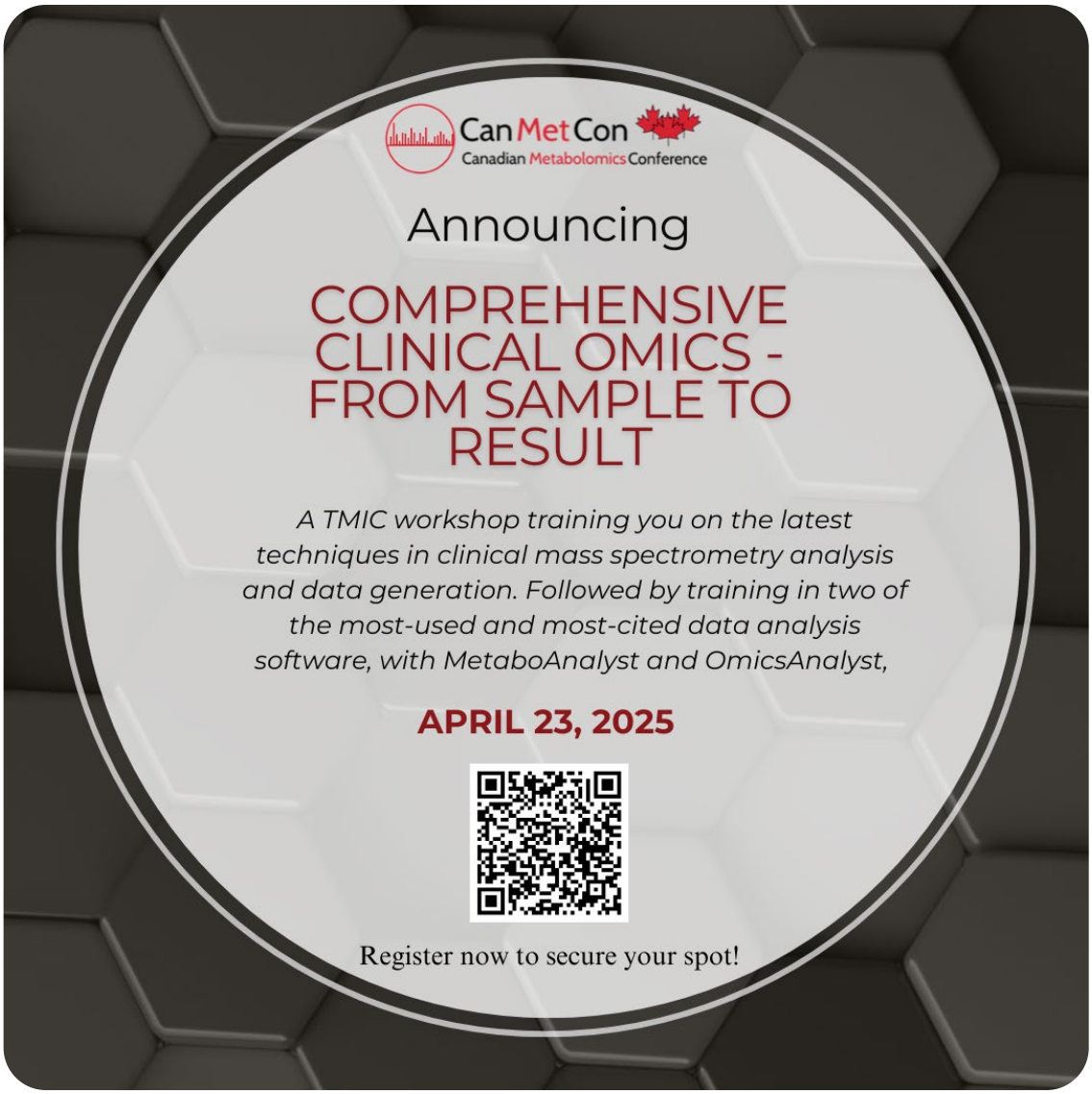
Metabolomics Society Career Medals

We are excited to continue the Society awards which seek to recognize the outstanding contributions of individuals to the field of metabolomics through the presentation of up to two Metabolomics Society Medals. These awards are open to all Society members who meet the eligibility criteria. While research contributions are of primary importance, other contributions, including the teaching of metabolomics and/or service to the field or the society will also be strongly considered. There will be up to two medals awarded each year in the following categories:

- The Metabolomics Society Medal is for mid-career members of the Society and is open to those members who have been awarded a PhD 10-15 years prior to the closing date for nominations in each round. In 2025 this means your PHD must have been awarded between 2009 and 2015.
- The President's Award recognizes outstanding achievements in metabolomics. It is available for Society members who have been awarded a PhD no more than 5-10 years prior to the closing date for nominations in each round. In 2025 this means your PHD must have been awarded between 2014 and 2019.
- Medal winners will have the opportunity to give a keynote presentation during the Society conference the same year they receive the award. Conference registration, and reasonable travel & hotel expenses will be reimbursed by the Society.

See https://metabolomicssociety.org/awards/career-medals/ for further details about Society career medals.

The application closing date is **January 31, 2025.**



Announcing **"Comprehensive Clinical Omics - From Sample to Result"**, a TMIC workshop from Dr. Christoph Borchers and Dr. Jianguo (Jeff) Xia on **April 23, 2025** at **CanMetCon 2025**.

Workshop Part 1: Attendees will have the opportunity to train at the Warren Y. Soper Clinical Proteomics Centre, one of Canada's only certified clinical metabolomics laboratories, on the latest techniques in clinical mass spectrometry analysis and data generation.

Workshop Part 2: Participants will learn how to explore this dataset and generate diagnostic insights, with MetaboAnalyst and OmicsAnalyst, two of the most-used and most-cited data analysis tools in metabolomics and multi-omics.

There are limited spaces available for each workshop register today to secure your spot!

Scan the QR Code or follow the link for registration details: Registration Link

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Early-Career Members Network (EMN)

Online Presence

The EMN MetSoc have recently expanded their online presence to BlueSky, and have already brought together 207 followers from across the metabolomics research community! This new platform will provide an exciting space to share insights, discuss the latest developments, and connect with colleagues passionate about advancing metabolomics. If you haven't joined us yet, follow along to stay updated on all things #earlycareer and #metabolomics.

ECR Voices 2024-2025

The EMN "ECR Voices" initiative to spotlight early-career researchers (PhD students, Postdocs, Young Investigators, etc.) on our Twitter/X account is continuing through 2024-2025! You can check out an example here: (https://x.com/EMN_MetSoc/status/1704787637591265456?s=20). We encourage everyone to participate! You can easily create your own ECR Voice slide using this link:**(**https://docs.google.com/presentation/d/1H43FIlp3gmtJMUYS6r-2XVd460N8PjBn/edit#slide=id.p15**).**

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

EMN Webinars 2024-2025

November Webinar

The EMN committee extends its sincere gratitude to Dr. Álvaro Fernández-Ochoa from the Bioactive Ingredients AGR-274 research group, Analytical Chemistry Department, Faculty of Science, University of Granada, Spain, for the insightful webinar on 28th November 2024 entitled "Untargeted Metabolomics Approaches in Nutritional Intervention Studies: Uncovering Insights into Bioactive Compounds". The webinar recording is now available on the MetSoc website and youtube channel:

https://metabolomicssociety.org/resources/multimedia/emn-webinars-2024/.

December Webinar

Additionally, the EMN committee expresses its deepest appreciation to Dr. Daniel Petras, assistant professor from the University of California, Riverside and the University of Tuebingen, and Dr. Paolo Stincone, a postdoctoral researcher from the University of Tuebingen who delivered a webinar on 11th December 2024 entitled: “A Functional Metabolomics Toolbox for Uncovering Small Molecule Dynamics in Microbial Communities”. The webinar recording will be available soon on the MetSoc website and you tube channel.

January Webinar

The first webinar of the new year will be hosted by Prof. Dr. Wout Bittremieux, assistant professor in the Adrem Data Lab at the University of Antwerp, Belgium, who will deliver a webinar on Wednesday, 22nd January 2024 15:00 UTC (16:00 CET) entitled: “Learning From Repository-Scale Untargeted Metabolomics Data”. Registration is available via the following Zoom link: https://zoom.us/webinar/register/WN_DArqO2CGRoGFjDMxAPV7Bw.

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

Task Groups Corner

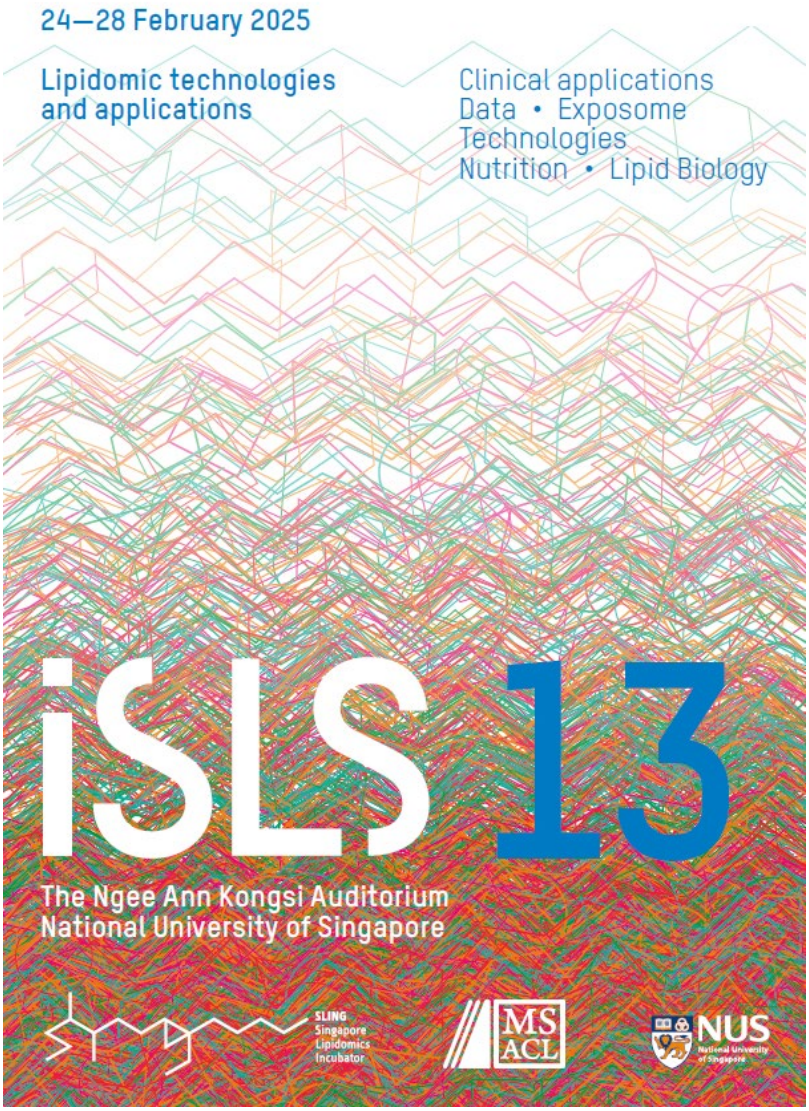
Lipidomics Task Group (LipidMet)

The 13th International Singapore Lipid Symposium (**iSLS13**) will take place in collaboration with Mass Spectrometry & Advances in the Clinical Lab (**MSACL**), hosted on-site at the National University of Singapore, The Ngee Ann Kongsi Auditorium, from **February 24–28, 2025**.

MSACL provides a forum for interaction and learning for participants from all stages of the development, advancement and use of analytical tools, including data analytics. While primarily addressing clinical mass spectrometry to improve patient care, also

research and service labs striving for highest quality will benefit from the workshops offered. This collaboration marks MSACL's first footprint in Asia.

In combination with the premier workshop series, this year's iSLS program features an excellent lineup of speakers with world leading expertise in metabolomics and lipidomics sciences. Key themes across the joint events are: exposome in health and analysis; nutrition science; lipidomics and biology; precision medicine; mass spectrometry technologies; metabolomics; standardisation in research; and data processing. Early registration is encouraged through this link: https://sling.sg/news-events/isls/



International Affiliates' Corner

Réseau Français de Métabolomique et Fluxomique (RFMF)

Visit http://www.rfmf.fr/

Next W4E Workshop in May 2025 in Rouen, France

Save the date! Analyze your data with Galaxy and the Workflow4metabolomics infrastructure! The next Workflow4Experimenters session (W4E2025) will take place in May 2025. During this one-week course (entirely in English), you will learn how to use the W4M infrastructure and analyze your own LC-MS, GC-MS, or NMR data. For this new session, the format changes:

- From April, 28th to 30th: online theoretical sessions (methods and tools).
- From May,12th to 16th: tutoring on your own data, PBS Laboratory Rouen (France, close to Paris). Online sessions are reserved for participants who attend the on-site session.

Details available here.

Invited speaker: Ultra-high resolution mass spectrometry and metabolomics, Hélène Lavanant (COBRA, Univ Rouen) & Isabelle Schmitz (PBS, CNRS, Rouen).

Scientific committee: C. Delporte (ULB, Bruxelles), C. Dalle (U.DAB IRBA, Brétigny-sur-Orge), Y. Guitton & J. Saint Vanne (Laberca INRAE, Nantes), C. Joly & M. Pétéra (PFEM INRAE, Clermont-Ferrand), G. Le Corguillé (Abims, Roscoff), B. Diémé (PFEM Université Clermont Auvergne), F. Souard (ULB, Bruxelles & Université de Grenoble), C. Canlet, M. Tremblay-Franco (Toxalim INRAE, Toulouse), I. Schmitz (PBS, CNRS, Rouen), S. Chéreau (INRAE, Rennes), H. Hecht (RECETOX, Brno), R. Weber (University of Birmingham), S. Dechaumet (CEA, Saclay).

Registration: https://sondages.inrae.fr/index.php/425432

Contact: workflow4metabolomics@proton.me

Sponsor: W4M is jointly developed and maintained by the French Bioinformatics

Infrastructure (IFB, Elixir) and the French Infrastructure for Metabolomics and Fluxomics (MetaboHUB).

Back to top

Spotlight Article

A Comprehensive LC–MS Metabolomics Assay for Quantitative Analysis of Serum and Plasma

Why was MEGA Developed?

The researchers of this publication recognized the distinction between the ability to analyze a large number of compounds through targeted metabolomics and untargeted metabolomics. Where untargeted metabolomics is more popular due to its broad metabolites coverage, low cost, and the ability to discover compounds which you may not expect. Targeted metabolomics strength is its ability to measure a predetermined and limited number of metabolites. Compared to the untageted method they are absolutely quantitative and well suited for high throughput studies.

In an effort to expand the coverage and improve accuracy of metabolite quantification the team decided to develop a comprehensive liquid chromatography–tandem mass spectrometry (LC–MS/MS) assay that could measure more than 700 metabolites in serum or plasma.

The Method

The MEGA assay employs an innovative combination of techniques to achieve high accuracy and throughput. These include:

- Chemical Derivatization: This step enhances the detection of metabolites during analysis.
- Reverse-Phase Liquid Chromatography–Tandem Mass Spectrometry (LC–MS/MS): This technique separates and identifies metabolites with high precision.
- Direct Flow Injection MS: Used in both positive and negative ionization modes for broader metabolite coverage.

- Multiple Reaction Monitoring (MRM): Combined with isotopic standards and multi-point calibration curves, this ensures the absolute quantification of targeted metabolites.
- 96-Well Plate Format: The assay is adapted for automated, high-throughput analysis, streamlining the workflow for large-scale studies.

The Results

The MEGA assay has demonstrated remarkable performance, with the capability to detect and quantify 721 metabolites across 20 diverse classes. These include amino acids, organic acids, biogenic amines, nucleobases, and a variety of lipids. Key highlights include:

- Sensitivity: Limits of detection range from 1.4 nM to 10 mM.
- Accuracy: Recovery rates are between 80% and 120%, with quantitative precision within 20%.
- Validation: When tested against the NIST® SRM® 1950 plasma standard, metabolite concentrations were found to be within 15% of NMR-quantified levels.

Conclusions

The MEGA Assay has been used to analyze more than 3000 serum/plasma samples at the Wishart Node, The Metabolomics Innovation Centre, demonstrating that it can be successfully used in a clinical metabolomics/exposomics study.

These new developments allow the MEGA assay to offer a comprehensive, high-throughput, and quantitative solution for metabolomics research. Its affordability and scalability make it a valuable tool for large-scale clinical studies, advancing our understanding of metabolite roles in health and disease.

For more detailed information, please refer to the full article: Read the Publication Here**.**

Looking Ahead

The MetaboNews Team is thrilled to announce that starting January 2025, our newsletter

will introduce a brand-new section: ***Perspectives*.** This exciting addition will feature exclusive insights from leading researchers in the field of metabolomics. Look forward to fresh ideas and unique viewpoints, alongside our regular *MetaboInterviews* and *Spotlight Articles*.

Back to top

MetaboReads

As 2024 draws to a close, it's worth celebrating a fantastic year in our field. This year's research has underscored the critical role of metabolomics in advancing our understanding of complex biological systems and its potential to transform healthcare and environmental science.This year has also seen a surge in multi-omics studies, which only reinforces the need for ongoing development of our collective bioinformatic infrastructure. The team here at MetaboNews is looking forward to seeing what new discoveries are to come in 2025. Happy holidays, and best wishes in the new year!

- The MetaboNews Team

The Metabolome and the Gut Microbiome

These four articles highlight how the gut microbiome and related microbial communities critically influence health, disease, and adaptation. From small vessel disease to long COVID interventions, from modulating obese and lean microbiomes to adjusting uric acid metabolism at high altitude, these investigations underscore how combined multi-omic analyses can pinpoint key microbial and metabolic links in various physiological states.

Characterizing the role of the microbiota-gut-brain axis in cerebral small vessel disease: An integrative multi-omics study

Song and colleagues in Neuroimage found that both gut microbial composition and fecal/blood metabolites differ significantly between CSVD patients and healthy controls. They performed multi-stage correlation analyses that tied these altered microbes and metabolites to neuroimaging measures of white matter integrity and global structural network topology. Their results showed that certain amino acid–related metabolic pathways were linked to cognitive and emotional statuses. This suggests that gut dysbiosis and altered metabolites play a role in the pathophysiology of CSVD. These findings open up the possibility of microbiota-targeted therapies to mitigate disease progression.

Beetroot juice intake positively influenced gut microbiota and inflammation but failed to improve functional outcomes in adults with long COVID: A pilot randomized controlled trial

Calvani and colleagues in Clinical Nutrition showed that two weeks of beetroot juice supplementation significantly altered gut microbial composition and inflammatory markers in long COVID participants. Although certain “beneficial” bacterial species increased in abundance, the study did not observe improvements in fatigue resistance or other functional parameters compared with placebo. The investigators noted higher levels of some inflammation-related cytokines, demonstrating that beetroot juice may have complex immunomodulatory effects. These results underscore the challenge in translating microbiota shifts into immediate clinical benefits. Further research is needed to optimize dosing and duration for long COVID recovery strategies.

Tailored impact of dietary fibers on gut microbiota: a multi-omics comparison on the lean and obese microbial communities

Dell’Olio and colleagues in Microbiome found that different apple-derived fibers, particularly pectin, differentially shaped obese versus lean gut microbiota in an in vitro system. Using metagenomics and metabolomics, they observed a reduction in potentially pathogenic species and an enrichment of beneficial bacteria such as Akkermansia in obese microbiomes when exposed to apple pectin. Their results also indicated altered production of short-chain fatty acids and indole metabolites, which are considered beneficial for metabolic health. This research suggests that selecting specific dietary fibers could serve as a personalized intervention strategy for metabolic disorders. It further underscores the potency of multi-omics approaches to unravel diet–microbiota interactions.

Rewiring of Uric Acid Metabolism in the Intestine Promotes High-Altitude Hypoxia Adaptation in Humans

Su and colleagues in Molecular Biology and Evolution showed that short- and long-term high-altitude exposure results in significantly decreased intestinal uric acid levels. By integrating fecal metabolomic and gut metagenomic data, they found that key uric acid–degrading bacteria, predominantly in the Lachnospiraceae family, thrive under hypoxic conditions. This shift helps maintain lower uric acid levels in the gut, which may be crucial for efficient acclimatization. Notably, these microbial dynamics were seen across multiple cohorts living at different high-altitude sites. Their findings highlight a novel intestinal metabolic mechanism contributing to human resilience in extreme environments.

Food and Agricultural Metabolomics

These studies highlight how metabolomics can shed light on everything from traditional cooking practices to medical dietary interventions. By analyzing shifts in amino acids, lipids, sugars, and other metabolites, researchers unravel the subtle ways that fermentation, heat treatment, and macronutrient composition shape both food quality and human physiology. From the dynamic changes in tea leaves and citrus peels to in vivo metabolic chamber experiments, the following

articles underscore the importance of capturing comprehensive metabolic profiles to guide nutrition science and improve food-based strategies. This integrated perspective not only helps optimize flavor and nutrient retention but also deepens our understanding of how diet interacts with human metabolism at large.

Widely targeted metabolomics and SPME-GC-MS analysis revealed the quality characteristics of non-volatile/volatile compounds in Zheng'an Bai tea

Liu and colleagues in Frontiers in Nutrition found that fresh leaves of Zheng'an Bai tea exhibit distinct changes in amino acids, polyphenols, and volatile aroma compounds during different developmental stages and processing steps. The authors identified 573 non-volatile metabolites, among which flavonoids, alkaloids, and terpenoids were significantly altered across samples. Volatile analysis revealed that moderate spreading enhanced the release of some aroma notes, whereas fixation caused a sharp decrease in many volatile metabolites. Nine key compounds, including linalool and geraniol, were deemed crucial to the tea's characteristic aroma. Overall, these insights provide a basis for refining processing protocols to preserve or enhance desirable tea qualities.

Metabolomic changes in Citrus reticulata peel after conventional and ultrasound-assisted solid-state fermentation with Aspergillus niger: A focus on flavonoid metabolism

Mamy and colleagues in Food Chemistry showed that ultrasound-assisted fermentation boosted protein and carotenoid content in fermented Citrus reticulata peels more effectively than conventional fermentation. They used an extensive metabolomic approach to detect 521 differential metabolites, including upregulated flavonoids, organic acids, and lipids. Additionally, higher levels of phenylalanine and tyrosine ammonia-lyase activity correlated with increased flavonoid accumulation under fermentation. This suggests that harnessing ultrasound-assisted methods can maximize flavonoid biotransformation and nutrient enrichment. Their work points to a sustainable strategy for converting citrus peel waste into value-added functional ingredients.

Integrative transcriptome and metabolome analyses reveal the mechanism of melatonin in delaying postharvest senescence in cowpeas

Liu and colleagues in International Journal of Biological Macromolecules found that exogenous melatonin treatment delayed senescence in postharvest cowpeas by maintaining color, firmness, and soluble solids. Through combined transcriptomic and metabolomic data, they demonstrated that melatonin upregulated genes associated with amino acid and carbohydrate metabolism while decreasing transcripts related to chlorophyll and cell wall degradation. This led to greater accumulation of essential amino acids and sugars, reinforcing the sensory quality of cowpeas during storage. Additionally, melatonin's anti-oxidative properties contributed to improved shelf life. Their findings highlight a promising natural approach to maintain freshness in postharvest produce.

Untargeted metabolomics reveals the alteration of metabolites during the stewing

process of Lueyang black-bone chicken meat

Wang and colleagues in Frontiers in Nutrition found that stewing leads to notable changes in the metabolomic profiles of black-bone chicken, particularly in amino acids, nucleic acids, and lipids. Many soluble metabolites, including certain amino acids and nucleotide derivatives, moved into the soup, enriching its nutritional and flavor profile. The fully cooked meat, however, remained enriched in beneficial unsaturated lipids, such as lysophosphatidylcholines. By comparing fresh meat to both partially and fully cooked samples, the authors highlighted that stewing can enhance overall dietary value by distributing select compounds between meat and broth. The study offers insights into how traditional cooking techniques improve both taste and nutrition.

Human metabolic chambers reveal a coordinated metabolic-physiologic response to nutrition

Perry and colleagues in JCI Insight found that transitioning between fasting and overfeeding states triggers predictable shifts in substrate oxidation and circulating metabolite profiles, detectable through advanced metabolic chamber measurements. Diets with higher fat content or prolonged fasting encouraged greater lipolysis and ketone generation, while high-carbohydrate loads skewed the metabolism toward glucose oxidation. These dynamic metabolic signatures, validated by targeted metabolomics, spotlight the body's remarkable flexibility in fuel usage. Their research demonstrates how precisely controlled feeding interventions can unravel the delicate interplay between diet composition and metabolic responsiveness.

The Metabolome and the Epigenome

Though we often think of epigenetic regulation as primarily a function of DNA- and histone-modifying enzymes, these four articles expand the growing pool of evidence showing that the metabolome plays a pivotal role in shaping the epigenome. Whether it is the availability of cofactors that power chromatin remodelers, the influence of metabolic byproducts on DNA methylation, or the interplay between energy pathways and histone acetylation, these studies show how shifts in cellular metabolism can have profound epigenetic consequences. They reveal that metabolic disturbances—ranging from low melatonin in obese mice to altered glycolysis in osteoblasts—propagate to the epigenome and reprogram gene expression. Taken together, this section underscores the tight feedback loop between the metabolome and the epigenome, influencing everything from plant seed dormancy to mammalian development and disease.

The BRAHMA-associated SWI/SNF chromatin remodeling complex controls Arabidopsis seed quality and physiology

Wrona and colleagues in Plant Physiology found that mutations in the SWI/SNF catalytic subunit BRM alter Arabidopsis seed size, yield, and longevity, partly through interactions with the key dormancy regulator DOG1. Their integrative transcriptomic and metabolomic analyses demonstrated that BRM and DOG1 coordinately modulate genes involved in glutathione homeostasis and other stress responses. BRM directly remodels the 3′ region of DOG1, which

overlaps with a long non-coding RNA promoter. These findings reveal how chromatin remodeling at a single locus can influence multiple seed traits. The study underscores a sophisticated interplay between transcriptional regulation and epigenetic modifications in plant seed biology.

TET3 regulates terminal cell differentiation at the metabolic level

Mulet and colleagues in Nature Communications showed that TET3 is essential for oxidative phosphorylation and normal enterocyte maturation in the mouse intestinal epithelium. Single-cell RNA sequencing revealed that Tet3 is predominantly expressed in differentiated enterocytes, and its absence halted their metabolic and identity transitions. Spatial metabolomics confirmed aberrant metabolite accumulation in Tet3 knockout enterocytes, contrasting with unaffected stem cells. By regulating key mitochondrial processes, TET3 ensures a proper shift to oxidative metabolism during final cell differentiation. These findings offer insight into how epigenetic enzymes modulate energy pathways in late-stage cell differentiation.

SIRT1 maintains bone homeostasis by regulating osteoblast glycolysis through GOT1

Jin and colleagues in Cellular and Molecular Life Sciences found that inducible osteoblast-specific Sirt1 knockout mice showed lower bone mass and diminished bone formation and resorption. Using metabolomics and acetyl-proteomics, they discovered that loss of SIRT1 increased the acetylation of GOT1, which in turn downregulated osteoblast glycolysis. This metabolic inhibition weakened bone growth and turnover. SIRT1's role as a deacetylase thus emerged as essential for sustaining osteoblast energy metabolism. These results point to the value of targeting osteoblast glycolysis pathways to treat bone-related disorders.

Maternal obesity may disrupt offspring metabolism by inducing oocyte genome hyper-methylation via increased DNMTs

Chao and colleagues in eLife found that high-fat diet–induced maternal obesity led to pronounced hypermethylation of the oocyte genome, some of which persisted in subsequent generations. Metabolomic analyses linked these epigenetic changes to lower circulating melatonin in obese mice, which appeared to upregulate DNMT3a and DNMT1. Supplementing melatonin reduced aberrant hypermethylation and partially restored metabolic phenotypes. This study underscores how maternal metabolic cues can have transgenerational effects through epigenetic reprogramming, potentially influencing offspring health.

The Metabolome and Oxidative Stress

These four articles illustrate that metabolic fluxes and intermediates are pivotal in driving or mitigating redox imbalance. From the preferential oxidation of guanine under bicarbonate-rich conditions to the role of taurine in radiation-induced injury, what we eat—or produce metabolically—shapes how cells respond to oxidative threats. Intracellular energy pathways, especially glycolysis and mitochondrial function, constantly intersect with ROS generation and scavenging mechanisms. By examining oxidative stress through the lens of metabolomics

researchers are gaining insight into a wide spectrum of disease contexts, including viral infections and neurodegeneration.

CO2 protects cells from iron-Fenton oxidative DNA damage in Escherichia coli and humans

Fleming and colleagues in PNAS found that bicarbonate levels under physiological conditions redirect the classic iron-Fenton reaction away from hydroxyl radicals toward carbonate radical anions. They used transcriptomics, electrochemical detection, and cell-based assays to show that carbonate radical anions preferentially oxidize guanine to 8-oxo-7,8-dihydroguanine (OG). This phenomenon became more pronounced under ferroptotic conditions, which increased labile iron and thus promoted bicarbonate-dependent oxidation. The work suggests that CO2_22/bicarbonate can act as a protective buffer against wide-ranging oxidative damage in nucleic acids.

Taurine ameliorates radiation-induced oxidative stress in bone marrow mesenchymal stromal cells and promotes osteogenesis

Chen and colleagues in Free Radical Biology and Medicine showed that taurine levels were elevated in irradiated mandibular stromal cells, yet overall taurine content in bone marrow mesenchymal stromal cells dropped after radiation. Supplementing taurine significantly reduced oxidative damage and DNA double-strand breaks, fostering enhanced osteogenic differentiation. Oral taurine administration also helped irradiated mice survive longer and improved bone regeneration in the jaw. By mitigating ROS accumulation, taurine appears to stabilize the redox balance in radiation-injured tissues. These insights propose taurine as a practical adjunct to combat osteoradionecrosis.

Influenza A virus-induced glycolysis facilitates virus replication by activating ROS/HIF-1α pathway

Zhang and colleagues in Free Radical Biology and Medicine found that WSN virus infection in mice and human cells triggered enhanced glycolysis, increased ROS levels, and upregulated lactate dehydrogenase. This, in turn, activated HIF-1α\alphaα signaling, which promoted viral replication. Pharmacological inhibition of glycolysis or HIF-1α\alphaα decreased viral propagation and protected lung tissue from severe damage. Their findings suggest that manipulating glycolytic flux or ROS/HIF-1α\alphaα pathways could be an effective therapeutic strategy against influenza A. It also highlights the importance of metabolic reprogramming during viral infection.

Functional implications of NHR-210 enrichment in C. elegans cephalic sheath glia: insights into metabolic and mitochondrial disruptions in Parkinson's disease models

Hameed and colleagues in Cellular and Molecular Life Sciences showed that knocking down nhr-210 in Caenorhabditis elegans bearing human alpha-synuclein disrupted dopaminergic behavior and mitochondrial functionality. Their experiments indicated altered levels of key metabolites such as ATP, betaine, and lactate, reflecting impaired metabolic balance.

Metabolomics further highlighted that nhr-210 depletion influenced multiple biochemical pathways, including glycine and tryptophan metabolism. These effects were associated with enhanced neurodegenerative phenotypes in the worms. The work suggests that glial NHR-210 is a critical regulator of neuronal health, opening new avenues for understanding Parkinson's disease.

Cardiovascular Metabolomics

These two articles illustrate how metabolomic shifts play a vital part in both aortic aneurysm pathology and ischemia-reperfusion injury in steatotic liver transplant recipients. By homing in on citrate transport, histone acetylation, and fatty acid binding proteins, researchers uncovered metabolic drivers that feed into inflammation, vascular remodeling, and tissue damage. Such insights highlight the interplay between metabolite accumulation, epigenetic regulation, and immune responses, all of which shape disease severity and outcomes. Taken together, these studies underscore the value of multi-omic approaches in diagnosing and targeting metabolic pathways that contribute to cardiovascular ailments.

ANK Deficiency-Mediated Cytosolic Citrate Accumulation Promotes Aortic Aneurysm

Wu and colleagues in Circulation Research found that downregulation of the citrate transporter ANK in vascular smooth muscle cells causes excess cytosolic citrate, fueling histone acetylation and proinflammatory gene expression. Using mass spectrometry–based metabolomics, they demonstrated that higher cytosolic citrate levels link directly to acetyl-CoA production, driving the pathological remodeling of the aorta. Overexpressing ANK or suppressing citrate cleavage alleviated these harmful changes, underscoring the potential to treat aneurysms by modulating citrate transport. These findings highlight a critical metabolic mechanism behind arterial wall vulnerability and inflammation, offering a new therapeutic target for aortic aneurysm.

Integrated multi-omic analysis identifies fatty acid binding protein 4 as a biomarker and therapeutic target of ischemia-reperfusion injury in steatotic liver transplantation

Yang and colleagues in Cellular and Molecular Life Sciences showed that increased fatty acid binding protein 4 (FABP4) in steatotic livers is tied to worse ischemia-reperfusion injury, partly via disrupted mitochondrial homeostasis and intensified oxidative stress. Through a combination of proteomics and metabolomics, they pinpointed FABP4's role in aggravating IR-induced liver damage. Inhibition of FABP4 rescued mitochondrial membrane integrity, reduced reactive oxygen species, and improved survival in transplanted steatotic grafts. Their multi-omic approach reveals a clear metabolic link between fatty acid trafficking and IR susceptibility, paving the way for targeted interventions in transplant medicine.

Back to top

|MC:SUBJECT|

Metabolomics Events

GRC: Metabolomics and Human Health - The Interaction Between Humans, Lifestyles and the Environment Viewed through Metabolism

February 2 - 7, 2025

Venue: Ventura, California, USA

Metabolomics is the comprehensive study of the metabolome, the repertoire of metabolites present in cells, tissues, and body fluids. More recently, these metabolites are being implicated in the development of unhealthy ageing and diseases, positive and negative impacts of interaction with the exposome and the promotion of human health. The human metabolic profile is influenced by a number of factors including diet, genetics, environmental factors and the microbiome. Understanding the influence of these factors at a cellular and systemic level is key to deciphering the role of metabolites in human health and promotion of lifespan. In this Gordon Conference series, we highlight state of the art metabolomics technologies and how such technologies can be used to study human health. The conference will cover exciting new applications in the field such as epidemiology, cancer, nutrition, analytical chemistry and bioinformatics and translation to human benefit.

Apply now

6th Annual Canadian Metabolomics Conference

(CanMetCon) 2025

April 24 - 25, 2025

Venue: Montreal, QC, Canada

The 6th Canadian Metabolomics Conference (CanMetCon) 2025 will be held at New Residence Hall, McGill University, Montreal, Quebec on April 24th–25th.

This year's theme, **"Clinical Metabolomics,"** highlights the growing role of metabolomics in healthcare and research. The Day 2 program will focus on four key areas:

- Clinical Metabolomics
- Computational Metabolomics and Machine Learning
- Nutrition and Health
- Public Health and Population Metabolomics

To kick off the conference, two hands-on workshops "Comprehensive Clinical Omics - From Sample to Result" will be held on April 23, led by Dr. Christoph Borchers and Dr. Jianguo (Jeff) Xia.

Workshop Part 1: Attendees will have the opportunity to train at the Warren Y. Soper Clinical Proteomics Centre, one of Canada's only certified clinical metabolomics laboratories, on the latest techniques in clinical mass spectrometry analysis and data generation.

Workshop Part 2: Participants will learn how to explore this dataset and generate diagnostic insights, with MetaboAnalyst and OmicsAnalyst, two of the most-used and most-cited data analysis tools in metabolomics and multi-omics.

Registration is open

EMBL-EBI Introduction to Metabolomics Analysis Course

May 20 - 23, 2025

Venue: Hinxton, United Kingdom

This course will provide an introduction to metabolomics through lectures and hands-on sessions, using publicly available data, software, and tools. Participants will become familiar with standardised workflows as well as with the current state of experimental design, data acquisition (LC-MS, MS imaging), processing, and modelling. In addition, they will learn about community standards and sharing in metabolomics, particularly through the use of EMBL-EBI's MetaboLights repository and Galaxy infrastructure. Participants will learn through hands-on tutorials to use tools available for data analysis and data submission. Additionally, case studies will be discussed to show how to employ the week's learning.

Check for more details

21st Annual Conference of the Metabolomics Society

Metabolomics 2025

June 22 - 26, 2025

Venue: Prague, Czech Republic

21st Annual International Metabolomics Conference of the Metabolomics Society will be held on June 22-26, 2024 in Prague, Czech Republic. The conference will follow the same pattern as previous years, with Workshops taking place on Sunday and Monday, and the full conference beginning on Monday afternoon and running through Thursday afternoon.

Call for workshops are now open - click here for details.
Deadline Extended: **January 10, 2025**

Check for more details

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

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

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

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

Back to top

Metabolomics Jobs

Metabolomics Jobs

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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
Metabolomics Senior Research Associate	Berkeley Lab's (LBNL) Environmental Genomics and Systems Biology (EGSB) Division	Bay Area, California, United States	Berkeley Lab
Chromatography and Mass Spectrometry Technologist	The James Hutton Institute	Dundee, United Kingdom	The James Hutton Institute
Postdoctoral Research Fellow Positions in Exposomics and	Department of Environmental Health at the Harvard T.H. Chan	Boston, MA, United States	Department of Environmental Health at the Harvard T.H.

Environmental Health	School of Public Health		Chan School of Public Health
Post Doctoral Fellow in Clinical Exposomics	Emory University	Atlanta, GA, United States	Emory University
Data Scientist / Senior Data Scientist		Oxford, England	Metabolomics Society

Back to top

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Fill Out Your Survey Here

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

Back to top

|MC:SUBJECT|