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MetaboNews

This month in metabolomics

July, 2026
Vol 16, Issue 6

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

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MetaboInterview
Constança Silva
(University of Toronto)

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

Members Corner

Board of Directors

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

Dear Metabolomics Society Members and metabolomics friends,

It was fantastic to see many of you at Metabolomics 2026 in Buenos Aires in June. This was the first ever Metabolomics Society conference in South America and all of the South American metabolomics community did us proud. This was planned to be a smaller conference and there were close to 500 attendees with a great diversity of science presented in the oral and poster sessions. I apologise to all who were not able to see my dance moves on stage.

I would like to thank many people and groups. Firstly, huge thanks to Maria, Ian and Monica as the local organisers and Aurelia as the conference committee chair. The planning process was very dynamic in the six weeks up to the conference and without these people the conference would not have been the success that it was. I would like to thank Breanna and the EMN team for organising a range of social events. I would also like to thank our many sponsors whose presence and financial support are critical for the success of

the conference. There are many others I would like to thank but space does not permit it, you know who you are and thank you.

The annual conference is always a busy time for the President and Board of Directors with many meetings and events. I really enjoyed the conference but was also happy to sit back and relax in front of the Brazil-Scotland soccer game on the Wednesday evening (with kilts and yellow Brazil shirts all around). I hope some of you also had time to enjoy the wonders of Argentina, I saw several groups at Iguazu Falls that I recognised from the conference.

Next year we are pleased that the annual conference will be hosted by our South Korean colleagues in Daegu and the team announced this in style in Buenos Aires. This will be an exciting conference in Asia and we are hoping for greater than 1000 attendees to beat our Asian record and so get this in to the diary now and think about travel grants. One of my team originates from Daegu and he waxes lyrical about the city and he has told me that this is important for Daegu also and local news outlets have already announced this.

Our annual elections for Directors is in operation. The Society is led through the voluntary efforts of the Board of Directors. While this provides motivated individuals a fantastic opportunity to contribute to the activities, communications and ultimate growth of our metabolomics community, it also requires a time commitment of typically 2 hours per week. Our new bylaws will ensure we have a broad geographical distribution of Directors and we are looking for increased numbers from the USA and North America, please do consider this in nominations (due by July 23rd) and when voting in August. We have three Directors up for re-election (Liz Want, Aurelia Williams and Nik Rattray), all have significantly contributed to the Society in an impactful way in their first term. A number of the board will step down at the end of September including the Secretary (Maria) and President (myself). More to follow on this in the next MetaboNews.

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

Early-career Members Network (EMN)

EMN Webinars

July EMN Webinar — Register Now!

The EMN committee is pleased to welcome **Dr Justin Carrard**, Senior Physician in Sport and Exercise Medicine at Lausanne University Hospital (CHUV) and Head of the Sport and Youth Health Unit at the Swiss Olympic Medical Centre, who will be presenting the July webinar entitled 'Metabolomics and Lipidomics in Sport and Exercise Medicine: a physician-scientist perspective'. The webinar will take place on Friday, 31 July at 15:00 CEST/13:00 UTC.

Register here:
https://zoom.us/webinar/register/WN_A9KeBbcfQrWcyOcOuEeOhg#/registration

Call for Abstracts: EMN & Affiliates Virtual Symposium

We are pleased to announce the first EMN & Affiliates - Virtual Symposium, a free global event for Early Career Researchers (ECRs), organized by the Early-Career Members Network (EMN) of the Metabolomics Society in collaboration with international affiliates: the Polish Metabolomics Society, the Spanish Metabolomics Society (SESMET), the Australian and New Zealand Metabolomics Society, and the Metabolomics Association of North America (MANA).

ECRs will have the opportunity to present their metabolomics research to a global audience as oral presentations. The symposium will take place on **Tuesday, November 3, 2026**, with regional sessions at

- Americas:14:00-16:30 EST
- Europe & Africa: 14:00-16:30 CET
- Asia & Oceania: 14:00-16:30 AEDT

Submit your abstract by July 26, 2026 (23:59 UTC):
https://forms.gle/ZDjtRGhYHYNRfrYK6
Participation is free. ECRs who are members of the Metabolomics Society or one of the affiliate societies are encouraged to submit an abstract and join the event.
Follow the EMN Metabolomics Society and affiliate societies on LinkedIn and X for updates. For questions, contact **info.emn@metabolomicssociety.org**.

EMN Elections

We are inviting early-career researchers to join the committee of the

Metabolomics Society's Early-career Members Network (EMN). We welcome applications from members* of the Metabolomics Society that are graduate students (Masters or PhD) or within 5 years post PhD (graduation date after 1 October 2021) while being in a training position (*e.g.* post-doc) in a metabolomics discipline or are actively engaged in metabolomics science. Applications to join the EMN committee will be open **July 27 - Aug 09 2026** (2359 Pacific Daylight Time (UTC/GMT -7)). Top candidates will be invited for an interview, which is expected to take place at the end of August/beginning of September. Successful candidates are expected to commence their EMN mandate in October 2026.

To apply, please visit this link. Please note that the form will not be accepting responses **until July 27**. Alternatively, we will be sharing the link on our LinkedIn account when applications open. As we strive for diversity and representation in our committees, we encourage applications from all corners of the globe and would strongly recommend ECRs from Asia, Africa and the Americas to apply. The full application call can be found here: Application Call 2026. Please follow the application guidelines carefully. Given the high number of applications we receive, applications that do not confer to guidelines will not be evaluated.

*current member or willing to become a member. EMN committee members receive a free Metabolomics Society membership for the time they serve on the committee.

EMN at the Metabolomics 2026 Conference in Buenos Aires

EMN Conference Workshop

A warm thank you to all participants of the EMN conference Workshop! The EMN is especially grateful to the invited panellists Alice Limonciel, Bart Ghesquiere, Fidele Tugizimana, Monica Cala, Rima Kaddurah-Daouk, and Susan Bird, who brought all the experience this workshop needed to be a success. Among the take-home messages to remember: (i) the career landscape in metabolomics goes beyond academia and covers diverse paths, (ii) your skills can be precious for multiple career paths, (iii) mentors and networking are key to defining your career path and achieving your goals and (iv) taking that first step is difficult, but is the first step towards your success! We hope to see you all at the next EMN Workshop at Metabolomics 2027 in Daegu!

Career Night Roundtable Discussions

We're incredibly grateful to everyone who participated in our Career Night Roundtable event. Each session was filled with thought-provoking dialogue, and enabled the exchange of experience, wisdom, and inspiration, helping participants navigate the world of metabolomics as an ECR.

Here's a special thank you to the discussion leaders:

Translating Research into Industry Applications
– Bart Ghesquière (KU Leuven, Belgium)
– Bashar Amer (Thermo Fisher Scientific, United States)

Career Transitions
– Silvia Radenkovic (UMC Utrecht, The Netherlands)
– Sarah Haynes (Enveda, United States)

Navigating the Post-doc Grey Zone
– Louis-Félix Nothias (Centre National de la Recherche Scientifique & Université Côte d'Azur, France)
– Julia Kuligowski (Health Research Institute La Fe, Spain)

International Employment Opportunities
– James MacRae (The Francis Crick Institute, UK)
– María Eugenia Monge (CIBION – CONICET, Argentina)

Networking & Collaboration
– Mariana S. Larraz Ferreira (UNIRIO - Federal University of the state of Rio de Janeiro, Brazil)
– Fabien Jourdan (INRAE-MetaboHUB, France)

Responsible Use of AI and LLMs
– Ricardo Roberto da Silva (University of São Paulo, Brazil)
– Fidele Tugizimana (University of Johannesburg & Omnia Group, Ltd., South Africa)

Career Resilience: handling rejection, failure & the imposter syndrome
– Aurelia Williams (North-West University, South Africa)
– Nicholas Rattray (University of Strathclyde, UK)

Grant Writing

– Liz Want (Imperial College London, UK)
– Lynn Vanhaecke (Ghent University, Belgium)

Science Communication
– Alice Limonciel (Biocrates life sciences ag, Austria)
– Roy Goodacre (University of Liverpool, UK)

Diversity, Equity, and Inclusion
– Rick Dunn (University of Liverpool, UK)
– Anne Bendt (National University of Singapore, Singapore)

Your contributions made this event a standout success. Thank you for fostering such a dynamic and supportive space for career exploration and growth.

EMN Reception
A heartfelt thank you to everyone who joined the EMN reception and quiz, making it a fantastic success! We hope you were able to find out a little more about what we do and will join us at future events. We want to extend special congratulations to our quiz winners as well all teams for their enthusiastic participation! We hope you all had a great time, made new connections, and enjoyed the spirit of friendly competition.

Travel Awardees
Congratulations once again to this year's EMN Travel Bursary Awardees: Ana Koifman, Federal University of the State of Rio de Janeiro (UNIRIO), Brazil (student award) and Joao Marcos Barbosa, Örebro University, Sweden (graduate award).

International Affiliates Corner

Benelux Metabolomics Centre (BMC)
Visit www.metabolomicscentre.nl/

Three days of Metabolomics at the University of Antwerp!
21 September, YoungBMC Symposium 2026 – FREE OF CHARGE EVENT

(FOR ECRs)!

This YoungBMC Symposium serves as a dynamic platform for PhD candidates, postdocs, early-career scientists, and metabolomics enthusiasts from across the Benelux region and beyond!
There are limited spots available!

Call for Abstracts Orals and Posters still open -> Deadline July 22nd- midnight
Register and upload your abstract here or use the QR code on the flyer.
More information
https://www.aanmelder.nl/beneluxmetabolomicsdays2026/ybmc-symposium-2026

22+23 September, Benelux Metabolomics Days 2026, Antwerp, Belgium
Organised by **Wout Bittremieux**, Adrem Data Lab & **Adrian Covaci,** Toxicological Centre from University of Antwerp. Join a dynamic meeting with top metabolomics keynotes and inspiring ECR presentations in an open, informal and engaging setting.

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Check out the programme here and below.

Register here! The call for abstracts for a poster spot is still open!
Conference website: BMD2026.

Benelux Metabolomics Days 2026		
uesday, 22 September 2026 (DAY 1)		
8:45 - 09:30	Arrivals + registration	
9:30 – 11:00	*Session 1: Chairs TBA*	
9:30-9:45	Welcome	**Welcome & Introduction**
9:45-10:15	**Erin Baker, University of North Carolina at Chapel Hill, NC, USA**	***When Nature Touches Us: Unraveling Environmental Signatures with Mass Spectrometry***
0:15-10:30	Laura Rosina Torres Ortega, Wageningen University & Research, NL	From defaults to principled networks: parameter tuning and bootstrap confidence for robust MS/MS molecular networking
0:30-10:45	Scientific sponsor talk	TBA
0:45-11:00	Maosen Zhao, University of Antwerp, BE	Nontarget Identification of Contaminants of Emerging Concern in Campus Indoor Dust Using Ion Mobility High-Resolution Mass Spectrometry
1:00-11:30	**Coffee break**	
1:30 –12:45	*Session 2: Exposomics & Environmental Health (Adrian Covaci, University of Antwerp, BE*	
1:30-12:00	**Arthur David, French School of Public Health, FR**	***Toward a Population Scale Map of the Human Chemical Exposome: Challenges, Strategies, and Opportunities***
2:00-12:15	Stelios Papazoglou, INRAE, FR	Optimized Ion Mobility CCS Approaches for PFAS Annotation in Fish Extracts: Implications for Food Safety and Exposomics
2:15-12:30	María del Mar Delgado-Povedano, University of Antwerp, BE	Metabolomic Signatures in a Flemish Population Exposed to Per- and Polyfluoroalkyl Substances
2:30-12:45	Ellen De Paepe, Ghent University, BE	A Validated Single-Tube Dual-Extraction Platform for Combined Placental Metabolomics and Lipidomics to Investigate In Utero Exposures
2:45-13:45	**Lunch**	
3:45-14:45	**Poster session 1**	
4:45 –16:00	*Session 3: Computational Metabolomics & AI (Wout Bittremieux, University of Antwerp, BE)*	
4:45-15:15	**Emma Schymanski, University of Luxembourg, LU**	***Exploring Relevant Chemical Space for Metabolomics and Exposomics with Open Science***
5:15-15:30	Gaetan De Waele, University of Antwerp, BE	Improving metabolomics transformers for chemical database retrieval
5:30-15:45	Matthijs Vynck, Ghent University, BE	Robust metabolomics data normalization across scales and experimental designs
5:45-16:00	Sponsor talk	TBA
6:00-16:30	**Coffee break + Snack**	
6:30 –17:45	*Session 4: Natural Products, Ecological & Plant Metabolomics (Geert Goeminne, VIB, Ghent University, BE)*	
6:30-16:45	Sandra Pous Torres, dsm-firmenich, NL	Metabolomics of Bad Taste: Hunting Plant Off-Notes
6:45-17:00	Meng Peng, VIB Center for Plant Systems Biology & Ghent University, BE	Identification of a biosynthetic gene cluster underlying three post-chorismate pathways in Arabidopsis thaliana
7:00-17:15	Huong T. Pham, Sookmyung Women's University, KR	Functional metabolomics-based reinvestigation of halogen promiscuity in Griseofulvin biosynthesis pathway
7:15-17:45	**Kyo Bin Kang, Sookmyung's Women University, KR**	***Qualitative Metabolomics Accelerates Function Studies of Natural Products***
7:45-18:45	**Poster session 2 + Drinks**	
9:00-20:30	**Dinner**	

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Online Benelux Metabolomics Seminars 2026

In 2021, the COVID-19 pandemic made physical meetings impossible. To maintain connections within the metabolomics community, the BMC Board at that time launched the **Benelux Metabolomics Seminars**—a series of online events designed to facilitate knowledge exchange, networking, and scientific discussion.

Since then, these seminars have been held on almost every the last Thursday afternoon of each month and typically last 60 to 90 minutes. They provide a platform for both senior principal investigators (PIs) and early-career researchers to present their work, followed by an interactive plenary discussion.

The seminars are **free of charge** and **open to all researchers interested in**

metabolomics and related fields. Over the past few years, the Benelux Metabolomics Seminars have grown beyond the Benelux region, attracting a diverse and international audience of researchers, including many young scientists. We warmly invite you to join our upcoming seminars and help us continue to grow this vibrant community by sharing the event series within your network.

Thursday 29 October, 15.00-16:30h, online
Online Benelux Metabolomics Seminar on "*Tracer Metabolomics*" organised by Bart Ghesquière,Lab Bart Ghesquiere, KU Leuven, BE
Please register here.

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

RFMF second thematic school on metabolomics in human health, deadline in September

Registration is now open for the 2nd RFMF Thematic School!

This thematic school, jointly organized by the RFMF and the French Society of Clinical Biology, will be supported by the CNRS.

The school will focus on metabolomics in human health.

Dates: October 5–9, 2026
Schedule: From Monday, October 5, 2026, at 12:00 p.m. to Friday, October 9, 2026, at 12:00 p.m.
Venue:
Centre de Vacances Paul Langevin
24 rue du Coin
73500 Aussois, France

All information is available on the website: RFMF Thematic School #2

Registration fees:

- Academic participants: €1,300
- Industry participants: €2,000
- FREE for CNRS staff, subject to availability

Places are limited. Registration deadline: September 2, 2026.

To register, please visit: Registration – RFMF Thematic School #2
We look forward to welcoming many of you for a full week of discussion around the numerous challenges facing metabolomics in health, identifying key barriers that need to be addressed, and helping to build and strengthen a community around this important field.

MetaboHUB training in metabolomics

TRAINING "Hands-On Metabolomics: From Bench to Data"
Why this training?

Want to integrate metabolomics into your research or analytical projects, but don't know where to start? Whether your focus is on agrosciences, nutrition, human health, environmental science, biotechnology, or animal health, this training designed by MetaboHUB is for you!

Information:
When? From November 23 to 27, 2026

Where? Toulouse, France, on the INSA Campus

Target audience? Researchers, engineers, technicians, doctoral and postdoctoral students, academics or industrials, biologists or analysts

What you will learn? Expert scientists from the MetaboHUB infrastructure will introduce you to the fundamental principles and cutting-edge techniques of metabolomics through a dynamic blend of theoretical and hands-on sessions !"

Extra Interactive format: Practical workshops, discussions, case studies, keynote and workshop Certification: Training certificate issued

Registration & Contact to fcq@insa-toulouse.fr : Hurry, limited space available!

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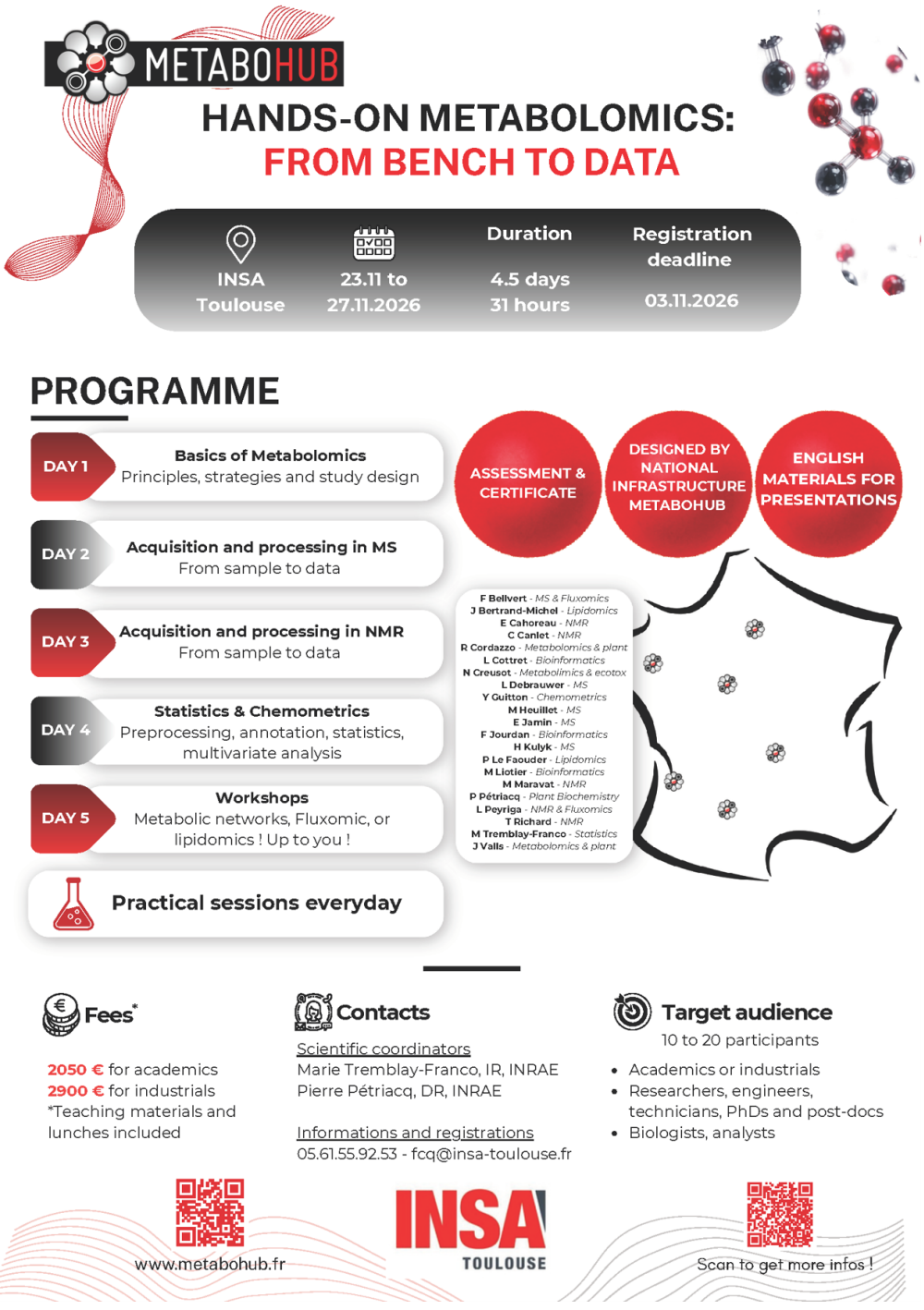

Nordic Metabolomics Society

Visit www.nordicmetsoc.org

NORDIC METABOLOMICS SOCIETY

Interested in joining our metabolomics conference?

The Fifth Nordic Metabolomics Conference 2026 will take place from September 28th-30th, 2026 in Uppsala, Sweden: https://nordicmetsoc.org/nmetc2026/.

Poster abstract submissions will be accepted until September 1st.

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MetaboInterview

Constanca Silva

Hi! I’m Constança, and I moved to Toronto, Canada from the Azores, Portugal, in 2020 to pursue post-secondary studies. My background is in nutrition, exercise, and lifestyle medicine. I recently completed an MSc in Nutritional Sciences at the University of Toronto, where I was first introduced to metabolomics through nutrition research. This experience sparked my interest in the field and its potential to advance personalized and preventive medicine. I’ll be starting medical school at the University of Toronto next, and I hope to continue working in this novel and fascinating area of research throughout my career!

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

Before starting my MSc, I had the opportunity to work on and explore different types of research projects, including systematic reviews and clinical trials. While I already had some experience with trials and reviews, metabolomics was completely new to me, which immediately made it exciting and intriguing. I

was drawn to the idea that small molecules in the body could provide such detailed insight into diet, metabolism, and disease risk. I decided to focus my MSc metabolomics work on characterizing a metabolomic signature of almond intake using samples from four Portfolio Diet trials. One of the main motivations behind this project was that almonds and other nuts are often poorly captured by traditional dietary assessment tools such as food frequency questionnaires (FFQs). People may eat almonds intermittently, in mixed dishes, or in forms that are difficult to quantify accurately through self-report alone. Metabolomics offers a more objective way to assess dietary exposure by capturing the biological response to food intake. What I found especially interesting was how metabolomics can bridge nutrition and precision medicine. It not only helps improve dietary assessment, but also provides insight into the metabolic pathways linking diet to cardiometabolic health. Working in this area showed me how powerful metabolomics can be in advancing nutrition research and personalized prevention strategies.

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

Working in metabolomics has definitely changed the way I think about nutrition and health, especially how interconnected biological systems are. Before my MSc, I mainly viewed nutrition through more traditional clinical and lifestyle perspectives, focusing on dietary patterns, risk factors, and health outcomes. Metabolomics added an entirely new layer to that understanding. What I find fascinating is that metabolomics allows us to move beyond simply asking what people eat and start exploring how the body actually responds to foods at a molecular level. It highlighted for me how dynamic and individualized metabolism is, and how diet can influence pathways related to inflammation, lipid metabolism, blood pressure, and overall cardiometabolic health in ways that are not always captured by conventional dietary assessment tools. Working on the almond metabolomic signature also reinforced how complex nutrition research can be. A single food does not act in isolation, and metabolomic profiles may reflect both the foods being consumed and the foods being displaced within a broader dietary pattern. That shifted my perspective away from thinking about nutrients or biomarkers individually and toward seeing health and disease as the result of interacting systems. Learning about metabolomics made biology feel more integrated and personalized, and it strengthened my interest in preventive and precision medicine as I move into more clinical studies in medical school.

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

The finding that surprised me the most was how much more strongly the almond metabolomic signature was associated with intermediate cardiometabolic outcomes compared with self-reported almond intake. I expected metabolomics to provide complementary information, especially because self-reported dietary data can be affected by recall bias, portion-size estimation, and variability in reporting. However, the magnitude of the difference was striking. In our analyses, most of the biomarkers we examined were significantly reduced in association with the almond metabolomic signature, whereas far fewer significant associations were observed with self-reported almond intake alone. These included reductions in blood pressure, weight, BMI, and several lipid markers. To me, this suggested that the metabolomic signature may be capturing more than almond intake in grams per day. It may also reflect individual differences in digestion, absorption, metabolism, adherence, and the broader dietary context in which almonds were consumed. This finding reinforced my interest in metabolomics as a tool to complement traditional dietary assessment and better understand biological responses to diet.

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

One advancement in metabolomics that I think deserves more attention is the development of metabolomic signatures as objective measures of dietary exposure. In nutrition research, we often rely on self-reported dietary assessment tools, such as food frequency questionnaires (FFQs) or diet records. These methods are useful, but they are also prone to measurement error, recall bias, and difficulty estimating portion sizes. This can be especially challenging for foods that are eaten intermittently, incorporated into mixed dishes, or not captured in detail by standard questionnaires. Metabolomics offers a powerful complementary approach because it can help identify biological signals related to what people eat and how they metabolize those foods. Rather than relying only on reported intake, metabolomic signatures may capture exposure, adherence, digestion, absorption, metabolism, and downstream biological responses. In my own work, this was particularly relevant for almonds, where the metabolomic signature appeared to show

stronger associations with several intermediate cardiometabolic outcomes than self-reported almond intake alone. I think this area deserves more attention because it has the potential to improve dietary assessment, strengthen nutrition research, and help us better understand diet-disease relationships. In the future, validated metabolomic signatures could be used alongside traditional dietary tools to support more personalized and preventive approaches to nutrition and medicine.

How do you see your work contributing to collaboration across disciplines or research communities?

I see my work as contributing to collaboration by sitting at the intersection of nutrition, metabolomics, epidemiology, and clinical research. Diet is one of the most important modifiable factors for chronic disease prevention, but studying it is challenging because dietary exposures are complex and difficult to measure precisely. Metabolomics can help address this challenge by adding a biological layer to traditional nutrition research. In my project, we used metabolomics to characterize a plasma signature of almond intake within Portfolio Diet trials and then examined how that signature related to intermediate cardiometabolic outcomes. This type of work requires collaboration across disciplines: nutrition scientists to understand dietary patterns and interventions, metabolomics experts to guide data generation and interpretation, biostatisticians and epidemiologists to build and validate signatures, and clinicians to help translate findings into meaningful health outcomes. I think this collaborative approach is especially important for moving toward more personalized and preventive medicine. Metabolomic signatures may help researchers better assess dietary exposure, monitor adherence, and explore mechanisms linking foods to disease risk. At the same time, clinical and public health perspectives are needed to ensure these tools are relevant, interpretable, and ultimately useful. As I move into medical training, I hope to continue building bridges between nutritional science, omics research, and patient-centred care.

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

One thing I wish more people understood about researchers and scientific work is that research is not done in isolation. Even when a project has one person presenting the results or writing the manuscript, the work behind it is almost

always the result of many people contributing their time, expertise, feedback, and support. My own research has been shaped by an incredible community. I have been very fortunate to work with supportive lab members, collaborators, and colleagues in the Department of Nutritional Sciences at the University of Toronto, who have helped me think through questions, troubleshoot challenges, and improve the way I communicate my work. I am especially grateful to my supervisor, Dr. John Sievenpiper, for his mentorship, encouragement, and continued support throughout my MSc. His guidance has played a major role in helping me grow as a researcher. I also think science requires a lot of humility and collaboration. Research is rarely a straight path, it involves uncertainty, revision, discussion, and learning from others. The final results are important, but so is the process of getting there, and that process depends heavily on mentorship, teamwork, and shared expertise. For me, one of the most rewarding parts of research has been being part of a community that is working together toward a common goal.

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

I see my research translating into real-world applications in a few ways. First, metabolomic signatures could help improve how we measure dietary intake in nutrition research. Traditional dietary assessment tools are important, but they can be affected by recall bias, misreporting, and difficulty estimating portion sizes. This is especially relevant for foods like almonds, which may be eaten in different forms, incorporated into mixed dishes, or consumed inconsistently. A metabolomic signature could provide an objective tool to complement self-reported intake. Second, this work may help us better understand how specific foods and dietary patterns influence cardiometabolic health. In my study, the almond metabolomic signature was associated with several intermediate outcomes, including blood pressure, weight, BMI, and lipid markers. These findings could help generate future hypotheses about the biological pathways linking almonds or plant-based dietary patterns to cardiovascular risk reduction. Finally, I think this type of work has longer-term potential for personalized and preventive medicine. If validated in independent studies, metabolomic signatures could eventually help monitor adherence to dietary interventions, identify individuals who respond differently to certain foods, and support more tailored nutrition recommendations. While more work is needed before clinical application, I see metabolomics as a promising bridge between nutrition science and real-world disease prevention.

What impact do you hope your research presented at CanMetCon 2026 will have in the next few years?

I hope the research I presented at CanMetCon 2026 contributes to the field at the research, clinical, and public health levels. From a research perspective, I hope it encourages further work on metabolomic signatures of individual foods and dietary patterns. Nutrition research has traditionally relied heavily on self-reported intake, and metabolomics offers a valuable complementary tool to better assess dietary exposure, adherence, and biological response. I hope this work helps support future validation studies and more mechanistic research on how plant-based foods influence cardiometabolic pathways. Clinically, I hope this research contributes to the long-term goal of more personalized and preventive medicine. While metabolomic signatures are not yet ready for routine clinical use, they may eventually help identify how individuals respond to dietary interventions and support more tailored nutrition recommendations for cardiometabolic risk reduction. At a public health level, I hope this work adds to the evidence supporting healthy plant-based dietary patterns, including foods such as nuts and legumes, as part of chronic disease prevention strategies. If we can better understand and measure how these foods influence inflammation and cardiometabolic health, we can strengthen dietary guidance and improve confidence in nutrition recommendations. Overall, I hope this research helps move the field toward more precise, objective, and actionable approaches to studying diet and health.

Outside of research, what helps keep you motivated, creative, or balanced during demanding projects?

Outside of research, spending time with friends and family is what helps keep me most grounded. Research can be demanding and, at times, very mentally consuming, so having a strong support system makes a big difference. Being around the people I love helps me step away from work, gain perspective, and return to projects with more energy and clarity. Exercise is also very important to me. I enjoy hiking, working out, and I also volunteer at a hot yoga studio, which has become a really meaningful part of my routine. Beyond the physical benefits, the sense of community there has been a great source of balance during busy periods. It reminds me of the importance of slowing down, being present, and taking care of myself. I also love cooking nutritious food, reading, and travelling. Cooking connects closely to my background in nutrition, but it is

also a creative outlet and a way to care for myself and others. Reading and travelling help me stay curious, inspired, and open-minded. I think these activities help me maintain balance by reminding me that creativity and motivation often come from making space for life outside of work.

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MetaboReads

Metabolic Reprogramming as a Driver of Disease

The common thread here is that altered metabolism is rarely just a consequence of disease and often an active force that holds a pathological state in place. Across leukemia, chronic liver failure, asthma, vitiligo, and the healthy brain, these studies move past cataloguing metabolic differences toward pinpointing the genes, metabolites, and signaling nodes that enforce them. Several converge on the same strategic payoff, a nominated target: RCC2 in asthmatic airway remodeling, the succinate receptor SUCNR1 in hyperglycemia-accelerated vitiligo, bile acid hub genes in liver failure progression, and MYC and mTOR-linked lipid programs in leukemic subtypes. Read together, they show how much of current mechanistic biology now runs through metabolite measurement rather than genetics alone. The

section also carries a caution, drawn from a study in which blocking a single biosynthetic step ripples across brain energy and lipid metabolism in ways that depend on sex, region, and developmental timing. That sensitivity argues against treating metabolic pathways as clean, isolable levers.

Integrated proteogenomic and metabolomic profiling of acute myeloid leukemias to identify molecular subtypes and associated therapy targets

Chu and colleagues in *Nature Cancer* reported that a thirteen-modality multiomics survey of 173 treatment-naive AML patients resolves the disease into distinct subtypes with characteristic metabolic and lipidomic wiring. Divergent MYC and mTOR activity emerged as a principal axis separating primitive from committed leukemias, driving extensive reprogramming of central metabolism and lipid handling. The integration ties genotype to phenotype and surfaces biomarkers and candidate vulnerabilities that any single omics layer would miss. For a malignancy this heterogeneous, the value lies in the map itself, which links pathobiology to actionable targets across the primitive-to-committed spectrum.

Decoupling lactylation-associated metabolic remodelling in Asthma: Integrated multi-omics and machine learning identify RCC2 as a potential therapeutic target

Feng and colleagues in *Computer Methods and Programs in Biomedicine* introduced an interpretable classifier that stratifies asthma by lactate metabolism and histone lactylation activity across airway cell lineages. Combining bulk and single-cell transcriptomes, they mapped a macrophage-predominant high-lactate state and a disease-associated module whose inflammatory programs track with metabolic subtype. Their Lactate Metabolic Biomarker Diagnosis framework outperformed single-pathway models on external validation and elevated RCC2 as the top-ranked feature. Knockdown of RCC2 in airway epithelial cells lowered intracellular lactate, suppressed glycolytic proteins, dampened pan-lactylation signals, and shifted redox and glycerophospholipid metabolism, positioning it as a hub linking glycolysis to epigenetic remodeling.

Integrated analysis of transcriptome and metabolome reveals key metabolites-related genes in chronic liver failure

Shu and colleagues in *Genomics* found that the progression from stable chronic liver failure toward acute-on-chronic failure carries a distinct bile acid signature. Weighted co-expression analysis of patient RNA-seq flagged gene modules enriched in innate immune pathways, while metabolomic profiling isolated 63 differential metabolites, among them four hydrophobic bile acids that scaled with severity. These bile acids correlated strongly and negatively with 33 hub genes, implicating bile acid biosynthesis as a node in severity progression. The cohort is small, so the bile acid and hub gene axis reads as a hypothesis worth testing at scale rather than a settled

biomarker.

Hyperglycemia aggravates vitiligo through succinate/SUCNR1-mediated T cell activation

Kang and colleagues in *Journal of Clinical Investigation* demonstrated that hyperglycemia worsens vitiligo by routing immune activation through succinate. A case-control study established the clinical correlation, and a mouse model confirmed that elevated glucose accelerates depigmentation. Targeted metabolomics singled out succinate as the mediating metabolite, acting via SUCNR1 to activate CD8+ T cells and, through stabilization of HIF-1α, to drive keratinocyte secretion of CXCL9 and CXCL10 that recruits those T cells to skin. The work supplies a mechanistic account for a long-noted clinical association and nominates SUCNR1 as a tractable target.

Blocking β-alanine synthesis triggers widespread perturbations of energy and lipid metabolism in the brain

Homaei and colleagues in *Molecular Metabolism* showed that deleting GADL1, the enzyme that generates β-alanine from aspartate, remodels brain energy and lipid metabolism in a strongly sex-dependent manner. Screening seven tissues and then profiling cerebrum, cerebellum, and olfactory bulb across sexes and ages, they saw oxidative stress and possible synaptic remodeling in mature females alongside pronounced lipid accumulation in males. The developing olfactory bulb showed lipid buildup in both sexes but inflammatory and energetic disturbance only in males. Because even a modest drop in β-alanine produced region, age, and sex-specific effects, the study argues against treating carnosine-related biochemistry as a uniform therapeutic lever.

Metabolomic Readouts of Therapeutic and Dietary Intervention

What unites this section is the use of metabolomics as a functional readout of intervention, showing not just whether a treatment works but how it reshapes systemic biochemistry. The interventions themselves span a deliberately wide range, from a classical Chinese herbal formula and a standardized olive leaf extract to incretin and gliflozin therapies and an aggressive ketogenic protocol. In each case the metabolite layer does work that clinical endpoints cannot, tracing mechanism in pulmonary fibrosis, linking periodontal recovery to shifts in inflammation and oxidative stress, separating two glucose-lowering drugs by their metabolic and microbial fingerprints, and grading hepatic vulnerability by metabolic flexibility. Two entries are trial protocols or pilots, a sign that metabolomic and microbiome endpoints are increasingly written into study design rather than bolted on afterward. The breadth reflects a field comfortable applying the same profiling toolkit to botanicals, biologics, and diet with equal seriousness. It also exposes the recurring

tension between mechanistic richness and the small samples that still characterize much of this work.

Multi-omics reveals the effects and mechanisms of Xinxue Granules against idiopathic pulmonary fibrosis through activating the cAMP/EPAC/CREB axis

Zhang and colleagues in *Journal of Ethnopharmacology* reported that the traditional formula Xinxue Granules blunts bleomycin-induced pulmonary fibrosis in mice by engaging cAMP signaling. Network pharmacology over twenty blood-absorbed components pointed to the cAMP pathway, and in vivo the formula reduced inflammation, fibroblast activation, and extracellular matrix deposition. Mechanistically it raised EPAC expression and CREB phosphorylation while lowering GLI3, and pharmacological EPAC inhibition partially reversed the antifibrotic and anti-EMT effects. The convergence of network pharmacology, transcriptomics, and metabolomics on a single axis lends the mechanistic claim more weight than any one approach would carry alone.

Adjuvant treatment with an oleuropein-enriched olive leaf extract improves periodontal outcomes in older adults with periodontitis: Metabolomic insights from a randomized controlled trial

Forbes-Hernandez and colleagues in *Phytomedicine* found that adding a standardized, oleuropein-enriched olive leaf extract to non-surgical periodontal therapy improved clinical outcomes in adults over fifty. In this double-blind, placebo-controlled trial, the treatment group achieved greater reductions in probing depth and larger attachment gains across multiple sites. Untargeted plasma metabolomics separated the groups on seventeen metabolites, with tentatively identified valine, cinnamic acid, 10-hydroxy-2-decenoic acid, and cortisol tracking periodontal improvement. The metabolite shifts map onto inflammation, oxidative stress, and tissue homeostasis, giving a plausible systemic mechanism for a local clinical benefit.

Dulaglutide versus empagliflozin as add-on therapy to metformin and sulfonylurea in type 2 diabetes: a randomized pilot study with exploratory metabolomic and microbiome analyses

Jun and colleagues in *Frontiers in Endocrinology* reported that dulaglutide and empagliflozin lowered HbA1c comparably when added to metformin and sulfonylurea, yet diverged in their metabolic and body-composition effects. Empagliflozin improved insulin resistance and produced earlier weight and fat loss, whereas dulaglutide raised beta-cell function and reduced weight more gradually. Exploratory LC-MS profiling and 16S sequencing hinted at modest, treatment-specific differences in plasma metabolites and microbiome-metabolic associations without shifting overall microbial diversity. As a small pilot, the study is best read as generating hypotheses about how these two drug classes differ beneath a shared

glycemic endpoint.

Can sodium-glucose cotransporter 2 (SGLT2) inhibition preserve renal structure and function in de novo kidney transplant recipients? Protocol for a randomised, double-blind, placebo-controlled trial assessing the efficacy of dapagliflozin on kidney structure, function and safety in kidney transplant recipients in Norway-the DEAK study

Kongerud and colleagues in *BMJ Open* described the DEAK trial, a protocol to test whether dapagliflozin can protect kidney structure and function in de novo transplant recipients, a group excluded from earlier SGLT2 inhibitor studies. The nationwide, placebo-controlled design will randomize 330 recipients to dapagliflozin or placebo for three years, with chronic eGFR slope as the primary endpoint. Beyond function and histology, the protocol writes in urinary metabolomics alongside biopsy inflammation, fibrosis scoring, and tissue mRNA and protein readouts. Embedding these exploratory metabolic endpoints in a transplant trial signals how routinely molecular phenotyping is now planned from the outset.

Very Low Energy Ketogenic Therapy Effects on Fibrosis-Dependent Metabolic Reprogramming: A Serum NMR Pilot Study

Donghia and colleagues in *Nutrients* found that very low energy ketogenic therapy reshapes the serum metabolome of obese patients, and that the response depends on underlying hepatic fibrosis risk. Serial 1H NMR across fifty samples captured rising ketone bodies after eight weeks, with acetone giving a clean quantitative marker of ketogenesis. Stratifying by fibrosis index revealed different metabolic flexibility, as lower-risk patients modulated TCA cycle intermediates while higher-risk patients held persistent alterations in aromatic amino acids and lipids. Correlations of tyrosine and β-alanine with clinical chemistry support a fibrosis-dependent signature and position circulating metabolites as noninvasive readouts of hepatic vulnerability.

Circulating Metabolite Profiling for Risk and Severity Assessment

The papers here treat the blood metabolome as a dense record of exposure and disease state, readable for both risk stratification and disease staging. One derives a circulating signature of ultra-processed food intake that predicts cardiovascular events better than dietary recall, and another tracks how plasma metabolism rewires step by step with COVID-19 severity. Both illustrate why untargeted profiling has become the preferred instrument when the biology is heterogeneous and self-report is unreliable. Their credibility rests on scale and validation in the first case and on careful clinical stratification in the second, two different routes to the same goal of trustworthy metabolite signatures. The section closes with a serum lipidomics protocol built on ion mobility and PASEF, the kind of methodological groundwork that determines whether such signatures replicate across labs. Method and application

belong in the same conversation, since a biomarker is only as good as the workflow that measures it.

Metabolomic signature of ultra-processed foods and cardiovascular morbidity and mortality

Wang and colleagues in *Clinical Nutrition* found that a blood metabolite signature of ultra-processed food intake predicts cardiovascular outcomes more strongly than reported intake itself. Across three prospective cohorts, they identified and then validated 43 circulating metabolites tied to consumption, several linked to incident coronary disease, cardiovascular death, and total mortality. The derived signature outperformed self-reported intake on every endpoint and explained most of the diet-disease association, with nucleoside and polyol markers among the standouts. By converting a notoriously noisy dietary exposure into a measurable biochemical trace, the work offers a sturdier handle on how these foods harm the heart.

Severity-dependent metabolic rewiring in COVID-19 based on untargeted metabolomic profiling of patient plasma

Majewska and colleagues in *PLOS ONE* showed that plasma metabolism tracks COVID-19 severity in an orderly, stage-specific way. Profiling 541 metabolites across four severity groups and healthy controls, they watched principal components fan out in step with pulmonary involvement and respiratory support. Monocarboxylic acid and phenylalanine perturbations dominated early to moderate disease, while the most severe cases pivoted toward pyrimidine metabolism consistent with heightened nucleotide turnover. Small as the cohort is, the graded signatures make a case for metabolomics-guided staging and stage-matched intervention.

Protocol for untargeted lipidomics of human serum using LC-TIMS-PASEF

Monteiro and colleagues in *STAR Protocols* described a reproducible workflow for untargeted serum lipidomics that couples reversed-phase separation with trapped ion mobility and PASEF fragmentation. The method profiles lipids from just 5 microliters of serum, annotating glycerophospholipids, glycerolipids, sphingolipids, sterols, and fatty acyls in one pass. Detailed guidance on project design, sample preparation, quality control, and data processing supports consistency across studies. The added mobility dimension raises annotation confidence, which matters directly for the biomarker programs featured elsewhere in this issue.

Microbial Metabolism and Microbiome-Host Crosstalk

These studies span the range from a single bacterium's internal chemistry to microbiome-driven pathology in a whole animal, held together by the idea that microbial metabolism has consequences reaching well beyond the microbe. One re-

analysis shows how sepsis-associated pathogens remodel amino acid metabolism under serum conditions in ways tied to antibiotic susceptibility, while another traces how gut dysbiosis actively drives a skeletal disorder in broilers through defined metabolite axes. A third places environmental chemistry in the loop, showing PFOS and ethanol converging on the gut-liver axis to amplify injury. Together they make the case that host phenotype often cannot be understood without accounting for microbial metabolic output. The causal experiments here, from serum-conditioned growth assays to fecal transplants, mark a shift from correlation toward demonstrated mechanism. That is a welcome trajectory for a subfield long criticized for stopping at association.

Genome-informed metabolomic re-analysis identifies serum-associated amino acid signatures in sepsis-associated bacterial pathogens

Ou and colleagues in *Frontiers in Medicine* reported that sepsis-associated pathogens carry a serum-conditioned amino acid signature that connects to antibiotic response. Re-analyzing paired whole-genome and metabolomic data from four species grown in serum or RPMI, they found the most consistent serum signature in Klebsiella, centered on branched-chain amino acid and aspartate metabolism. Validation in K. quasipneumoniae showed that serum exposure restrained growth, raised cell-associated levels of these amino acids, and pushed meropenem and ciprofloxacin inhibitory endpoints upward. The finding suggests host-like conditions reshape pathogen metabolism in ways that blunt drug susceptibility, offering candidate signatures for mechanistic follow-up.

Gut microbiota dysbiosis induced by tibial dyschondroplasia in turn accelerates disease pathogenesis through the gut-bone axis in broilers

Song and colleagues in *Poultry Science* demonstrated that gut dysbiosis is a causal contributor to tibial dyschondroplasia rather than a bystander. Fecal transplants from diseased birds transferred the phenotype to healthy broilers, while transplants from healthy donors failed to reverse it in affected birds. All disease groups showed depleted Lactobacillus and enriched Streptococcus and Escherichia-Shigella, and metabolomics isolated seven stably dysregulated metabolites. Chenodeoxycholic acid tracked positively with Lactobacillus and bone mineral content while 2-methoxyestradiol moved inversely, defining a Lactobacillus and bile acid axis as a target for prevention.

Integrated Multi-Omics Reveals Synergistic Hepatotoxicity of Ethanol and PFOS Co-Exposure

Stem and colleagues in *Chemico-Biological Interactions* found that the environmental contaminant PFOS and ethanol act together to worsen liver injury beyond either exposure alone. In a murine model, co-exposure reduced survival and produced marked hepatomegaly and mixed steatosis despite lower cumulative ethanol intake.

Multi-omic, spatial lipidomic, and metagenomic analyses traced the synergy to disrupted β-oxidation, mitochondrial and bile acid transport failure, hepatocyte-scale phospholipid remodeling, and depletion of microbiome-derived indole metabolites. Severe dysbiosis and loss of commensal anaerobes place gut-liver crosstalk at the center of the interaction, framing PFAS exposure as a modifier of alcohol-associated liver disease.

Environmental, Ecological, and Agricultural Metabolomics

This section gathers work on how organisms and managed systems remodel their metabolism in response to environment, diet, and human intervention. A castration study in yak connects an endocrine change to fat deposition and fatty acid composition through defined regulatory genes, while a survey of plateau pikas along an altitudinal gradient couples foraging strategy to liver metabolism and detoxification. Two further entries turn metabolomics on environmental problems directly, one dissecting how a marine Klebsiella strain routes carbon toward nitrate assimilation for potential use in wastewater treatment, the other mapping neonicotinoid uptake and biotransformation in rice with its attendant phytotoxicity. The shared move is to read ecology and agronomy through a biochemical lens, treating metabolite profiles as sensitive indicators of adaptation and stress. What stands out is the practical horizon, from meat quality and conservation physiology to bioremediation and food safety. These are reminders that metabolomics has real utility well outside the clinic.

Transcriptomics and Metabolomics Signatures of Fat Deposition Following Orchiectomy in Yak

Xiong and colleagues in Animals found that castration enhances fat deposition in male yaks and enriches subcutaneous fat with polyunsaturated fatty acids. Pairing GC-MS fatty acid measurement with transcriptomic and metabolomic profiling of adipose tissue, they tied the effect to the PPAR signaling pathway, the citrate cycle, and insulin resistance. The integration nominated FASN, ACACA, SCD, and SLC2A4 among others as controllers of fat quantity, with FADS2, LPL, and ACSL4 governing PUFA content. For a trait that shapes both herd management and meat quality, the gene set offers concrete handles for selection and functional study.

Dietary Divergence Along an Altitudinal Gradient Is Associated With Liver Transcriptomic and Metabolic Remodeling in a Small Mammal

Yao and colleagues in FASEB Journal showed that plateau pikas shift both diet and liver metabolism across an altitudinal gradient in a coordinated way. High-altitude animals moved from selective foraging on forbs to tolerance foraging on hardy sedges and toxic locoweeds, a change mirrored in their hepatic chemistry. Their

livers accumulated antioxidant compounds and upregulated xenobiotic detoxification and energy metabolism genes, whereas low-altitude populations favored biotic stress responses, cell growth, and immune pathways. The result reads out a tightly coupled diet-gene-metabolism axis, showing how a foraging decision redirects physiology from biotic toward abiotic stress defense.

Adaptive reprogramming of carbon-nitrogen metabolism in Klebsiella aerogenes under nitrate-rich conditions

Chen and colleagues in Frontiers in Microbiology reported that a marine Klebsiella aerogenes strain reroutes central carbon metabolism to support efficient nitrate assimilation. Under nitrate-rich conditions the strain incorporated more than 83 percent of supplied nitrate into biomass, releasing little as gaseous nitrogen. Metabolomics showed upregulated TCA intermediates and amino acids alongside lower isocitrate and acetyl-CoA, signatures of carbon skeletons redirected toward nitrogen use. With lysine degradation, glyoxylate, and taurine pathways implicated, the authors frame the strain as a candidate for sustainable nitrate removal in aquaculture and wastewater.

Uptake, metabolism, and underlying mechanisms of neonicotinoid insecticides in rice plants (Oryza sativa L.)

Wei and colleagues in Journal of Hazardous Materials found that rice readily takes up three common neonicotinoids and moves them preferentially into aboveground tissues, with acetamiprid reaching the highest shoot concentrations. The insecticides underwent extensive biotransformation through hydroxylation, sulfonation, cyanation, dechlorination, and other reactions, generating multiple transformation products. Exposure disturbed mineral nutrient balance and triggered oxidative stress, while untargeted metabolomics flagged perturbations in flavonoids, amino acids, and lipids. Transcriptomics pointed to secondary metabolite biosynthesis and core metabolic pathways, giving a mechanistic picture of both accumulation and phytotoxicity with clear food-safety implications.

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Metabolomics Events

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MANA SODAMeet

August 11, 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

MANA 2026

8th Annual Conference

September 8 - 11, 2026

Venue: UC Davis, California, USA

The Metabolomics Association of North America (MANA) is a non-profit organization that brings together a community of dedicated scientists and professionals in the field of metabolomics. With members from Canada, Mexico, and the USA, MANA is committed to fostering cooperation, coordination, and the advancement of metabolomics research in North America.

The 8th Annual MANA Conference will be hosted at the University of California. Check out the website for program information, speakers, events, registration, awards, and more.

Check for more details

Benelux Metabolomics Days 2026

September 22 - 23, 2026

Venue: Antwerpen, Belgium

The Benelux Metabolomics Days is the annual conference of the Benelux Metabolomics Centre (BMC), bringing together the metabolomics community from the Netherlands, Belgium, and Luxembourg. It will take place at Stadscampus – Hof van Liere, University of Antwerp (Belgium). Hosted by Professor Wout Bittremieux and Professor Adrian Covaci, the conference will feature keynote lectures and sessions highlighting emerging and topical areas in metabolomics. Oral and poster presentations by early-career researchers will be selected through the abstract submission process.

Visit the website for more details

Introduction to Applying GC-MS in Untargeted Metabolomics

September 22 - 24, 2026

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

CMMC Symposium 2026 – Metabolic Control of Tissue Regeneration and Degeneration

September 28 - 30, 2026

Venue: Cologne, Germany

The CMMC Symposium 2026 will focus on the emerging role of metabolic programs and metabolites as key regulators of tissue regeneration and degeneration. Beyond providing energy and cellular building blocks, metabolic pathways control fundamental processes such as cell proliferation, differentiation, reprogramming and immune responses. By linking mechanistic insights with clinical perspectives, the symposium will address major challenges in molecular medicine and human disease.

Keynote speakers:

- Elly Tanaka (IMBA, Vienna, AT)
- Axel Roers (University Hospital Heidelberg, DE)
- Gerald I. Shulman (Yale School of Medicine, US)

The meeting is open to all and free of charge but **free registration is required**.

Visit the website for more details

5th Nordic Metabolomics Conference 2026

September 28 - 30, 2026

Venue: Uppsala, Sweden

The 5th Nordic Metabolomics Conference is the official annual conference of the Nordic Metabolomics Society and will be organized at Uppsala Konsert & Kongress (UKK) in Uppsala, Sweden. The city hosts Uppsala University, who has a longstanding tradition in Analytical Chemistry and Mass Spectrometry. The conference will host the entire depth of the metabolomics community in the Nordic Countries, high profile (inter)national speakers, will include an Early Career Event, and a dinner at Uppsala Castle.

Abstract submission deadline for poster presentations - **September 1, 2026**

Check for more details

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.

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Check for more details

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.

Abstract submission deadline - **July 17, 2026**
Early bird registration deadline - **August 7, 2026**

Visit website for more details

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Job Title	Employer	Location	Source
ARISE Fellowship program	ARISE Career Accelerator for Research Infrastructure	Six EMBL sites	European Molecular Biology Laboratory (EMBL)

		Scientists	
Postdoctoral Scholar-Fixed Term	Michigan State University	East Lansing, Michigan, United States	Michigan State University

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