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MetaboNews

This month in metabolomics

October, 2026

Vol 16, Issue 9

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



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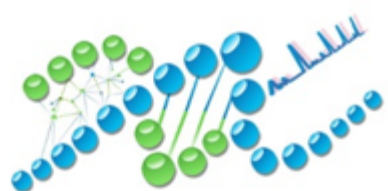
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The Metabolomics Society is an independent, non-profit organization dedicated to promoting the growth, use, and understanding of metabolomics in the life sciences.

General Enquiries

info@metabolomicssociety.org



METABOLOMICS SOCIETY
EARLY- CAREER MEMBERS NETWORK

Members Corner

Board of Directors - Words from the Chair

Dear Members and Colleagues,

It is a great honour to share my first message to you as President of the Society. I am humbled by the opportunity to serve our metabolomics community over the next two years.

I would like to begin by sincerely thanking our previous President, Warwick Dunn, for his outstanding leadership during his term, and our outgoing Secretary, María Eugenia Monge, for her invaluable contribution to the smooth running of the Society.

I would also like to acknowledge our returning Board members for their continued commitment and for the energy and enthusiasm they bring to our meetings and initiatives. In particular, Elizabeth Want will serve her second term as director, Candice Ulmer Holland will continue as Treasurer for another year, and Nicholas Rattray will take over as Secretary. I wish all our Officers every success as they work together to implement key decisions and initiatives that will shape the future of the Society.

I am pleased to welcome our four new Directors, Ian Castro-Gamboa, Facundo Fernandez, Nicola Gray and Huiru Tang, as well as Carolina Dalmeida who serves

as our EMN Chair. I am confident that the fresh perspectives and insights they bring will serve us well as we continue to build a diverse, inclusive and sustainable Society that serves our members and the wider metabolomics community.

Building on the Society's current momentum and increasingly global representation, my vision for the next two years is to strengthen a connected, inclusive and forward-looking Society that responds to regional priorities while advancing our shared global goals. In particular:

- Strengthen global participation and collaboration by broadening engagement across regions, with particular attention to underrepresented regions. Our Annual Conference provides an immediate opportunity to encourage workshops that are co-developed and delivered across regions, bringing different communities and expertise together.
- Expand access to global expertise and opportunities by strengthening connections between our international experts and underrepresented regions. A particular priority will be to seek funding and partnerships that enable international experts to deliver workshops and capacity-building activities in Africa and other underrepresented regions.
- Strengthen the Society's identity, visibility and membership engagement through more active marketing and communication, regularly sharing exciting Society developments and clearly communicating the opportunities and benefits of membership to grow engagement, membership and long-term sustainability.

Planning for our 2027 Annual Conference is already well underway, and the team is actively preparing for what we hope will be another successful event. Further details will be shared soon.

I hope to see many of you there. It will be an important opportunity to reconnect, share ideas and hear your feedback on the changes and developments taking place within the Society. Your input will be vital as we shape its future together.

My special thanks go to Snap for their continued administrative support. Leslie, Bridget and their team play an important role in the Society's day-to-day work, and their contribution is greatly appreciated.

Finally, I look forward to an exciting year ahead and to working with all of you to strengthen and grow our Society.

Regards and best wishes,

Aurelia Alvina Williams
North-West University, South Africa
President, Metabolomics Society

Early-career Members Network (EMN)

Welcome to our new EMN Committee members!

We are delighted to welcome the new members joining the EMN Committee for the 2026–2027 term:

- Andrés Rogelio Martínez Bilesio – Germany
- Stefan Pieczonka – Australia
- João Marcos Gonçalves Barbosa – Sweden
- Akhona Myoli – South Africa
- Eduardo Solano Pina dos Santos – Brazil
- Lidiia Rumiantseva – Belgium
- Samaria Johana Gutiérrez Felix – Mexico

We are excited to have them on board. The EMN Secretary and Treasurer for the 2026–2027 term will be elected at our first committee meeting and announced in the next issue of MetaboNews. Stay tuned!

EMN & Affiliates Virtual Symposium – REGISTER NOW!

The EMN-MetSoc, in collaboration with the Polish Metabolomics Society, Spanish Metabolomics Society, Australian and New Zealand Metabolomics Society, and Metabolomics Association of North America, is pleased to announce the EMN & Affiliates Virtual Symposium.

The symposium will feature keynote and ECR presentations and will take place virtually on Tuesday, November 3rd, with regional sessions for Europe/Africa (14:00–16:30 CET) and Asia/Oceania (14:00–16:30 AEDT).

Register here:

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

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

October EMN Webinar – Thank you!

The EMN Committee would like to thank Dr Zoe Hall, Associate Professor, and Dr Aleksandra Gruevska, Postdoctoral Researcher at Imperial College London (UK), for their excellent webinar, “Spatial metabolomics to explore metabolic microenvironments in liver disease and cancer.”

We also thank everyone who joined us for the session. The webinar recording will be available on the Metabolomics Society website.

Metabolomics Society Webinar

November 5th at 1pm UCT

Turning Methods into Open, Citable Protocols: A Practical Webinar with protocols.io

Reliable methods are the foundation of metabolomics research, yet they rarely stand still. Recording the full methodological context in a form that others can easily find, reuse and build on is often harder than it should be. This practical webinar will show how to convert experimental methods into open, citable, version-controlled protocols that link directly to your publications, strengthening the credibility, discoverability and reproducibility of your work.

Attendees will also find out how to make the most of the protocols.io Premium access available exclusively to Metabolomics Society members. Premium goes beyond protocol publishing, offering private protocol management through a dynamic, interactive methods repository that your whole team can use.

The session will be particularly valuable if you have ever:

- hunted for specific method details that were missing from a paper
- repeated work because methodological information was hard to locate or reuse
- lost track of which version of a protocol was the most current
- wanted to make your methods more open, reproducible and useful to the wider community

Invited speaker: Dr Julia Kurz, Scientific Engagement Manager, protocols.io (part of Springer Nature)

Please use the link below to register:

https://zoom.us/webinar/register/WN_-Vu6PjumST2PWAz6aL2S2Q#/registration

International Affiliates Corner

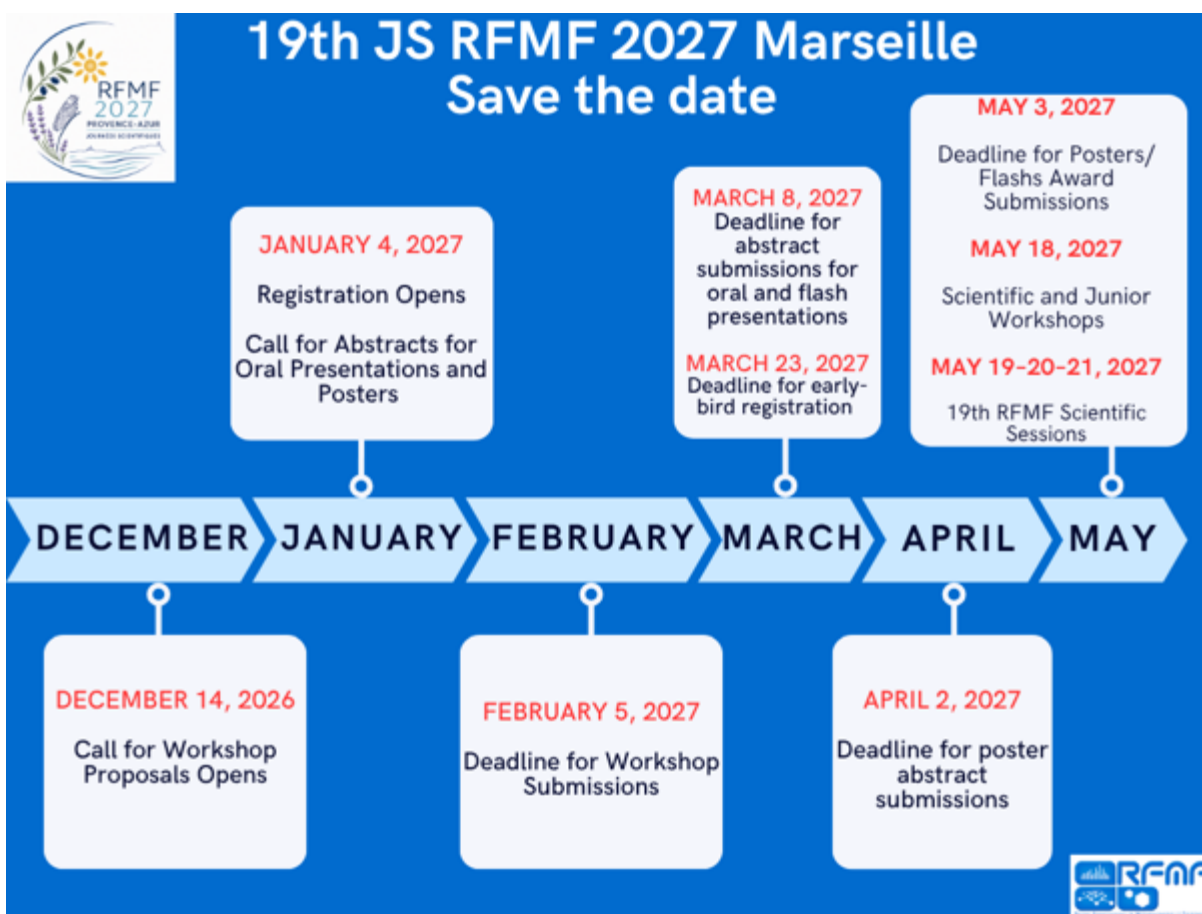


Réseau Français de Métabolomique et Fluxomique (RFMF)

Visit <http://www.rfmf.fr/>

Save the date! The 19th RFMF Days will take place from May 19-21, 2027.

Take note of these key dates, from the opening of registration and abstract submissions to the deadlines for workshop, oral, flash and poster presentations. And don't miss the Scientific and Junior Workshops on May 18th!



Next W4E 2027 session in Rennes, France



Save the date! Analyze your data with **Galaxy** and the **Workflow4metabolomics** infrastructure!

The next **Workflow4Experimenters session (W4E2027)** will take place in April 2027. 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, format changes:

- From April, 5th to 9th: online theoretical sessions (methods and tools)
- From April, 26th to 30th: tutoring on your own data, Pôle Numérique Rennes Beaulieu in Rennes (France).

Online sessions are reserved for participants who attend to on-site session

Invited speaker: to be announced soon

Scientific Committee: C. Delporte (ULB, Bruxelles), C. Dalle (U.DAB IRBA, Brétigny-sur-Orge), Y. Guitton (Laberca INRAE, Nantes), D. Centeno & 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)

Pre-registration: to be communicated soon

Cost: Academic 1300€; Private 2500€

In case of RFMF membership, 100€ discount

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).



See you soon in Rennes !

Preliminary program

1- Webinars

Start	End	MONDAY 28th April		TUESDAY 29th April		WEDNESDAY 30 April
08:30	09:00					
09:00	09:30					
09:30	10:00					
10:00	10:30	Introduction		Statistical analysis M. Pétéra / M. Tremblay-Franco		Advanced topic(s)
10:30	11:00					
11:00	11:30	Galaxy session : initiation and data management M. Pétéra / Y. Guitton / G. Le Corguillé				
11:30	12:00					
12:00	12:30					
14:00	14:30	[MS] Data Preprocessing M. Pétéra / Y. Guitton	[NMR] Data Preprocessing C Canlet / M. Tremblay-Franco	[MS] Annotation Y. Guitton / R. Weber	[NMR] Annotation C. Canlet	
14:30	15:00					
15:00	15:30					
15:30	16:00					
16:00	16:30	Signal Drift and Batch-Effect Correction - M. Pétéra				

2- On-site training

Start	End	MONDAY 12th May	TUESDAY 13th May		WEDNESDAY 14th May	THURSDAY 15th May		FRIDAY 16th May			
08:30	09:00		[MS] Data Preprocessing	[NMR] Data Preprocessing	Statistical analysis	[MS] Annotation MS and MSMS	[NMR] 1D and 2D Annotation	Advanced topic(s)			
09:00	09:30										
09:30	10:00		Tutoring	Tutoring	Tutoring	Tutoring	Tutoring				
10:00	10:30										
10:30	11:00		Break		Break	Break		Break			
11:00	11:30			Tutoring	Tutoring	Tutoring	Tutoring	Tutoring	Week debrief and Survey		
11:30	12:00	Welcome and lunch boxes	Signal Drift and Batch-Effect Correction								
12:00	12:45		Tutoring								
12:45	14:00		Buffet lunch		Buffet lunch	Buffet lunch		Lunch boxes			
14:00	14:30	Introduction and round table	Invited speakers H���								

MetaboHUB is hiring!

Several exciting opportunities are opening in **bioinformatics, software development, metabolomics, flux modelling and data processing**, with positions based at **MetaboHUB facilities in France**.

Start date: January 1st, 2027

Interested in joining a leading research infrastructure in metabolomics and contributing to cutting-edge data, technology, and analytical workflows?

Check out the individual job offers and apply:

<https://www.metabohub.fr/emplois-et-stages.html>

Please share with anyone who might be interested!

4th MetaboHUB webinar | November 13th, 2026

What role does p53 play in regulating metabolism?

Join us for this new MetaboHUB webinar, which will bring together complementary expertise in metabolomics, lipidomics and fluxomics to explore this complex biological question.

« Deciphering the role of p53 in the control of metabolism »

November 13th, 2026

1.30–3.30 (UTC+1)

On the agenda:

- Introduction and presentation of MetaboHUB's expertise
- The p53 pathway and metabolism
- Data visualisation and acquisition
- Statistical integration of data
- Multi-technology and multi-site data management
- The benefits of MetaboHUB in tackling complex biological challenges
- Questions & conclusions

Sign up here (free but mandatory) : <https://framaforms.org/coming-soon-webinar-metabohub-registration-is-freebut-mandatory-1782993241>

Come and find out how the MetaboHUB national infrastructure can support your complex biological projects.

MetaboHUB training in metabolomics

TRAINING "Hands-On Metabolomics: From Bench to Data" – Places Still Available!

There are still places available for the upcoming MetaboHUB training! If you are interested in learning how to integrate metabolomics into your research or analytical projects, this is a great opportunity to gain both theoretical knowledge and practical, hands-on experience.

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? November 23–27, 2026

Where? Toulouse, France – INSA Campus

Who is it for? Researchers, engineers, technicians, doctoral and postdoctoral

students, academics and industry professionals, biologists and analysts

What will you learn?

Expert scientists from the MetaboHUB infrastructure will introduce you to the fundamental principles and cutting-edge techniques of metabolomics through a dynamic combination of **theoretical and hands-on sessions**.

Interactive format:

- Practical workshops
- Discussions and case studies
- Keynotes and workshops
- **Training certificate provided**

Registration & contact: fcq@insa-toulouse.fr

Limited places are still available – register soon to secure your spot!

i All the information is available in the picture below.



HANDS-ON METABOLOMICS: FROM BENCH TO DATA




INSA
Toulouse


23.11 to
27.11.2026

Duration
4.5 days
31 hours

Registration
deadline
03.11.2026

PROGRAMME

DAY 1

Basics of Metabolomics
Principles, strategies and study design

DAY 2

Acquisition and processing in MS
From sample to data

DAY 3

Acquisition and processing in NMR
From sample to data

DAY 4

Statistics & Chemometrics
Preprocessing, annotation, statistics, multivariate analysis

DAY 5

Workshops
Metabolic networks, Fluxomic, or lipidomics ! Up to you !



Practical sessions everyday

**ASSESSMENT &
CERTIFICATE**

**DESIGNED BY
NATIONAL
INFRASTRUCTURE
METABOHUB**

**ENGLISH
MATERIALS FOR
PRESENTATIONS**

F Bellvert - MS & Fluxomics
J Bertrand-Michel - Lipidomics
E Cahoreau - NMR
C Canlet - NMR
R Cordazzo - Metabolomics & plant
L Cottret - Bioinformatics
N Creusot - Metabolomics & ecotox
L Debrauwer - MS
Y Guitton - Chemometrics
M Heuillet - MS
E Jamin - MS
F Jourdan - Bioinformatics
H Kulyk - MS
P Le Faouder - Lipidomics
M Liotier - Bioinformatics
M Maravat - NMR
P Pétriacq - Plant Biochemistry
L Peyriga - NMR & Fluxomics
T Richard - NMR
M Tremblay-Franco - Statistics
J Valls - Metabolomics & plant

Fees*

2050 € for academics
2900 € for industrials
 *Teaching materials and lunches included

Contacts

Scientific coordinators
 Marie Tremblay-Franco, IR, INRAE
 Pierre Pétriacq, DR, INRAE

Informations and registrations
 05.61.55.92.53 - fcq@insa-toulouse.fr

Target audience

10 to 20 participants

- Academics or industrials
- Researchers, engineers, technicians, PhDs and post-docs
- Biologists, analysts



www.metabohub.fr

INSA

TOULOUSE



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REGISTRATION:



canmetcon.com



TWO DAYS OF CURRENT
METABOLOMICS RESEARCH





POSTER PRESENTATIONS
& LIGHTNING TALKS



MEET INDUSTRY
EXPERTS

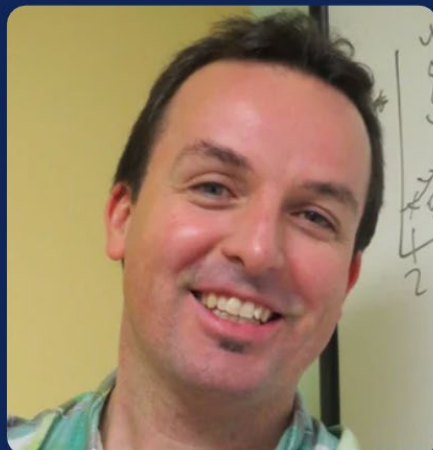
8TH ANNUAL CANADIAN METABOLOMICS CONFERENCE

MAY 6TH - 7TH, 2027

Hear the latest research and connect with the metabolomics community in **Canmore, Alberta**. Featuring plenary and invited talks and all nine TMIC node leaders.

[MetaboTalks](#)

Meet the Speakers!



Dr. Philip Britz-McKibbin

McMaster University



Dr. Rafa Montenegro Burke

University of Toronto

METABOTALKS
Brought to you by TMIC

November 18th, 2026

ONLINE @ 10AM MDT

Thank you to everyone who joined us for our October edition of **MetaboTalks**, featuring **Dr. Sheri Schmidt from the University of Alberta!**

Join us on **November 18, 2026, at 10:00 AM MDT** for the next edition of **MetaboTalks**, TMIC's monthly webinar series bringing together experts in metabolomics and related fields.

This session features **Dr. Philip Britz-McKibbin** of McMaster University and **Dr. Rafa Montenegro Burk** of the University of Toronto. Join us to hear from these researchers as they share their expertise and perspectives on advancing metabolomics research.

Date: November 18, 2026

Time: 10:00 AM MDT

Location: Online

Additional details: <https://metabolomicscentre.ca/science/metabotalks/>

Stay tuned for more details and registration information. We look forward to seeing you there!

 **BIOGNOSYS**
GROUP

Webinar

October 27, 2026 | 4 PM CEST

Hybrid Metabolomics Now Standardized

- **Confident discovery** with Bruker's timsMetabo™
- **Robust quantitation** with the *biocrates MxQuant kit*
- **Streamlined workflow** in an integrated software ecosystem

Click here to register



[MetaboReads](#)

Open Software for the Full Analytical Chain

Data processing remains the least standardized stage of most metabolomics studies, and the three contributions in this section each address a different link in the chain that runs from raw vendor files to biological interpretation. Two present the latest MetaboAnalyst release in protocol form, one written for general untargeted work and one built around the specific demands of exposomics, while the third assembles an open pipeline for targeted MRM data, a corner of the field that has long depended on proprietary software and hand-curated peak integration. Read together, they show tool developers converging on a shared

set of priorities: raw spectral processing inside the analysis environment, MS2-based annotation as a default rather than an add-on, and an audit trail that a second laboratory can follow. The protocol format matters as much as the software. Step-by-step procedures with worked datasets and stated run times lower the barrier for groups without a dedicated informatician, and they make it easier for reviewers to ask exactly which settings were used. With dose-response modeling and causal inference now sitting beside PCA and pathway enrichment in the same interface, the bar rises for what a routine exposure or cohort study can be expected to report.

[Using MetaboAnalyst 6.0 for exposomics data analysis: from LC-MS² spectra processing to dose-response modeling and causal inference](#)

Pang and colleagues in *Nature Protocols* described how MetaboAnalyst 6.0 can carry an exposomics study from raw LC-MS/MS spectra through to causal inference, extending the group's 2022 protocol in the same journal. The workflow runs in four stages: spectral processing with MS2-based compound identification, exposome-aware data processing and exploratory analysis, dose-response modeling of metabolic responses to exposure level, and the use of known genetic associations to test whether a metabolite plausibly lies on a causal path to disease. Stages one to three are demonstrated on a recent blood exposomics dataset concerning electronic waste exposure, and stage four on a proposed causal link between L-isoleucine and type 2 diabetes. The authors estimate about two hours for spectral processing, depending on server load, and roughly 90 minutes for everything that follows, which puts a full exposomics analysis within reach of groups without in-house informatics support.

[Metabolomics Spectral Processing, Data Analysis, and Multiomics Integration Using MetaboAnalyst 6.0](#)

Pang and colleagues in *Methods in Molecular Biology* presented eight new or substantially revised protocols for MetaboAnalyst 6.0, updating the twelve procedures the group published for version 4.0 in 2019. The earlier set leaned toward targeted metabolomics, whereas this one is organized around untargeted LC-MS, beginning with raw spectral processing with or without MS2 data, MS2 spectral annotation, and functional analysis of untargeted datasets. Further protocols cover multifactor statistical designs, dose-response analysis, pathway and joint-pathway analysis with other omics layers, and causal analysis. A final protocol moves the same workflows into MetaboAnalystR for batch processing, giving laboratories a route from point-and-click exploration to scripted, repeatable runs on larger studies.

[MStargetR: a reproducible, containerised workflow for end-to-end targeted \(MRM/SRM\) mass spectrometry data processing in R](#)

Szemray and colleagues in *Metabolomics* introduced MStargetR, an R-native, containerized workflow that takes targeted MRM/SRM data from vendor files to a finished QC report in a single pipeline. Its three modules handle conversion to mzML through msConvert, peak

boundary optimization and integration executed through Skyline, and normalization, concentration calculation, signal and batch correction, and reporting; a Shiny interface and a standalone correction module sit alongside. Third-party tools are pinned in versioned Docker images with Apptainer support for HPC, and every plate produces a populated Skyline document so that integrations can be inspected by a person and reimported. On a published targeted lipidomics dataset of 128 plasma samples and 1,161 lipid species, the pipeline recovered every targeted feature, 949 of which met an RSD below 30% across long-term reference QCs, and processing scaled linearly to 4,200 samples at about 4.1 seconds per sample.

Natural Products and the Search for Mechanism

Traditional remedies and marine organisms continue to supply candidate therapeutics, and what now separates convincing work from routine screening is whether a chemical inventory can be tied to a defined molecular target. The four studies here sit at different points along that path. At one end, LC-MS/MS molecular networking annotates and organizes a family of sesterterpenoids from a strongly cytotoxic sponge extract; at the other, metabolomics locates a specific lesion, succinate accumulation in failing liver, and pharmacological inhibition of the responsible enzyme is used to test whether a herbal formula acts through it. Two of the papers concern hepatic injury, and both arrive at redox and mitochondrial metabolism, through ferroptosis in one case and the TCA cycle in the other. That convergence reflects how often untargeted profiling in liver models points back to glutathione, lipid peroxidation and succinate, and it argues for designing follow-up experiments around those nodes from the start. The persistent weakness across this literature is the distance between tentative annotation and an isolated, quantified compound, a gap these studies narrow without fully closing.

[Metabolomic profiling and antiproliferative activity of the marine sponge *Phyllospongia foliascens* using LC-MS/MS-based molecular networking](#)

Alsharif and colleagues in *Scientific African* reported that a crude extract of the Red Sea sponge *Phyllospongia foliascens* is strongly cytotoxic toward human cancer cell lines, with IC₅₀ values of 0.2 µg/mL against MCF-7, 1.5 µg/mL against HepG2 and 5.7 µg/mL against HCT116. LC-MS/MS profiling yielded tentative annotations for 42 scalarane-type sesterterpenoids. Molecular networking was then used to map the structural and biosynthetic relationships within this compound class. Because the activity data come from the whole extract, attributing potency to individual scalaranes will require fractionation and testing of purified constituents.

[Metabolomics analysis of *Brassica rapa* leaves and validation of its action as a natural remedy for pain, pyrexia and inflammation through modulating JAK/STAT3/MCP1 signaling pathway](#)

El-Abd and colleagues in *Tissue & Cell* found that a methanolic extract of turnip (*Brassica*

rapa) leaves has analgesic, antipyretic and anti-inflammatory activity in rats, lending experimental support to the plant's traditional uses. UPLC-MS/MS tentatively identified 39 compounds, mainly flavonoids, phenolics and glucosinolates, and GC-MS identified fifteen, with glucobroteroin making up 87.61% of that profile; glucobrassicin, cetyl palmitate, p-coumaric acid and luteolin were isolated outright. The extract lengthened response latency in hot-plate and tail-flick tests, and at 200 mg/kg it controlled yeast-induced fever and reduced carrageenan paw edema. Its anti-inflammatory effect came with lower oxidative stress and reduced p-STAT3, JAK, MCP1, IL-1 β , TNF- α and iNOS, consistent with action through JAK/STAT3 signaling.

[Alleviation of hepatic ischemia-reperfusion injury by ginsenoside Rg5 and deoxyandrographolide through inhibition of SLC7A11/GPX4-mediated ferroptosis](#)

Su and colleagues in *International Immunopharmacology* demonstrated that ginsenoside Rg5 and deoxyandrographolide, identified as bioactive constituents of Shenfu Injection, protect against hepatic ischemia-reperfusion injury in mice and in AML12 hepatocytes subjected to oxygen-glucose deprivation and reoxygenation. Combined treatment lowered serum ALT and AST, restored antioxidant capacity, and reduced inflammation, hepatocyte apoptosis and histological damage. Transcriptomic and metabolomic profiling converged on ferroptosis, glutathione metabolism and lipid peroxidation, and docking with molecular dynamics predicted that both compounds interact with SLC7A11 and GPX4. Treatment raised SLC7A11 and GPX4 at the mRNA and protein levels and suppressed PTGS2 in vivo and in vitro, consistent with protection through the SLC7A11/GPX4 ferroptosis axis.

[Wenyang Jiedu Huayu Formula targets succinate metabolism to alleviate acute-on-chronic liver failure](#)

Zhou and colleagues in *World Journal of Gastroenterology* showed that the Wenyang Jiedu Huayu formula relieves acute-on-chronic liver failure in rats at least partly by clearing accumulated succinate. Targeted energy metabolomics identified succinate buildup and TCA cycle dysfunction in ACLF liver, both reversed by treatment. The formula increased succinate dehydrogenase activity and SDHA/B expression, driving succinate-to-fumarate conversion and lowering HIF-1 α , and it also restored mitochondrial ultrastructure and ATP content and reduced CD68+ macrophage infiltration. Co-administration of an SDH inhibitor partially abolished these benefits, which gives the mechanistic claim more weight than correlation alone would and points to succinate metabolism as a therapeutic target in ACLF.

Regulatory Control of Pigment Metabolism

Color is one of the few metabolic phenotypes a grower or consumer can read directly, which makes pigment pathways an obvious target for combined metabolomic and transcriptomic work. The three studies in this section trace pigmentation in two fruit species and an edible mushroom back to the factors that control it. In fig and blue honeysuckle, the control points are MYB and bHLH transcription factors acting on anthocyanin biosynthesis, found by tracking gene expression against metabolite accumulation through ripening or cold

exposure. The honeysuckle work goes a step further: the same anthocyanin machinery, together with iridoid synthesis, contributes to cold tolerance, so pigment production and stress defense run through one regulatory program. The mushroom study finds its lever in redox status, where glutathione metabolism shifts the balance between eumelanin and pheomelanin. Where these papers are strongest, metabolite profiling narrows the candidate list and a direct manipulation, overexpression in fig or chemical treatment in the mushroom, supplies the causal test.

Integrated metabolomic and transcriptomic analyses reveal the regulatory role of FcMYB6 in promoting anthocyanin biosynthesis in fig (*Ficus carica* L.) fruit

Wang and colleagues in *Plant Science* found that the MYB transcription factor FcMYB6 promotes anthocyanin accumulation in the peel of the red fig cultivar 'Red Orphan'. Metabolomic profiling across fruit development identified 13 anthocyanin-related metabolites, with pelargonidin and pelargonidin-3-(6'-malonylglucoside) the likely main contributors to red coloration. Transcriptomic and correlation analyses flagged 26 candidate MYB regulators, of which FcMYB6 tracked anthocyanin content most closely and was most highly expressed in strongly pigmented fruit. Overexpression of FcMYB6 enhanced anthocyanin accumulation, giving breeders a defined target for improving fig color.

Adaptive cold-environmental strategies of *Lonicera caerulea*: synergistic regulation of anthocyanin and iridoid pathways in cold tolerance and fruit ripening

Wang and colleagues in *Horticulture Research* reported a chromosome-level genome assembly for wild blue honeysuckle (*Lonicera caerulea*) from the Changbai Mountain region and used it, with transcriptomic and metabolomic data, to explain how the species tolerates cold and ripens fruit in early spring. Under cold stress, an LcODO1/LcMYB15-LcSLAS module promotes iridoid accumulation while an LcbHLH62/LcMYB3R5-LcF3GT module enhances anthocyanin biosynthesis, and the two together raise cold resistance. During ripening the pathways diverge, with anthocyanins rising in both pulp and peel while bitter iridoids fall sharply in the pulp. The genome and regulatory modules give breeders gene resources for improving cold tolerance and fruit quality in this crop.

From dark-brown to yellow: metabolomics reveals ROS alterations regulating glutathione metabolism to control cap color changes in *Flammulina filiformis*

Liang and colleagues in *Food Research International* showed that reactive oxygen species control cap color in dark-brown strains of *Flammulina filiformis* by way of glutathione-mediated redox balance. Exogenous application of the ROS scavenger DMTU faded caps from dark brown to yellow, lowered the activity of melanin biosynthetic enzymes and raised the pheomelanin-to-eumelanin ratio. Metabolomics showed strong activation of glutathione metabolism after DMTU treatment, and applying either GSH or GSSG reproduced the faded phenotype. qRT-PCR confirmed upregulation of glutathione synthesis and regeneration genes alongside repression of melanin synthesis genes, giving breeders a redox-based framework for selecting cap color.

Light and Drought as Metabolic Signals in Plants

Plants read their environment largely through metabolism, and the three studies in this section use multi-omics to follow how light quality and water supply are translated into changes in chemical composition. Two of them run closely comparable spectral designs, exposing potato tubers and tall fescue to monochromatic and mixed light, and both find that blue light drives the strongest photosynthetic or pigment responses while green light does comparatively little. Both are also careful about the limits of their data, the potato study warning against extrapolating peel-enriched glycoalkaloid levels to whole tubers and the fescue study reporting where transcript and metabolite layers fail to agree. That candor is a useful corrective to multi-omics papers that report only the pathways where everything lines up. The drought study, on a desert xero-halophyte, adds a time dimension by sampling recovery as well as stress, and finds that the metabolome does not return to baseline after rewatering, a persistence that invites testing under repeated drought cycles. The applied stakes differ in each case, from glycoalkaloid safety in stored potatoes to turf quality under supplemental lighting and the use of desert shrubs as models for drought adaptation.

[Light spectrum differentially regulates postharvest tuber greening and steroidal glycoalkaloid accumulation in potato through coordinated metabolic and transcriptional reprogramming](#)

Sa and colleagues in *Postharvest Biology and Technology* found that light spectrum shapes how strongly harvested potato tubers green and accumulate steroidal glycoalkaloids (SGAs). Among dark, UV-A, blue, green, red and white treatments, blue and white light induced the most chlorophyll, carotenoid, anthocyanin and SGA accumulation, green light the least, and red light comparatively low pigment but relatively high SGA. Chlorophyll content correlated positively with total SGA, and SGA in periderm-enriched outer tissue exceeded the commonly cited 200 mg/kg FW benchmark under every light treatment except green, although the authors caution against extrapolating those values to whole tubers or consumer exposure. Integrated metabolomic and transcriptomic data pointed to spectrum-dependent reprogramming of chlorophyll, carotenoid, mevalonate-sterol and SGA biosynthesis linked to HY5-PIF transcriptional responses.

[Light quality-dependent carbon allocation in tall fescue: Integrated transcriptomic and metabolomic evidence](#)

Ding and colleagues in *Environmental and Experimental Botany* reported that light quality changes how tall fescue divides carbon among photosynthesis, storage and structural fractions. Blue light raised photosynthetic capacity and whole-plant carbon stock without matching gains in leaf non-structural carbon or cell wall fractions, whereas red light favored turf quality and the accumulation of starch, hemicellulose and lignin. Red-blue light gave the highest sucrose content and strong antioxidant responses, and green light the weakest growth and photosynthesis. Multi-omics analysis found treatment-specific responses rather

than a shared UDP-glucose-centered pathway, with red-blue light showing concordant enhancement of unsaturated fatty acid biosynthesis across both omics layers and green light showing coordinated suppression along the phenylpropanoid-flavonoid axis.

[Metabolomic insights into tolerance mechanisms of the desert shrub *Haloxylon salicornicum* during drought and recovery](#)

Ezzine and colleagues in *Acta Physiologiae Plantarum* described organ-specific metabolic responses to drought and rewatering in seedlings of the desert xero-halophyte *Haloxylon salicornicum*. After 15 days without water, 25 metabolites accumulated in shoots and 24 in roots, with glutathione, leucine and N-acetylputrescine rising in both organs as candidate drought markers. Shoots built up xylulose, xylitol and galacturonate, linked to cuticle and cell wall remodeling, along with aspartate, asparagine and TCA cycle intermediates, while roots accumulated osmolytes such as β -alanine and GABA as well as putrescine, glycerol and UDP-glucuronate. Fifteen days of rewatering did not restore the pre-stress profile, and several stress-related metabolites stayed elevated.

Processing, Provenance and Product Quality

Much applied metabolomics is ultimately asked a commercial question: does a change in how a product is grown, fed or processed alter its chemistry in ways that matter for quality? The four studies here put that question to a medicinal herb, cured tobacco, coconut and duck meat. Two of them treat processing as chemistry to be decoded, linking stir-frying temperature or staged curing parameters to defined shifts in the metabolome and in color or sensory traits. The coconut study is a useful counterweight, because its factorial design across varieties and landscapes found little separation in untargeted profiles and reported that null result plainly; carefully designed negative findings of this kind are scarce in the food metabolomics literature. The duck feeding trial pairs metabolomics with proteomics to connect a dietary intervention to creatine biosynthesis and amino acid metabolism in muscle. Across the section, the more persuasive studies are those that tie metabolite changes to a measured quality endpoint rather than stopping at a list of differential features.

[Wine processing as a chemical driver for reprogramming the metabolomic profile and color phenotype of *Radix Paeoniae Rubra*: an integrative molecular networking and thermochemical study](#)

Gao and colleagues in *Food Research International* demonstrated that rice wine processing reprograms both the metabolome and the color of *Radix Paeoniae Rubra*, and they built an interpretable framework linking processing parameters to chemical change. A four-factor, multilevel processing design was combined with CIE L*a*b* color phenotyping, UPLC-Q-TOF-MS metabolomics and consensus feature selection across PLS-DA, random forest, SVM-ROC and FDR-corrected ANOVA, which retained 399 processing-responsive features. Stir-frying temperature was the factor most strongly associated with metabolic divergence, with a model-estimated transition region near 90 °C rather than a precisely resolved threshold. Feature-based molecular networking suggested a cascade of lipid and ester hydrolysis, glycoside degradation, oxidation and Maillard-like nitrogen incorporation,

with rice wine supplying organic acids, amino acids and acetaldehyde as exogenous reactants. The authors treat thermochemical estimates and IBM RXN reaction predictions as auxiliary evidence only and frame provisional structures for two nitrogen-containing features as testable hypotheses.

[Multi-platform metabolomics reveals the effects of different staged curing processes on tobacco quality and metabolic mechanisms](#)

Zhao and colleagues in *Industrial Crops and Products* found that adjusting process parameters at specific stages of flue-curing changes tobacco leaf chemistry and quality in distinct ways. Working with B2F and B3F grade leaves of Yunyan 87, they compared treatments that modified the yellowing and color-fixing stages together (SG), the color-fixing stage alone (SS) and the stem-drying stage (SW), profiling leaves by LC-MS and GC-TOF-MS. SG produced the lowest starch, the highest sugars and polyphenols, and the best sensory scores and average price, with accumulation of phenylpropanoid aroma precursors and downstream flavonoids. SS moved in the same direction less effectively, whereas SW led to indole derivatives from tryptophan metabolism and excess organic acids from the tyrosine pathway; differences between grades traced to richer terpenoid and flavonoid content and fewer irritant compounds in B2F leaves.

[Physicochemical, mineral, and metabolic variation across coconut varieties and coastal landscape types](#)

Cardona and colleagues in *European Food Research and Technology* reported that compositional variation among coconut varieties and coastal production landscapes is trait-specific and, for most measures, small. Their 2 × 3 factorial design covered alluvial and fluvio-marine plains and the Manila Red, Hybrid and Alto Pacífico varieties, with 36 biological replicates each pooling six fruits from six palms. Kernel circumference differed by variety and the kernel-to-water ratio by landscape, but moisture, oil content and the physicochemical traits of coconut water and milk showed no significant effects. Mineral composition was where differences emerged, with calcium tracking variety and magnesium and potassium showing variety-by-landscape interactions. Untargeted UPLC-ESI-QTOF-MS profiling of coconut milk retained 709 features after QC filtering, yet PCA showed no clustering by variety or landscape and no valid PLS-DA model could be built.

[Yeast-fermented feed improves growth and meat quality in meat duck: Integrated metabolomics and proteomics reveal amino acid metabolic mechanisms](#)

Liu and colleagues in *Poultry Science* showed that adding 5% yeast-fermented feed to the diet of Cherry Valley ducks for 42 days improves late-phase growth, feed efficiency and carcass yield while making breast meat leaner. Supplemented birds reached a higher final body weight with a lower feed-to-gain ratio and higher semi-eviscerated and eviscerated yields, and their breast muscle contained less crude fat and more phenylalanine and lysine. Metabolomics and proteomics identified 179 differential metabolites and 388 differential proteins converging on glycine, serine and threonine metabolism, arginine and proline metabolism, and aminoacyl-tRNA biosynthesis. Creatine biosynthesis stood out, with

glycocyamine, sarcosine, creatine, creatinine and the enzymes GATM, GAMT and Ckmt1 all upregulated, marking the pathway as a candidate biomarker set for feed-driven meat quality.

Pollutants, Microbial Communities and Barrier Inflammation

Microbial communities sit between many environmental inputs and the outcomes researchers measure, whether that outcome is a degraded pollutant or an inflamed tissue. The three studies in this section pair metabolomics with metagenomic, microbiome or host transcriptomic data to explain how community function and host barriers respond to stress. In an engineered system the variable is hydrodynamics, and changing stirring speed reshapes which microbes and which degradative genes dominate a wastewater reactor. In fish, chronic pyrethroid exposure disrupts the gut microbiota, the epithelial barrier and host energy metabolism at the same time. In laying ducks, cloacal inflammation is traced to coordinated changes in immune genes and in taurine- and lipid-related metabolites. Each study reports an integrated correlation structure rather than a single causal chain, and the next step for all three will be interventions that test which of the linked microbial or metabolic changes are drivers and which are passengers.

[Hydrodynamic regulation drives azo dye transformation and hydrolysis acidification by reshaping microbial metabolism in the micro-aerobic hydrolysis acidification reactor](#)

Hui and colleagues in *Journal of Hazardous Materials* demonstrated that hydrodynamic conditions govern how a micro-aerobic hydrolysis acidification reactor degrades the sulfonated azo dye Acid Red GR. A moderate stirring speed of 120 rad/min balanced turbulence intensity with flow uniformity, giving favorable oxygen transfer and the highest biodegradability (0.50) and VFA production (140.38 mg/L). This condition enriched hydrolytic, facultative and fermentative genera including *Klebsiella*, *Enterobacter*, *Bacteroides*, *Propionivibrio* and *Bacillus*, along with genes for azo reduction, aromatic intermediate transformation, pyruvate generation and acidogenesis. Combined metagenomic, metabolomic and functional group evidence traced a degradation route through azo reduction, deamination, desulfonation and aromatic ring cleavage to acidogenic products.

[Chronic bifenthrin exposure disturbs intestinal homeostasis in common carp via mitochondrial dysfunction, epithelial barrier injury, gut dysbiosis, and metabolic reprogramming](#)

Feng and colleagues in *Pesticide Biochemistry and Physiology* found that 30 days of exposure to bifenthrin at 0.1 to 2 µg/L disrupts intestinal homeostasis in common carp on several fronts at once. Exposed fish showed altered digestive enzyme activity, histopathological damage, oxidative imbalance, impaired mitochondrial function and increased apoptosis, together with barrier failure marked by altered tight junction proteins and higher serum diamine oxidase and D-lactate. Raised intestinal and serum

lipopolysaccharide and pro-inflammatory cytokines indicated persistent inflammation, while the microbiota shifted toward potential opportunists at the expense of dominant commensals. Metabolomics revealed disrupted energy metabolism, lipid mediator imbalance and altered redox metabolism, and microbiome-metabolome correlation linked the dysbiosis to metabolic signatures of intestinal damage.

[Integrated transcriptomic and metabolomic analyses reveal host-metabolite interactions underlying cloacal inflammation in laying Pekin ducks](#)

Xu and colleagues in Animal Bioscience reported host-metabolite interactions associated with cloacal inflammation, a welfare and productivity problem often accompanied by prolapse, in laying Pekin ducks. Histology showed a loose, disorganized cloacal sphincter in inflamed birds, and transcriptomics identified differentially expressed genes enriched in immune signaling, inflammatory response and epithelial repair. Metabolomic profiling of cloacal tissue and contents revealed changes in taurine- and lipid-related pathways. Cross-omics integration linked immune-related genes including COL6A3, SPARC, PPEF1, HSD17B2 and KCNG2 to metabolites such as Hydroxytyrosol-Ac, phytol, MeCys-SO and PEA-glu, pointing to their involvement in immune activation and epithelial barrier dysfunction.

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Introduction to Applying LC-MS in Untargeted

Metabolomics

October 26 - 28, 2026

Venue: Liverpool, United Kingdom

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

Registration and additional event details

Webinar - Hybrid Metabolomics Now Standardized

October 27, 2026

Venue: Online

Metabolomics researchers often face a trade-off between confident, targeted quantification and broad, untargeted discovery, limiting the insight available from a single experiment. Hybrid metabolomics removes the need to choose between these complementary strategies, enabling both robust quantification and comprehensive profiling from the same measurement. The result is a more standardized workflow that conserves valuable sample, time, and resources.

In this webinar, explore the principles and scientific potential of an integrated approach to quantification and discovery, and hear how early adopters are applying hybrid metabolomics to aging and cardiometabolic disease research.

Attendees will gain practical perspectives on bridging hypothesis-driven and discovery-based science to address a broader range of research questions.

Attend this webinar to:

- Learn how standardized hybrid metabolomics workflows integrate targeted quantification and untargeted discovery
- Discover how hybrid workflows expand biological insight beyond traditional approaches
- Learn how early adopters apply hybrid metabolomics to aging and cardiometabolic research.

[Click here to register](#)

X Symposium of the Mexican Proteomics Society

November 9 - 13, 2026

Venue: Mexico City

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

[Visit website for more details](#)

Imperial College London Metabolomics training course:

Hands-on Data Analysis for Metabolomics

December 7 - 11, 2026

Venue: Online

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

[Visit website for more details](#)

MANA SODAMeet

December 8, 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](#)

Introduction to Applying GC-MS in Untargeted Metabolomics

February 2 - 4, 2027

Venue: Liverpool, England, United Kingdom

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

[Registration and event details](#)

2027 Metabolomics and Human Health Gordon Research Conference and Gordon Research Seminar

February 27 - March 5, 2027

Venue: Liverpool, United Kingdom

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

Health-Disease-Environment Interface Through Emerging Technologies.”

Gordon Research Conference

Gordon Research Seminar

8th Annual Canadian Metabolomics Conference

CanMetCon 2027

May 6 - 7, 2027

Venue: Canmore, Alberta, Canada

Join us for the 8th Annual Canadian Metabolomics Conference 2027 in Canmore, Canada, from May 6 - 7, 2027. The conference brings together researchers, professionals, and students from across the metabolomics community for an engaging program of scientific presentations, networking, and knowledge exchange. For more details about the program, speakers, and registration, please check our website regularly for updates.

Early-Bird registration is **open**.

Registration and event details

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Job Title	Employer	Location	
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Assistant Professor in Cancer Prevention	Fred Hutchinson Cancer Center: Public Health Sciences Division	Seattle, WA, US	Fred Hutchinson Cancer Center
ARISE2 Fellowship program	ARISE Career Accelerator for Research Infrastructure Scientists	Six EMBL sites	European Molecular Biology Laboratory (EMBL)

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