



BePAc26

BELGIAN PROTEOMICS ASSOCIATION CONFERENCE



13 & 14 October 2026

LIÈGE • BELGIUM

PROGRAMME & BOOK OF ABSTRACTS

5 keynotes 14 talks 4 sponsor talks 30 posters

📍 University of Liège • Campus du Sart Tilman
Building B8 • Quartier Agora, L'Agora 1, 4000 Liège

Organised by the **Belgian Proteomics Association** in partnership with



BePAc26

BELGIAN PROTEOMICS ASSOCIATION CONFERENCE · LIÈGE, 13–14 OCTOBER 2026

VENUE

University of Liège, Campus du Sart Tilman
Building B8 – Maison des Étudiants & Exèdre Dick Annegarn

ORGANISED BY

Belgian Proteomics Association (BePA)
with KVCV and SRC · hosted by the MSLab, ULiège

ONLINE

belgianproteomics.be/events/bepac26

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01 About the organisers

Belgian Proteomics Association (BePA)



The Belgian Proteomics Association is embodied by a workgroup that aims to bring together the Belgian proteomics community. Founded on 13 March 2012 in Brussels, BePA is the national member society of the European Proteomics Association (EuPA) and represents Belgian proteomics at the European level.

BePA is open to everyone, from experts to proteomics users in other scientific fields. The association dedicates part of its efforts to introducing researchers to the fundamentals of proteomics: it organises workshops where the basics of proteomics are taught, and an annual Proteomics Summer School. Members have free access to all BePA workshops.

Every year BePA organises the Belgian Proteomics Association Conference, BePac — two days full of Belgian proteomics, an opportunity to network within the Belgian proteomics community, to initiate collaborations with closely located researchers and to broaden one's proteomics view. BePac26 is the 2026 edition, hosted in Liège by the Mass Spectrometry Laboratory of the University of Liège.

BePA is organised as the Proteomics section of the KVCV, with a parallel section being set up within the SRC: members of the Proteomics section are automatically members of BePA and of EuPA.

Source: belgianproteomics.be and kvcv.be/secties/sectie-proteomics

Koninklijke Vlaamse Chemische Vereniging (KVCV)



The KVCV is the professional association of all Flemish chemists, regardless of their diploma. Its mission is to bridge the gap between education, industry and society in the field of chemistry. Through a programme of conferences, symposia, lectures and study days, it connects chemists working in academia, industry and teaching.

The association is structured in ten thematic sections — among them Analytical Chemistry, Computational Chemistry, Medicinal Chemistry and Chemical Biology, Organic and Bio-organic Chemistry, Nutrition, Education and Training, History and Philosophy of Chemistry, the young chemists' section Jong KVCV, Kekulé, and the Proteomics section, which carries the activities of BePA: representing Belgian proteomics in Europe, networking the Belgian proteomics researchers, organising the annual BePac conference and the yearly Proteomics Summer School. Registration for BePac26 is handled through the KVCV ticketing platform.

Source: kvcv.be

Société Royale de Chimie (SRC)



The Société Royale de Chimie is the French-speaking Belgian chemical society. It was founded on 14 April 1887 as the Association Générale des Chimistes Belges — later the Association Belge des Chimistes — and received its royal title in 1987, on the occasion of its centenary. Its members are chemists from academia and industry, and several of them have been distinguished by the Belgian Royal Academy, the Institut de France and the Nobel Committee.

The SRC promotes research and the dissemination of knowledge in chemistry, works to improve the public image of chemistry, and is active in a multitude of domains involving chemistry, from industry to biotechnology and pharmaceuticals, with a strong commitment to European integration and to scientific education. It organised the first International Congress of Applied Chemistry in 1894, publishes the magazine Chimie Nouvelle (founded in 1983) and runs international congresses and autumn scientific days through its thematic divisions and local sections. A Proteomics section mirroring that of the KVCV is being set up within the SRC.

Source: src.ulb.be

02 Our hosts

BePac26 is hosted on the Sart Tilman campus of the University of Liège by the Mass Spectrometry Laboratory (MSLab) and the GIGA Proteomics platform.

University of Liège (ULiège)



1817

founded

11

faculties

~30 000

students

4

campuses

70

partner countries

Founded in 1817 under William I of the Netherlands, the University of Liège is a major public research university of the Wallonia–Brussels Federation. Its 11 faculties offer 243 master's programmes to almost 30,000 students (29,972 in 2025–2026), across three cities and four campuses: the historic city centre of Liège, the wooded **Sart Tilman campus** that welcomes BePac26, Gembloux Agro-Bio Tech and Arlon. With more than 6,000 staff members, over 1,850 research agreements and partners in 70 countries, ULiège covers the full spectrum of knowledge, from the life and health sciences to engineering, the humanities and astrophysics — its TRAPPIST telescopes in Chile and Morocco helped reveal the TRAPPIST-1 planetary system. The university counts Nobel laureate Albert Claude (Physiology or Medicine, 1974) among its alumni; its motto is *Scientia optimum*.

Sources: uliege.be (key figures 2025–2026), Wikipedia.

Mass Spectrometry Laboratory (MSLab)

MOLSYS RESEARCH UNIT · DEPARTMENT OF CHEMISTRY

The MSLab brings together chemists and biologists with expertise in mass spectrometry and optical spectroscopy. Part of the MolSys Research Unit of the Faculty of Sciences, it is directed by Prof. Gauthier Eppe (deputy director Prof. Loïc Quinton) and builds on the long tradition of mass spectrometry in Liège established by Prof. Edwin De Pauw. Its research is organised in thematic groups — **MSLab-Analytics** (food safety, contaminants, microplastics), **MSLab-Biology** (bioactive peptides, venom toxins, structural MS by cross-linking and H/D exchange), **MSLab-Fun** (ion formation, gas-phase structure and data processing), **MSLab-Vib** (vibrational spectroscopy) and **MSLab-Omics** (proteomics, post-translational modifications, microproteomics and single-cell proteomics) — with mass spectrometry imaging as a cross-cutting tool.

MSLab-Omics

Headed by **Gabriel Mazzucchelli**, Associate Professor and Research Logistics Director (*Directeur logistique de recherche*, MolSys) and local organiser of BePac26. Main themes: single-cell and low-input proteomics on a timsTOF SCP recently upgraded with the Athena Ion Processor (AIP); spatial proteomics with MMI laser microdissection and the Pixel2Proteomics (P2P) method; human sweat proteomics, including the **SmartSweat** project (a passive patch for overnight sweat collection); and microfluidic chips for single-cell processing (ChipOmics).

The team gratefully acknowledges the support of the F.R.S.-FNRS, the Walloon Region and the Fondation contre le Cancer.

Sources: mslab.uliege.be, molsys.uliege.be, news.uliege.be, giga.uliege.be.

GIGA – Interdisciplinary biomedical research institute

UNIVERSITY HOSPITAL (CHU) · SART TILMAN

2003

created

600+

scientists

40+

nationalities

1 / day

peer-reviewed article

100+

patent applications

GIGA is the University of Liège's interdisciplinary biomedical research institute. Created in October 2003 around some twenty laboratories using genoproteomic approaches, it moved in 2007 into the University Hospital on the Sart Tilman campus and has kept growing ever since, with the arrival of neurosciences, cardiovascular biology, in vivo imaging and stem-cell research. Today GIGA brings together more than 600 scientists from over 40 countries — physicians, pharmacists, veterinarians, biologists, chemists, physicists, mathematicians and engineers — working on cancer, immunobiology, metabolism and cardiovascular biology, molecular and computational biology, and neuroscience. Its core technology platforms (genomics, proteomics, cell imaging, flow cytometry, immunohistology, viral vectors, animal facility and cyclotron) are open to academic and industrial partners, and its lab-hotel incubator supports start-ups and spin-offs. GIGA hosts the highest concentration of ERC grantees in Wallonia.

Source: giga.uliege.be.

GIGA Proteomics platform

BUILDING B6C · QUARTIER AGORA

GIGA Proteomics is the proteomics core facility of GIGA, located in the Faculty of Sciences next to the conference venue and run in close partnership with the MSLab. The platform is headed by **Dominique Baiwir**, platform manager, with platform experts Nancy Rosière and Lisette Trzpiot and in close collaboration with Gabriel Mazzucchelli (MSLab-Omics). It offers academic and industrial users services ranging from accurate mass determination to the identification and label-free quantification of thousands of proteins — from biopsies, cell extracts or laser-microdissected FFPE tissues —, protein sequencing and characterisation of post-translational modifications, absolute quantification, quality control of protein batches and molecular imaging. Since 2025, the platform is part of the **SpatialP2PDissectOmics** infrastructure (F.R.S.-FNRS, €720,000), which couples an ultra-high-resolution automated laser microdissector — unique among Belgian universities — with the GIGA cell imaging, immunohistology and proteomics platforms.

proteomics.giga@uliege.be · +32 4 366 34 48 · gigaproteomics.uliege.be

Sources: gigaproteomics.uliege.be, giga.uliege.be.

Organising committees

BePA board. An Staes (President), Gabriel Mazzucchelli (Vice-President), Simon Devos (Secretary), Simon Daled (Treasurer); board members Didier Vertommen, Dieter Deforce, Francis Impens, Gerben Menschaert, Kris Gevaert, Laurent Gatto, Lennart Martens and Liesbet Temmerman.

Local organising committee (University of Liège). Gabriel Mazzucchelli, Dominique Baiwir, Maximilien Fléron, Christopher Kune, Matthieu Hodeige and Amine Mohamed Berkal.

Source: belgianproteomics.be/board

03 Our sponsors

BePac26 is made possible by the generous support of our sponsors. We warmly thank them and invite all participants to visit their stands in Le Foyer (1st floor).

★ GOLD SPONSORS



BigOmics Analytics

Lugano, Switzerland

Founded in 2018 by Ivo Kwee and Murodzhon Akhmedov as a spin-off of the Institute of Oncology Research in Bellinzona, BigOmics Analytics develops Omics Playground, a code-free platform that lets biologists analyse and visualise their own transcriptomics, proteomics and metabolomics data — from quality control and differential expression to pathway enrichment, biomarker discovery and multi-omics integration. It is used by more than 4,000 scientists in academia and industry.

www.bigomics.ch



Bruker

Bruker Belgium NV, Kontich · Headquarters: Billerica, MA, USA

Founded in 1960 in Karlsruhe, Germany, Bruker develops high-performance scientific instruments that allow researchers to explore life and materials at the molecular, cellular and microscopic levels. Through Bruker Daltonics, it is a leading provider of mass spectrometry for life sciences, including the timsTOF platform, which couples trapped ion mobility with high-resolution TOF for 4D-proteomics — from single-cell and spatial proteomics to high-throughput plasma studies.

www.bruker.com



MS Wil

Aarle-Rixtel, The Netherlands

Founded in 1978 in Wil, Switzerland, by Peter Weibel, MS Wil moved its headquarters to Aarle-Rixtel in the Netherlands in 2019. True to its motto “Making Science Work”, it is a one-stop shop for fine mass spectrometry tools: sample-preparation products, nano-LC columns and emitters, ion-source and MS supplies, and data-analysis software such as Mascot and the NIST libraries — a long-standing partner of proteomics laboratories across Europe.

www.mswil.com



SCIEX

AB Sciex NV, Halle, Belgium

For more than 50 years, SCIEX has delivered precise solutions for the quantitation and characterisation of molecules. It launched the first commercially successful triple-quadrupole mass spectrometer in 1981 and has since pioneered LC-MS/MS and capillary electrophoresis technologies. For proteomics, its portfolio includes the ZenoTOF systems with Zeno trap and electron-activated dissociation (EAD), high-sensitivity triple quadrupoles for targeted quantitation and robust microflow LC workflows. SCIEX is part of Danaher.

www.sciex.com

★ SILVER SPONSORS

**Evosep***Odense, Denmark*

Evosep is a Danish company whose mission is to make sample separation ten times faster and one hundred times more robust. Its Evosep One and Evosep Eno LC systems, combined with disposable Evotip sample-loading tips and standardised pre-formed gradients, deliver reproducible high-throughput LC-MS — up to 300 samples per day — from discovery to clinical proteomics.

www.evosep.com**PreOmics***Planegg / Martinsried, Germany*

PreOmics was founded in 2016 as a spin-off of Matthias Mann's laboratory at the Max Planck Institute of Biochemistry. It develops standardised, easy-to-use sample-preparation solutions for MS-based proteomics — the iST kit family for cells, tissues and body fluids, ENRICH-iST for deep plasma proteomics, the BeatBox tissue homogeniser and automation-ready workflows. PreOmics is part of the Biognosys Group.

www.preomics.com**Promega***Promega Benelux, Leiden, The Netherlands · Headquarters: Madison, WI, USA*

Founded in 1978 in Madison, Wisconsin, Promega is a privately held life-science company providing innovative solutions and technical support to researchers, clinical and applied laboratories and drug developers. Proteomics laboratories know Promega for its high-quality proteases — Sequencing Grade Modified Trypsin, Trypsin/Lys-C Mix, rapid digestion kits and specialty enzymes — and for its bioluminescent technologies (NanoLuc, HiBiT) for protein detection and interaction studies.

www.promega.com**Thermo Fisher Scientific***Merelbeke, Belgium · Headquarters: Waltham, MA, USA*

Thermo Fisher Scientific is the world leader in serving science, with the mission of enabling its customers to make the world healthier, cleaner and safer. Through its Thermo Scientific brand, it is the home of Orbitrap mass spectrometry, a technology at the heart of proteomics research worldwide — today with the Orbitrap Astral and Orbitrap Exploris families — complemented by Vanquish UHPLC systems, consumables and Proteome Discoverer software.

www.thermofisher.com**Waters***Waters NV, Antwerp, Belgium · Headquarters: Milford, MA, USA*

Founded in 1958, Waters has pioneered chromatography, mass spectrometry and thermal analysis for more than 65 years, and introduced UPLC technology in 2004. Its portfolio for proteomics and biopharmaceutical characterisation spans ACQUITY UPLC and M-Class LC systems, Xevo and SELECT SERIES Cyclic IMS mass spectrometers with ion mobility, columns, sample-preparation chemistries and informatics.

www.waters.com

04 Practical information

VENUE

Building B8 – Maison des Étudiants & Exèdre Dick Annegarn

University of Liège, Campus du Sart Tilman – Quartier Agora, L'Agora 1, B-4000 Liège · GPS 50.5847 N, 5.5705 E

Talks, welcome & closing

Conference room « Exèdre Dick Annegarn »

Registration, breakfast, coffee breaks, lunch & sponsor exhibition

« Le Foyer », 1st floor

Poster sessions

« PhD House », 1st floor

⚠ To reach the PhD House, please just walk through the student cafeteria — do not stay there.

REGISTRATION

The registration desk opens on **Tuesday 13 October at 08:30** in Le Foyer (1st floor), together with the morning coffee. Please collect your badge before the welcome talk at 09:00 by Gabriel Mazzucchelli (local organiser) and An Staes (BePA President).

PRESENTATIONS

Keynotes last 35–45 min and talks 20 min, **questions included (5 min)**. Sponsor talks last 20 min. All presentations take place in the Exèdre Dick Annegarn.

POSTERS

All posters are displayed in the PhD House on both days. Poster sessions take place during the lunch breaks (**Tue 12:10–14:20, Wed 12:10–13:30**). Posters P13–P30 accompany the talks and sponsor talks. A **poster prize of €150** is awarded at the closing session (Wed 16:10).

GALA DINNER

Tuesday 13 October, 20:00

Brasserie Li Sku Mel

4 Rue Lulay des Fèbvres, 4000 Liège (city centre)

REGISTRATION REQUIRED

WI-FI ACCESS

Wi-Fi login details are available at the registration desk (Le Foyer, 1st floor).



THIS BOOK ONLINE

The complete programme and all abstracts are available at belgianproteomics.be/events/bepac26

GETTING THERE

From Liège-Guillemins station, bus **B2** reaches the campus in 20–25 min (stop « Sart-Tilman Amphithéâtres », 175 m from B8). By car, parkings B, C and D on the campus are free.

Full Access & Accommodation Guide: p. 34.

CONTACTS

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05 Programme at a glance

Day 1 Tuesday 13 October 2026

♦ Talks: **Exèdre Dick Annegarn** · Building B8

08:30–09:00	Registration & morning coffee	♦ Le Foyer · 1st floor
09:00–09:10	Welcome talk · Gabriel Mazzucchelli & An Staes (BePA President)	♦ Exèdre Dick Annegarn
Session A-1	Less Is More: Single-Cell, Spatial, and Beyond in Low-Input Proteomics	09:10–10:35
09:10–09:55	Keynote A Combining Spatial Proteomics and Lipidomics in Precision Oncology <i>Michel Salzet</i> — University of Lille	
09:55–10:15	Talk A1 (P13) Trap-Refocusing-Elute nanoLC-MS: a robust strategy combining trap-elute loading with direct-injection chromatographic resolution <i>Christopher Kune</i> — MSLab, University of Liège	
10:15–10:35	Talk A2 (P14) Low-input proteomics uncovers molecular determinants of neural migration in mouse and human brain <i>Sylvia Tielens</i> — GIGA Neurosciences, University of Liège	
10:35–11:10	Coffee break	♦ Le Foyer · 1st floor
Session A-2	Less Is More	11:10–12:10
11:10–11:30	Talk A3 (P15) Linking spatial to functional proteomics on heterogeneous samples: the “pixel-by-pixel” shotgun proteomic approach <i>Matthieu Hodeige</i> — MSLab, University of Liège	
11:30–11:50	Talk A4 (P16) Single-cell proteomics for determination of mouse cardiomyocyte heterogeneity: the SCarP strategy <i>Blandine Chazarin</i> — ProtMic, UMONS	
11:50–12:10	Sponsor talk AS1 (P17) Sponsor presentation: Bruker	
12:10–14:20	Lunch & poster session	♦ Lunch: Le Foyer · Posters: PhD House
Session B-1	Zooming Out: Proteomics in the Bigger Picture	14:20–15:45
14:20–15:05	Keynote B From Molecules to Mechanisms: Exploring Biology Through Multi-Omics <i>Bart Ghesquière</i> — KU Leuven	
15:05–15:25	Talk B1 (P18) Development of an analytical framework to evaluate antivenom efficacy through magnetic beads and biolayer interferometry <i>Thomas Crasset</i> — MSLab, University of Liège	
15:25–15:45	Talk B2 (P19) From surfaceome discovery to therapeutic opportunities: proteomic targets in patient-derived glioblastoma stem-like cells <i>Anna Laurent</i> — Laboratory for the Analysis of Medicines, University of Liège	
15:45–16:30	Coffee break	♦ Le Foyer · 1st floor
Session B-2	Zooming Out	16:30–17:30
16:30–16:50	Talk B3 (P20) Interaction between the FET fusion FUS::DDIT3 and the cohesin loader NIPBL remodels the 3D chromatin structure in myxoid liposarcoma <i>Élise Gilson</i> — Gene Expression and Cancer, GIGA, University of Liège	
16:50–17:10	Talk B4 (P21) Proteomic identification of THSD7A in a case of PLA2R-negative membranous nephropathy and potential implications for clinical management <i>Annelore Vandendriessche</i> — VIB Proteomics Core, Ghent University	
17:10–17:30	Talk B5 (P22) Mapping EWSR1::FLI1 interactions with the cohesin loader complex in Ewing sarcoma <i>Fateme Shaabanpouraghamaleki</i> — Gene Expression and Cancer, GIGA, University of Liège	
20:00	Gala dinner · Brasserie Lî Sku Mel, Liège (p. 8)	♦ Registration required

Day 2 Wednesday 14 October 2026♦ Talks: **Exèdre Dick Annegarn** · Building B8

08:45–09:10	Morning coffee	♦ Le Foyer · 1st floor
Session C-1	Going Big: High-Throughput LC-MS Strategies for Scale and Depth	09:10–10:35
09:10–09:55	Keynote C Boosting Proteomics: Enhancing Peptide Recovery, Automation, Chromatographic Robustness and Performance <i>Gabriel Mazzucchelli</i> — MSLab Omics, University of Liège	
09:55–10:15	Talk C1 P23 Reading metabolic routing off the histone epigenome: a dual DDA/DIA framework for time-resolved ¹³ C incorporation analysis <i>Thijs Lefever</i> — ProGenTomics, Ghent University	
10:15–10:35	Sponsor talk CS1 P24 Sponsor presentation: BigOmics Analytics	
10:35–11:10	Coffee break	♦ Le Foyer · 1st floor
Session C-2	Going Big	11:10–12:10
11:10–11:30	Talk C2 P25 Sweat proteomics: a non-invasive approach for biomarker discovery with optimized and semi-automated sample preparation <i>Amine Mohamed Berkal</i> — MSLab, University of Liège	
11:30–11:50	Sponsor talk CS2 P26 Sponsor presentation: SCIEX	
11:50–12:10	Sponsor talk CS3 P27 Sponsor presentation: MS Wil	
12:10–13:30	Lunch & poster session	♦ Lunch: Le Foyer · Posters: PhD House
Session D-1	Processing and Interpreting Proteomic Data: The Promise and Pitfalls of Bioinformatics and AI	13:30–14:35
13:30–14:15	Keynote D1 Proteomics in the Age of Artificial Intelligence <i>Wout Bittremieux</i> — University of Antwerp	
14:15–14:35	Talk D1 P28 Development of a de novo human immunopeptidomics map <i>Moira Breëns</i> — Adrem Data Lab, University of Antwerp	
14:35–14:55	Coffee break	♦ Le Foyer · 1st floor
Session D-2	Processing and Interpreting Proteomic Data	14:55–16:10
14:55–15:30	Keynote D2 Cloud Pipelines Followed by AI-Assisted Downstream Analysis and Interpretation <i>Henry Emanuel Webel</i> — DTU	
15:30–15:50	Talk D2 P29 Characterization of the immunopeptidome of drug-tolerant persister cells in acute myeloid leukemia <i>Charline Faville</i> — GIGA Hematology, University of Liège	
15:50–16:10	Talk D3 P30 Characterizing unexpected peptides in human proteomics data using de novo peptide sequencing <i>Fatemeh Mirzadeh Sarcheshmeh</i> — Adrem Data Lab, University of Antwerp	
16:10–16:25	Poster prize & closing remarks · Gabriel Mazzucchelli & An Staes (BePA President)	♦ Exèdre Dick Annegarn

Keynotes (35–45 min) and talks (20 min) include 5 min for questions. **P13** Every talk and sponsor talk is accompanied by a poster (P13–P30), displayed in the PhD House.

06 Posters

All posters are on display in the **PhD House (1st floor)** during both days. Poster sessions take place during the lunch breaks — **Tue 12:10–14:20** and **Wed 12:10–13:30**; a poster prize of €150 is awarded at the closing session.

▲ To reach the PhD House, please just walk through the student cafeteria — do not stay there.

Poster contributions · P1–P12

abstracts p. 26

- P1** **Evaluation of Protein Module Detection Analysis for Single Cell Proteomics**
Enes Sefa Ayar — CBIO, de Duve Institute, UCLouvain
- P2** **Genome-wide characterization of aberrantly expressed tumor antigens through proteogenomics**
Gabriele Carriglio — Laboratory of Hematology, GIGA, University of Liège
- P3** **Step-by-step method optimization with standard proteins for structural characterization of therapeutic megadalton virus-like particles**
Charles Delvaux — MSLab, University of Liège
- P4** **Understand the lack of immune response to mRNA vaccine for haemodialyzed patients**
Lise Demulles — ProtMic, UMONS
- P5** **Optimized FFPE Tissue Processing: Complete workflow for in-depth proteome analysis of multiple FFPE formats**
Adam Hughes — PreOmics GmbH – Biognosys Group
- P6** **Dissection and modulation of mitochondrial pathways during activation and transdifferentiation of cardiac fibroblasts into cardiomyocytes**
Guillaume Paulissen — URBC, NARILIS, University of Namur
- P7** **A living proteomics benchmark for comprehensive evaluation of deep learning-based de novo peptide sequencing tools**
Marina Pominova — Bittremieux Lab, University of Antwerp
- P8** **Inhibitors of Tax1-PDZ Interactions Block HTLV-1 Viral Transmission by Changing EV Composition**
Jedidja Puttemans — Viral Interactomes Network Lab, GIGA, University of Liège
- P9** **Scop3P-Toolkit: executable structure-aware workflows linking PTMs, peptides, and mutations to protein function**
Natalia Tichshenko — CompOmics, VIB – Ghent University
- P10** **Advancing Plasma Proteomics Through a Next-Generation Single-Particle Enrichment Workflow for Deeper and More Quantitative Biomarker Discovery**
Karin Yeoh — PreOmics GmbH – Biognosys Group
- P11** **Biological Relevance of Measuring Low Abundant Proteins in Human Plasma**
Rajendra Kumar Chauhan — Illumina
- P12** **Smarter Libraries for Faster DIA: A Sequential Digestion Strategy to Enhance Proteome Coverage in DDA-based Spectral Libraries**
Alia Gillet — MSLab Omics, University of Liège

Posters accompanying the oral presentations · P13–P30

abstracts with the talks, p. 13

- P13** **Trap-Refocusing-Elute nanoLC-MS: a robust strategy combining trap-elute loading with direct-injection chromatographic resolution**
Christopher Kune — MSLab, University of Liège Talk A1 · Tue 09:55
- P14** **Low-input proteomics uncovers molecular determinants of neural migration in mouse and human brain**
Sylvia Tielens — GIGA Neurosciences, University of Liège Talk A2 · Tue 10:15
- P15** **Linking spatial to functional proteomics on heterogeneous samples: the “pixel-by-pixel” shotgun proteomic approach**
Matthieu Hodeige — MSLab, University of Liège Talk A3 · Tue 11:10

- P16** **Single-cell proteomics for determination of mouse cardiomyocyte heterogeneity: the SCarP strategy**
Blandine Chazarin — ProtMic, UMONS Talk A4 · Tue 11:30
-
- P17** **Bruker — sponsor poster**
Bruker — Gold sponsor Sponsor talk AS1 · Tue 11:50
-
- P18** **Development of an analytical framework to evaluate antivenom efficacy through magnetic beads and biolayer interferometry**
Thomas Crasset — MSLab, University of Liège Talk B1 · Tue 15:05
-
- P19** **From surfaceome discovery to therapeutic opportunities: proteomic targets in patient-derived glioblastoma stem-like cells**
Anna Laurent — Laboratory for the Analysis of Medicines, University of Liège Talk B2 · Tue 15:25
-
- P20** **Interaction between the FET fusion FUS::DDIT3 and the cohesin loader NIPBL remodels the 3D chromatin structure in myxoid liposarcoma**
Élise Gilson — Gene Expression and Cancer, GIGA, University of Liège Talk B3 · Tue 16:30
-
- P21** **Proteomic identification of THSD7A in a case of PLA2R-negative membranous nephropathy and potential implications for clinical management**
Annelore Vandendriessche — VIB Proteomics Core, Ghent University Talk B4 · Tue 16:50
-
- P22** **Mapping EWSR1::FLI1 interactions with the cohesin loader complex in Ewing sarcoma**
Fateme Shaabanpouraghamaleki — Gene Expression and Cancer, GIGA, University of Liège Talk B5 · Tue 17:10
-
- P23** **Reading metabolic routing off the histone epigenome: a dual DDA/DIA framework for time-resolved ¹³C incorporation analysis**
Thijs Lefever — ProGenTomics, Ghent University Talk C1 · Wed 09:55
-
- P24** **BigOmics Analytics — sponsor poster**
BigOmics Analytics — Gold sponsor Sponsor talk CS1 · Wed 10:15
-
- P25** **Sweat proteomics: a non-invasive approach for biomarker discovery with optimized and semi-automated sample preparation**
Amine Mohamed Berkal — MSLab, University of Liège Talk C2 · Wed 11:10
-
- P26** **SCIEX — sponsor poster**
SCIEX — Gold sponsor Sponsor talk CS2 · Wed 11:30
-
- P27** **MS Wil — sponsor poster**
MS Wil — Gold sponsor Sponsor talk CS3 · Wed 11:50
-
- P28** **Development of a de novo human immunopeptidomics map**
Maira Breëns — Adrem Data Lab, University of Antwerp Talk D1 · Wed 14:15
-
- P29** **Characterization of the immunopeptidome of drug-tolerant persister cells in acute myeloid leukemia**
Charline Faville — GIGA Hematology, University of Liège Talk D2 · Wed 15:30
-
- P30** **Characterizing unexpected peptides in human proteomics data using de novo peptide sequencing**
Fatemeh Mirzadeh Sarcheshmeh — Adrem Data Lab, University of Antwerp Talk D3 · Wed 15:50
-

07 Detailed programme & abstracts

Day 1 Tuesday 13 October 2026

08:30–09:00 Registration & morning coffee — Le Foyer (1st floor)

09:00–09:10 Welcome talk by Gabriel Mazzucchelli (local organiser) & An Staes (BePA President) — Exèdre Dick Annegarn

Session A-1

Less Is More: Single-Cell, Spatial, and Beyond in Low-Input Proteomics

09:10–10:35

09:10–09:55 ★ KEYNOTE A

Combining Spatial Proteomics and Lipidomics in Precision Oncology

Michel Salzet — Professor, University of Lille — PRISM, Inserm U1192; Institut Universitaire de France

Mass spectrometry (MS)-based spatial proteomics provides a robust framework for investigating tumour ecosystems. It achieves this by identifying markers that distinguish cancer cells from immune and stromal populations, and by resolving phenotypically distinct tumour clones within the same lesion. By preserving tissue architecture, untargeted MS approaches can generate diagnostic, prognostic, and therapeutic information that is firmly rooted in the tumour microenvironment. The combination of mass spectrometry imaging (MSI) and large-scale, non-targeted spatial proteomics is proving to be particularly promising. MALDI-MSI can map lipids and tryptic peptides in workflows that are compatible with formalin-fixed, paraffin-embedded tissues. Meanwhile, image segmentation can guide microproteomics of selected phenotypes, niches, and invasion fronts. Machine learning strategies can also be used to connect lipid MSI profiles with protein networks, signalling pathways, immune infiltration and candidate therapeutic vulnerabilities, including patient-derived organoids for drug repurposing and treatment prioritisation. In longitudinal breast cancer cohorts, spatial proteomics indicates that tumour evolution follows a limited number of phenotypic trajectories, with clonal dynamics being strongly influenced by local microenvironmental constraints. These observations can be cross-validated using single cell proteomic, targeted MS-based proteomics, including high-plex MALDI immunohistochemistry with click-chemistry-enabled antibodies or aptamers for immune cell and immune checkpoint panels. A significant step towards translation is SpiderMass technology, a water-assisted laser desorption/ionisation ambient MS approach, that uses endogenous water as a matrix to acquire molecular fingerprints with minimal invasiveness and without the need for sample preparation. When coupled with AI, SpiderMass enables real-time ex vivo and in vivo tissue classification, margin assessment, and molecular stratification during surgery. Recent applications in glioblastoma have demonstrated that SpiderMass fingerprints can stratify IDH-wild-type patients, achieving over 90% diagnostic accuracy following cross-validation and supporting prognosis assessment and the inference of immune infiltration. Emerging studies are now extending this strategy to include topographic 3D molecular maps, cancer patient digital twins, bacterioscores, and margin delineation in breast and gastro-oesophageal cancers. Meanwhile, robotic SpiderMass MSI is paving the way for interpretable, surgeon-facing molecular feedback. Together, these developments are moving spatial proteomics towards subcellular analysis through tissue expansion and towards intraoperative precision oncology through SpiderMass-guided decision-making.

09:55–10:15 TALK A1 (P13)

Trap-Refocusing-Elute nanoLC-MS: a robust strategy combining trap-elute loading with direct-injection chromatographic resolution

Christopher Kune — MSLab, University of Liège

Chromatographic resolution is a major bottleneck in nanoLC-MS proteomics. Users must currently choose between Direct Injection (DI), which offers sharp peaks but limited loading capacity, and Trap-and-Elute (TE), which loads more sample and desalts online but produces noticeably broader peaks. We developed Trap-Refocusing-Elute (TRE), a simple upgrade to

standard TE setups that addresses this gap. An auxiliary pump adds a tunable water flow between the trap and analytical columns. This flow dilutes the organic solvent reaching the analytical column, which restores strong peptide retention at the column head and refocuses peptides immediately before separation.

Using a HeLa digest standard on a timsTOF SCP, TRE reduced median peak width (Full Width at Half Maximum, FWHM) to 3.1 s. This compares to 4.7 s for TE and 3.6 s for DI, matching or surpassing DI while retaining the practical advantages of TE. This improvement was accompanied by 24% more peptide identifications and 13% more proteins than standard TE, alongside improved run-to-run reproducibility. A dedicated control experiment confirmed that the auxiliary water flow itself, rather than the trap, drives this improvement. The benefit was also maintained when injecting nine times more sample volume, demonstrating that TRE remains effective for dilute or precious samples.

TRE requires no additional hardware beyond a pump already present on many nanoLC systems. This makes it a straightforward, low-cost upgrade for laboratories running trap-based workflows. It positions TRE as particularly relevant for single-cell proteomics, clinical samples, and high-throughput pipelines, where sensitivity and robustness are especially critical.

10:15–10:35 **TALK A2** **P14**

Low-input proteomics uncovers molecular determinants of neural migration in mouse and human brain

Sylvia Tielens — GIGA Neurosciences, University of Liège

Neuronal diversity in the developing cerebral cortex arises from tightly coordinated migration and identity-acquisition programs in GABAergic cortical interneurons (cINs) and oligodendrocyte precursor cells (vOPCs). While transcriptomics has extensively mapped these processes, the proteomic determinants of migratory behaviour and subtype identity remain largely unexplored, mainly because these are rare, transient cell populations yielding very limited starting material.

We combined FACS-purification of genetically labelled cINs and vOPCs from transgenic mouse embryos with a downscaled sample-preparation workflow enabling label-free quantitative proteomics on as few as ~1,000–7,000 cells. This *in vivo* mouse approach was complemented by human *in vitro* models, including hiPSC-derived dorsal/ventral cerebral assembloids and *ex vivo* human fetal brain tissue (GW10–13), allowing cross-species comparison of interneuron proteomes.

Comparative proteomics of cINs and vOPCs uncovered distinct enriched pathways: cell-cycle/DNA-replication signatures in cINs versus myelin- and cytoskeleton-remodelling signatures in vOPCs, which we functionally linked to differential nucleokinesis and growth-cone dynamics during live-imaging of migration. Longitudinal profiling of cINs across two developmental waves (E13.5 vs E16.5) revealed a shift from translation/mitochondrial-metabolism pathways to mRNA-processing and chromatin-related pathways, coinciding with migration into progressively stiffer tissue environments, a relationship we further probed using stiffness-controlled hydrogels. Moreover, comparison of mouse and human interneuron proteomes identified shared and species-specific candidates.

Together, these downscaled proteomic workflows, applied in parallel across *in vivo* and *in vitro* mouse and human models, provide a novel level of resolution to unravel the molecular logic of neuronal migration and identity acquisition during corticogenesis. This work illustrates how proteomics can zoom out from single-cell molecular mechanism to a translational understanding of human brain development.

10:35–11:10 Coffee break — Le Foyer (1st floor)

Session A-2 **Less Is More (cont'd)**

11:10–12:10

11:10–11:30 **TALK A3** **P15****Linking spatial to functional proteomics on heterogeneous samples: the “pixel-by-pixel” shotgun proteomic approach****Matthieu Hodeige** — *MSLab, University of Liège*

Proteins are crucial for assessing cell health and activity, yet proteomics of biological tissues faces challenges due to sample heterogeneity. Mass spectrometry imaging offers spatial information with limited functional insights, while laser capture microdissection (LCM) shotgun proteomics provides detailed proteome data but sacrifices spatial resolution. We propose a technique, called pixel-by-pixel shotgun proteomics (Pixel2Proteomics, P2P), combining laser microdissection with proteomics. This approach was evaluated on mouse squamo-columnar junctions that connect a stratified squamous epithelium to a glandular epithelium. The interest of this tissue lies in the well-established emergence of precancerous lesions in these junctions. Tissues were initially preserved in formalin-fixed paraffin-embedded (FFPE) form and sectioned into 5 µm slices. The 5 µm tissues were microdissected into areas of 1600 µm² (10–20 cells), following a systematic grid pattern. A key challenge in developing this approach was identifying a laser microdissection system that could combine high recovery efficiency with high-throughput sampling. To this end, we used the CellCut laser microdissection system from MMI. Several critical parameters affecting the performance of the workflow were investigated, including recovery efficiency related to static electricity, laser cutting precision, tissue degradation, and the implementation of sample preparation following microdissection. On average, 1000–1500 proteins were identified per successfully recovered and analyzed 1600 µm² pixel. Using this approach, we were able to demonstrate distinct proteomic profiles across the three tissue regions despite their histological similarities. We further identified proteins that were differentially abundant in the junctional region and characterized the biological functions associated with these proteomic differences. These results demonstrate the potential of P2P for spatially resolved proteomic characterization of heterogeneous tissues at high resolution.

11:30–11:50 **TALK A4** **P16****Single-cell proteomics for determination of mouse cardiomyocyte heterogeneity: the SCarP strategy****Blandine Chazarin** — *ProtMic, UMONS***B. Chazarin**, A. Binek, J. V. Janssens, J. Cantlon, Y. Zirem, A. Karlstaedt, J. V. Van Eyk

Single-cell proteomics (SCP) has traditionally faced technical limitations when applied to tissue-isolated primary cells. This study presents Single Cardiomyocyte Proteomics (SCarP), a novel workflow specifically tailored to dissect the proteomic heterogeneity of primary mouse cardiomyocytes isolated directly from adult tissue. SCarP integrates cell sorting and miniaturized sample preparation using the CellenONE X1 system—including photographic imaging and automated cell length measurement—in 384-well plates. Proteomic acquisition is conducted via data-independent acquisition (DIA) on a TimsTOF SCP mass spectrometer, supported by real-time quality control monitoring. Analysis of 425 individual cardiomyocytes across four adult hearts yielded 2,634 unambiguously quantified proteins covering five orders of magnitude, defining four distinct cell clusters based on unique proteomic signatures. Remarkably, the myosin heavy chain Myh7b—previously reported to be absent in adult hearts due to alternative splicing—was detected in 6.6% of single cells, confirmed by five proteotypic peptides, and independently validated in cardiac myofilaments using Orbitrap Astral MS. Myh7b expression strongly correlated with proteins involved in calcium signaling, pointing to a potential regulatory role in cellular calcium responses. Metabolic profiling across all clusters confirmed functional features of viable primary cardiomyocytes, including robust representation of oxidative phosphorylation and branched-chain amino acid degradation.

11:50–12:10 **SPONSOR TALK A51** **P17****Sponsor presentation: Bruker**

Company profile in “Our sponsors” (p. 6). Visit the stand in Le Foyer (1st floor).

12:10–14:20 **Lunch (Le Foyer) & poster session (PhD House, 1st floor)**

Session B-1 **Zooming Out: Proteomics in the Bigger Picture**

14:20–15:45

14:20–15:05 ★ **KEYNOTE B****From Molecules to Mechanisms: Exploring Biology Through Multi-Omics****Bart Ghesquière** — *Full Professor, KU Leuven — Metabolomics Expertise Center, VIB-KU Leuven*

Modern mass spectrometry provides unprecedented opportunities to characterize biological systems across multiple molecular layers. Yet, measuring more molecules does not necessarily result in better biological understanding. The potential of multi-omics lies in integrating complementary information from proteins, metabolites and lipids with spatial and functional information.

Mass spectrometry-based multi-omics strategies can move beyond molecular inventories towards a mechanistic understanding of cellular metabolism. Integration of proteomics, metabolomics and lipidomics with stable-isotope tracing adds a dynamic dimension, revealing pathway activity and metabolic rewiring.

These concepts are increasingly being extended towards smaller and spatially defined samples through workflows that extract multiple omics layers from the same sample, imaging mass spectrometry, and emerging single-cell and subcellular approaches. Applications in biomedical research demonstrate both the opportunities and challenges associated with these technologies. Ultimately, the goal is not to generate as many omics layers as possible, but to integrate the right layers to answer biological questions and translate complex molecular datasets into testable mechanisms.

15:05–15:25 **TALK B1** **P18****Development of an analytical framework to evaluate antivenom efficacy through magnetic beads and biolayer interferometry****Thomas Crasset** — *MSLab, University of Liège*

Snake envenomation remains a major public health concern in subtropical areas of Asia, Africa, and the Middle East, mainly affecting rural populations. Each year, an estimated 81,000 to 138,000 people die from snakebite envenoming, while approximately two to three times as many suffer long-term disabilities. As a result, the World Health Organization has classified snakebite envenoming as a neglected tropical disease. Although antivenoms remain the only specific treatment available, they consist of a mixture of toxin-specific and undesired non-specific IgGs, are often thermally unstable, and may induce adverse reactions. Consequently, several next-generation alternatives, including nanobodies, monoclonal antibodies, and ADDomers (adenovirus-derived multivalent nanoparticles), are currently under development.

Current antivenomics methods designed to assess antivenom-venom binding lack throughput and quantitative resolution. We developed a novel antivenomics workflow combining protein G magnetic beads with high-resolution ion mobility mass spectrometry for toxin identification and quantification, using a label-free, automatable workflow. Protein G magnetic beads were coupled with EchiTabG IgGs, a monospecific antivenom prepared against *Echis romani* toxins, and incubated with the corresponding venom. Following immunocapture, eluates were analyzed by LC-IM-MS/MS after tryptic digestion to identify and quantify the bound toxins. In parallel, bio-layer interferometry was used to determine the apparent avidity of the whole antivenom against the crude venom, providing a metric comparable across antivenoms and emerging therapeutic alternatives.

Our results revealed a clear saturation profile of EchiTabG toward *E. romani* venom, supporting clear binding between the antivenom and the venom used for immunization. The proteomics workflow enabled the identification and relative quantification of the toxin families captured by the antivenom, while requiring only small sample amounts and offering compatibility with automation. Together, these complementary methodologies provide a robust framework for evaluating antivenom specificity, affinity, and toxin recognition and could be implemented as routine quality-control tools for both conventional antivenoms and next-generation toxin-neutralizing therapeutics.

15:25–15:45 TALK B2 (P19)

From surfaceome discovery to therapeutic opportunities: proteomic targets in patient-derived glioblastoma stem-like cells

Anna Laurent — *Laboratory for the Analysis of Medicines, University of Liège*

A. Laurent¹, G. Cobraiville¹, A. Allard¹, M. C. Köse², A. Lombard³, C. Lemoine³, V. Neirinckx³, M. Fillet¹

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Glioblastoma (GBM) is the most common and aggressive primary brain tumor in adults, with limited treatment options and systematically fatal outcomes, highlighting the urgent need to find new therapeutic approaches. Cell surface proteins (CSP) represent attractive therapeutic targets because of their accessibility and their involvement in key physio-pathological processes.

To identify novel target CSP candidates in GBM, untargeted cell surface proteomic analysis was performed on patient-derived glioblastoma stem-like cell (GSC) cultures. Proteomic data were integrated with RNA-seq and publicly available databases to prioritize therapeutically relevant targets. This workflow identified five CSPs of interest: PTK7, PTPRZ1, OSMR, CSPG4, and IGDCC4. To further investigate these candidates, a targeted UHPLC-multiple reaction monitoring (MRM) assay was developed and optimized to assess their expression and relative abundance across different GSC models and cell passage levels, providing insights into their intra- and inter-cell cultures variability. These results were then further supported by qPCR analysis across cell passage and target localization confirmation by flow cytometry and western blot analyses.

Overall, these observations support PTK7, PTPRZ1, OSMR, CSPG4, and IGDCC4 as promising therapeutic targets in GBM. Furthermore, this study illustrates the strength of combining multi-omics and translational approaches as well as the interest of clinically relevant three-dimensional patient-derived GSC models in drug target discovery.

Source: Laurent, A.; Cobraiville, G. ; Allard, A. ; Köse, M.C., Lombard, A. ;Lemoine, C. ;Neirinckx, V. ; Fillet, M. Identification of glioblastoma cell surface proteins and assessment of their expression across patient-derived stem-like cell cultures. *J. Proteome Res.* (2026) 25 (9): 4744–4756. doi: 10.1021/acs.jproteome.6c00267

15:45–16:30 Coffee break — Le Foyer (1st floor)

Session B-2 Zooming Out (cont'd)

16:30–17:30

16:30–16:50 TALK B3 (P20)

Interaction between the FET fusion FUS::DDIT3 and the cohesin loader NIPBL remodels the 3D chromatin structure in myxoid liposarcoma

Élise Gilson — *Gene Expression and Cancer, GIGA, University of Liège*

Chromosomal translocations involving FET proteins and transcription factors (TFs) lead to the formation of oncogenic fusion proteins that play a central role in the development of several sarcoma subtypes. These chimeric proteins disrupt cellular function, notably by reshaping the three-dimensional organization of chromatin and disturbing key regulatory mechanisms. Previous studies have shown that certain TFs, such as the glucocorticoid receptor, interact with NIPBL, the cohesin-loading factor, to recruit cohesin to specific chromatin sites. This suggests that the ability to interact with NIPBL may be a shared feature of TFs. Whether FET fusion proteins exploit this interaction to disrupt chromatin architecture and gene expression in cancer cells remains unknown.

In this project, we will investigate the interaction between FUS::DDIT3, the FET fusion causing myxoid liposarcoma, and NIPBL. Co-immunoprecipitation assays will allow us to determine whether a physical interaction occurs between these proteins in cancer cells. To map the interacting domains with higher precision, we will employ a split-luciferase complementation assay. Chromatin immunoprecipitation followed by sequencing (ChIP-seq) will be used to assess whether the presence of FUS::DDIT3 leads to abnormal cohesin loading at specific genomic loci. To evaluate the broader

consequences on genome organization, we will perform Micro-C, a chromatin conformation capture technique capable of revealing disruptions in chromatin folding. Finally, transcriptomic profiling by RNA-seq will link the observed structural changes to downstream effects on gene expression.

We hypothesize that FUS::DDIT3 will recruit NIPBL by direct interaction, promoting aberrant cohesin loading at genomic regions characteristic of this fusion protein. This mislocalization is expected to induce alterations in 3D chromatin organization, including loop formation and domain boundaries, leading to widespread transcriptomic dysregulation. These findings will shed light on a novel mechanism by which FUS::DDIT3 drives sarcomagenesis and could identify potential therapeutic targets for disrupting its oncogenic activity.

16:50–17:10 **TALK B4** (P21)

Proteomic identification of THSD7A in a case of PLA2R-negative membranous nephropathy and potential implications for clinical management

Annelore Vandendriessche — *VIB Proteomics Core, Ghent University*

Membranous nephropathy (MN) is an autoimmune glomerular disease most commonly associated with antibodies against phospholipase A2 receptor (PLA2R). In PLA2R-negative disease, identification of alternative target antigens can resolve diagnostic uncertainty and provide clinical information. We report a case in which proteomic analysis identified THSD7A as the disease-associated antigen in a patient with progressive, treatment-resistant MN.

A 65-year-old man presented with nephrotic syndrome and progressive renal dysfunction. Kidney biopsy showed MN, while circulating anti-PLA2R antibodies were negative and tissue PLA2R staining was initially weak and inconclusive. Subsequent serological testing detected anti-THSD7A antibodies, but without available THSD7A immunohistochemistry, the disease-associated antigen remained unconfirmed at the tissue level. Despite supportive treatment and B-cell depletion with rituximab, nephrotic syndrome persisted and renal function deteriorated. A repeat kidney biopsy was referred for mass spectrometry-based proteomic analysis. Abnormal glomeruli were isolated from FFPE tissue by laser microdissection in 2 technical replicates (~100,000 μm^2 each). Following low-input sample preparation, peptides were analyzed by DIA nanoLC-MS/MS on an Orbitrap Astral and processed using DIA-NN. Proteomic analysis of the glomeruli identified THSD7A, providing tissue-based molecular confirmation of THSD7A-associated MN and resolving the discordant PLA2R findings. Given persistent disease and progressive renal dysfunction, treatment was switched to obinutuzumab. After treatment, anti-THSD7A antibodies became undetectable, followed by improved renal function, normalization of serum albumin and a reduction in proteinuria to a subnephrotic range.

CONCLUSION. This case illustrates how mass spectrometry-based proteomic analysis of laser-microdissected glomeruli from routine FFPE kidney tissue can identify the disease-associated antigen in serologically unresolved MN. Although THSD7A was identified only after treatment failure and progressive renal decline, its identification raises an important clinical question: could earlier proteomic characterization of the initial biopsy have enabled earlier, more informed therapeutic decisions and potentially altered the clinical course? Integrating tissue proteomics earlier in the diagnostic workup of serologically unresolved MN may help move clinical management toward a more precise, antigen-informed approach.

17:10–17:30 **TALK B5** (P22)

Mapping EWSR1::FLI1 interactions with the cohesin loader complex in Ewing sarcoma

Fateme Shaabanpourghamaleki — *Gene Expression and Cancer, GIGA, University of Liège*

INTRODUCTION. Ewing sarcoma is an aggressive pediatric cancer driven by the EWSR1::FLI1 fusion transcription factor, which profoundly rewires gene expression and 3D genome organization. Intracellular communication within the nucleus relies on coordinated chromatin interactions that regulate long-range transcriptional programs. Since the cohesin loader NIPBL plays a central role in genome topology and chromatin communication, we investigated whether EWSR1::FLI1 exploits NIPBL-mediated chromatin remodeling to sustain oncogenic transcriptional networks in Ewing sarcoma.

METHODS. Protein interactions between EWSR1::FLI1 and NIPBL were analyzed using GPCA assays. Domain mapping and mutational analyses were performed to identify interaction interfaces. Functional relevance was assessed through transactivation assays, siRNA-mediated depletion of EWSR1::FLI1 and NIPBL in A673 cells, RNA sequencing, qPCR validation, knockdown-rescue (KD-rescue) experiments, and colony formation assays.

RESULTS. We identified a direct interaction between EWSR1::FLI1 and the N-terminal region of NIPBL mediated by both the N- and C-terminal domains of EWSR1::FLI1. GPCA and mutational analyses revealed that an LLxLL-containing amphipathic α -helix within the EWSR1::FLI1 C-terminus is critical for NIPBL binding. Transcriptomic analyses demonstrated a strong overlap between EWSR1::FLI1- and NIPBL-regulated genes, with 91.1% of shared targets altered in the same direction. qPCR further confirmed co-regulation of PPP1R1A, PRKCB, and ICAM1. Importantly, KD-rescue and colony formation assays showed that NIPBL-binding deficient mutants exhibited impaired target gene rescue and reduced clonogenic potential, highlighting the functional importance of the EWSR1::FLI1–NIPBL interaction in oncogenic signaling and transcriptional regulation.

CONCLUSION. Our findings identify NIPBL as a critical cofactor of EWSR1::FLI1 and support a model in which EWSR1::FLI1 hijacks cohesin-loading machinery to reprogram intracellular chromatin communication networks and sustain oncogenic transcriptional programs in Ewing sarcoma. These results provide new insights into the role of chromatin-mediated communication in cancer progression and highlight the EWSR1::FLI1–NIPBL interaction as a promising therapeutic target.

20:00

Gala dinner — Brasserie Lî Sku Mel, Liège city centre (registration required)

Day 2 Wednesday 14 October 2026

08:45–09:10 Morning coffee — Le Foyer (1st floor)

Session C-1

Going Big: High-Throughput LC-MS Strategies for Scale and Depth

09:10–10:35

09:10–09:55 ★ KEYNOTE C

Boosting Proteomics: Enhancing Peptide Recovery, Automation, Chromatographic Robustness and Performance**Gabriel Mazzucchelli** — MSLab Omics, University of LiègeC. Kune¹, A. Gholizadeh², M. Ska², A. M. Berkal¹, S. Tielens³, M. Fléron⁴, D. Baiwir⁴, D. Vandormael⁵, A. Bruffaerts⁶, A. Mottais⁶, L. Nguyen³, S. Gohy⁶, G. Eppe¹, T. Gillet², **G. Mazzucchelli**^{1,4}¹Mass Spectrometry Laboratory (MSLab), MolSys Research Unit, University of Liège, Belgium²Microfluidics Lab, University of Liège, Belgium³GIGA Stem Cells, Molecular Regulation of Neurogenesis, University of Liège, Belgium⁴GIGA Proteomics Facility, University of Liège, Belgium⁵Sirris, Belgium⁶Pole of Pneumology, ENT and Dermatology (LUNS), Institute of Experimental and Clinical Research (IREC), UCLouvain, Brussels, Belgium

Single-cell proteomics and clinical biofluid studies both generate hundreds to thousands of samples, each with a very low protein content. Scaling up these studies requires workflows that are sensitive, but also automated, robust and fast.

In single-cell proteomics, each cell is a sample, and in spatial proteomics, each laser microdissection is a sample (talk A3, M. Hodeige). At such low amounts, peptide adsorption to surfaces is a key bottleneck. Using HeLa tryptic digests, we showed that adsorption follows a Langmuir model, with substantial signal loss at very low concentrations. By optimizing a one-pot protocol with polymer-based vials (PMMA or PET) and nonionic detergents (PEO or DDM), we improved peptide recovery up to 16-fold. As part of our ChipOmics developments, this DDM-based protocol was then transferred to WellOmics, a microfluidic chip in a 384-well plate format operated solely by centrifugation. WellOmics automates sample preparation from single-cell FACS sorting to LC-MS injection, with minimal manual handling and sub-microliter volumes, allowing up to 384 cells to be processed in parallel on a single plate.

To analyse these samples, we developed the Trap-Refocusing-Elute (TRE) nanoLC mode (talk A1, C. Kune), which combines the sharp peaks of direct injection with online desalting and flexible injection volumes (1 to 10 µL). TRE ensures complete sample transfer and enables 25-minute analysis cycles on standard UPLC platforms, which corresponds to more than 50 runs per day, with the robustness needed for long acquisition series. In addition, a DIA spectral library built by double (sequential) enzymatic digestion and peptide fractionation (poster P12, A. Gillet) identified 282,008 peptides and 9,588 proteins, supporting consistent identification across large sample sets.

Finally, I will present our strategy to increase sample collection and cohort sizes for human sweat proteomics, developed within the SmartSweat project (Win2Wal, Wallonia) with the ULiège Microfluidics Lab, Sirris and UCLouvain. The project aims at a low-cost wearable microfluidic patch that passively collects a defined volume of sweat, including unstimulated sweat collected overnight, and stabilises it by drying until analysis. Since no sweat stimulation or immediate processing is needed, sampling becomes simple, including in newborns, and compatible with large clinical cohorts. The collected samples are then analysed with our semi-automated sweat proteomics workflow (talk C2, A. M. Berkal), with the long-term goal of building a sweat proteome database for personalised health monitoring.

These developments improve peptide recovery, automation and analytical throughput, and make it possible to apply proteomics to large numbers of single cells and to large clinical cohorts.

09:55–10:15 TALK C1 (P23)

Reading metabolic routing off the histone epigenome: a dual DDA/DIA framework for time-resolved ^{13}C incorporation analysis

Thijs Lefever — ProGenTomics, Ghent University

A cell must constantly adapt to what its environment offers, and much of that adaptation is written onto chromatin. Histone post-translational modifications (hPTMs) are built from metabolites such as acetyl-CoA and S-adenosylmethionine, and hPTM removal often depends on metabolic cofactors such as NAD⁺ and alpha-KG, which places epigenetics right where metabolism meets gene regulation. This metabolic-epigenetic cross-talk is thought to be a key driver of how cells respond to nutrient changes and how they establish their identity. At ProGenTomics, we developed a mass spectrometry workflow that profiles the metabolome, proteome and histone epigenome from a single cell pellet. Yet even such a complete snapshot has a blind spot: abundances show what is present, not how actively it is being made or removed.

Stable isotope tracing fills that gap. When cells are fed ^{13}C -labelled nutrients such as glucose or glutamine, the heavy carbon follows the metabolic routes the cell actually uses. Where it turns up downstream shows which pathways are active and how fast they run. We extended this idea beyond metabolites to histone peptidofoms, following ^{13}C from the nutrient all the way onto chromatin. The tracer ends up both in the amino acid backbone and in the modifications themselves, so two processes run in parallel at different rates. To separate them, we built 'EnvelopeFlux', a DDA-based tool that combines custom isotopic envelope extraction with isotope distribution modelling to estimate amino acid and PTM incorporation for every histone peptidofom.

Using a time-course design, we determined the fraction of each PTM at each residue that was newly synthesised from the tracer, and how quickly it turned over. DIA measurements of the same samples, based on MS2 fragment ions, gave incorporation parameters consistent with the MS1 precursor analysis. This opens the way to incorporation analysis at the level of single peptidofoms.

This framework turns the histone epigenome into a readout of metabolic activity and brings us closer to causality and directionality in phenotype networks. It can be applied to any cellular model and is especially relevant to cancer biology, where metabolic and epigenetic reprogramming go hand in hand. In drug testing, it can also show how a treatment rewires metabolism and histone modifications over time.

10:15–10:35 SPONSOR TALK CS1 (P24)

Sponsor presentation: BigOmics Analytics

Company profile in "Our sponsors" (p. 6). Visit the stand in Le Foyer (1st floor).

10:35–11:10 Coffee break — Le Foyer (1st floor)

Session C-2 Going Big (cont'd)

11:10–12:10

11:10–11:30 TALK C2 (P25)

Sweat proteomics: a non-invasive approach for biomarker discovery with optimized and semi-automated sample preparation

Amine Mohamed Berkal — MSLab, University of Liège

Sweat is a promising biofluid for biomarker discovery due to its non-invasive collection and rich molecular content. Its proteome reflects key physiological processes and offers opportunities for disease monitoring via mass spectrometry-based proteomics. We developed a semi-automated workflow combining NanoOrange™ protein quantification with a streamlined One-Pot digestion protocol, enabling direct analysis of raw sweat without pretreatment steps that can cause protein loss. The study included 422 sweat samples and 6 pooled quality controls, covering several diseases—cystic fibrosis, asthma, bronchiectasis, respiratory infections/cough, and growth or digestive disorders—alongside healthy individuals. A total of 3,380 proteins were identified; after stringent quality filtering, 1276 proteins with 92% data completeness were retained. Identified proteins participate in different important biological processes, including innate immunity, oxidative stress, and

metabolic pathways. After adjusting for age, sex, and Body Mass Index (BMI), differential expression analyses revealed several candidate biomarkers distinguishing cystic fibrosis, along with additional disease-associated biomarkers across the cohort. These results demonstrate the strong potential of sweat as a non-invasive source for disease characterisation and health monitoring. Ongoing work aims to validate the identified biomarkers and further establish sweat-based proteomics as a reliable tool for clinical applications.

11:30–11:50 **SPONSOR TALK CS2** **P26**

Sponsor presentation: SCIEX

Company profile in “Our sponsors” (p. 6). Visit the stand in Le Foyer (1st floor).

11:50–12:10 **SPONSOR TALK CS3** **P27**

Sponsor presentation: MS Wil

Company profile in “Our sponsors” (p. 6). Visit the stand in Le Foyer (1st floor).

12:10–13:30 Lunch (Le Foyer) & poster session (PhD House, 1st floor)

Session D-1

Processing and Interpreting Proteomic Data: The Promise and Pitfalls of Bioinformatics and AI

13:30–14:35

13:30–14:15 ★ **KEYNOTE D1**

Proteomics in the Age of Artificial Intelligence

Wout Bittremieux — Assistant Professor, University of Antwerp

Proteomics is now generating unprecedented volumes of mass spectrometry data, driven by increasingly powerful instrumentation and large-scale studies. Yet our ability to translate these measurements into biological knowledge remains a major challenge. The limiting factor is no longer data generation, but our capacity to extract meaningful insights from increasingly complex molecular datasets.

Artificial intelligence (AI) is beginning to reshape every stage of the proteomics workflow. Early applications focused on improving established computational approaches, where machine learning models enhanced conventional database search strategies by predicting peptide properties and improving peptide-spectrum match scoring. More recently, deep learning models are learning directly from tandem mass spectra for de novo peptide sequencing, enabling new discoveries.

The next evolution will be AI-driven proteomics experiments, where models actively contribute to experimental decision-making. Rather than simply analyzing measurements after acquisition, AI could guide instruments toward collecting the most informative data, transforming proteomics from a strategy of measuring more toward one of measuring smarter.

Ultimately, the greatest opportunity lies in moving beyond individual spectra and molecular identifications toward biological understanding. By integrating diverse omics measurements, AI may enable predictive representations of cellular systems and provide new ways to understand the complexity of life.

I will explore the ongoing transformation of proteomics through AI: from models that enhance existing workflows, through systems that directly interpret molecular signals, toward intelligent technologies that could redefine how we perform experiments and uncover biological knowledge.

14:15–14:35 TALK D1 **P28**

Development of a de novo human immunopeptidomics map

Moira Breëns — *Adrem Data Lab, University of Antwerp*

Peptides bound to major histocompatibility complex (MHC) proteins are presented on the cell surface to the adaptive immune system, which can recognise these epitopes, and subsequently eliminate infected or malignant cells through an immune response. Mass spectrometry can be used to analyse these immune peptides, but current research is limited by the usage of a database-driven approach. An alternative approach, not limited by the content of the database, is based on de novo sequencing tools such as Casanovo, followed by identification of these peptides and their origin. As this approach isn't constrained by matching against a fixed database, this could enable the discovery of novel findings that would otherwise be missed, providing opportunities for generating new hypotheses.

We aim to build a human immunopeptidome map, including both human peptides, fusion peptides and foreign peptides (e.g. bacterial or viral) presented to the immune system by these MHC complexes. Casanovo output is filtered on a dual PSM-confidence threshold and pooled in a biologically relevant manner, e.g. by sample or tissue. Next, our pipeline screens peptides for contaminants before matching them against the human proteome. Peptides without a clear human match are then searched against a relevant, broader database, and hits are prioritised towards those known to infect humans or be present within the environment, allowing each peptide to be assigned a likely taxonomic origin and an overview of the outside actors presented to our immune system.

A preliminary analysis on the HLA Ligand Atlas, using a combination of PeptideMapper and BLAST on the de novo output from Casanovo, confirms the presence of a majority of human peptides, but also contaminants (such as protein A from *Staphylococcus aureus*) and well-known viral and bacterial epitopes. This included established epitopes from Epstein-Barr virus and Cytomegalovirus, which are known to impact human health and disease. These results contribute to insight into the adaptive immune system and could aid the development of immunotherapies and vaccines.

14:35–14:55 Coffee break — *Le Foyer (1st floor)*

Session D-2 Processing and Interpreting Proteomic Data (cont'd)

14:55–16:10

14:55–15:30 ★ KEYNOTE D2

Cloud Pipelines Followed by AI-Assisted Downstream Analysis and Interpretation

Henry Emanuel Webel — *Senior Data Scientist, Novo Nordisk Foundation Biotechnology Research Institute for the Green Transition (NNF-BRIGHT), DTU*

At the Novo Nordisk Foundation Biotechnology Research Institute for the Green Transition (NNF-BRIGHT), we are developing a multiomics cloud-based infrastructure built around Nextflow pipelines, facilitating automated processing, downstream analysis, and AI-assisted interpretation and consultation across diverse sustainability applications. Through our Data Catalog, users can register and upload data and metadata to the Data Catalog and subsequently launch nf-core-based processing pipelines on their datasets. We have curated and integrated a collection of community-standard, nf-core workflows to process different data types. For proteomics, we run quantms and quantmsdiann, which are two quantitative proteomics pipelines that I actively help maintain. Quantmsdiann provides DIANN output tables that can be then used for downstream analysis. We are using Seqera platform for pipeline execution monitoring, and easy and fast access to execution logs and results. The entire results folder of a pipeline run is stored back to our Data Lake.

With three custom Python packages for statistical analysis (acore), visualization (vuecore) and report generation (vuegen), we can produce standard reports for common data types, demonstrated for this event with MS-based proteomics datasets. On top of these automated reports, we are building an Agentic Omics Reasoning and Analysis (AORA) library designed to interpret, contextualize, and extend results generated from the standard reports. AORA can be used to orchestrate access to data and resources, and to augment the analysis. In my talk I will highlight some of the ways we envision to augment results to biological meaning in an interactive way.

The results interpretations will end up in a VueGen report that can generate multiple report formats based on a result folder, including interactive Streamlit reports. The Streamlit report has an interface to a chatbot that help users in interpreting results and augmenting the analysis according to their research questions and custom requirements.

The downstream analysis and the automatic interpretation are built on open-source Python libraries and language models – which can be open-source or not – enabling transparent, customizable, and reproducible end-to-end omics workflows, from automated data processing to AI-assisted biological interpretation.

15:30–15:50 **TALK D2** **P29**

Characterization of the immunopeptidome of drug-tolerant persister cells in acute myeloid leukemia

Charline Faville — GIGA Hematology, University of Liège

C. Faville, B. E Silva, A. Daubry, L. Correia Da Cruz, G. Carriglio, S. Charles, A. De Voeght, M. Fléron, D. Baiwir, G. Mazzucchelli, L. Willems, F. Baron, G. Ehx

Acute myeloid leukemia (AML) is the most frequent and lethal leukemia among adults. High dose of chemotherapy (cytarabine) is the first-line treatment and leads to high remission rate. However, most patients eventually relapse. Relapse is mediated by drug-tolerant persister cells (DTPs, residual cells surviving the treatment) that present a vast transcriptomic reprogramming characterized by the expression of stress responses. In this work, we hypothesized that DTPs present specific and immunogenic MHC-I-associated peptides (MAPs) induced by stress responses and tried to identify MAPs specifically expressed by DTPs to design immunotherapy. To do so, five cell lines and ten primary samples were treated in vitro with cytarabine for 3 days and collected later to characterize the immunopeptidome of DTPs through a proteogenomic approach (RNA sequencing and mass spectrometry).

MAPs were isolated from cells by immunoprecipitation and analysed by a high-performance liquid chromatography system, coupled with trapped ion mobility spectrometry time-of-flight instrument. After MAPs filtering based on their length and predicted MHC-I binding profile, differential presentation analyses evidenced a global reduction of MAPs presentation in DTPs. Based on immunogenicity predictions and BamQuery, we could segregate 296 MAPs in cell lines and 507 in primary samples, which were predicted to be highly immunogenic and overexpressed by AML cells. These MAPs were flagged as tumor antigens (TAs). Among them, 75 in cell lines and 157 in primary samples were highly specific to AML and flagged as tumor-specific antigens (TSAs). At peptide level, TAs are globally downregulated, suggesting the immunogenicity of DTPs is reduced. Transcriptomic analyses suggested that DTPs present a globally decreased protein translation rate, possibly explaining the depletion of the peptide pool feeding the MHC-I machinery. By flow cytometry, we also observed that DTPs upregulated total MHC-I molecules at their surface but downregulated peptide-loaded MHC-I molecules.

Altogether, these results suggest that DTPs may evade T-cell recognition through a decreased presentation of immunogenic MAPs. However, TSAs are still presented by DTPs, which make promising targets to eradicate cells expressing them.

15:50–16:10 **TALK D3** **P30**

Characterizing unexpected peptides in human proteomics data using de novo peptide sequencing

Fatemeh Mirzadeh Sarcheshmeh — Adrem Data Lab, University of Antwerp

Mass spectrometry samples usually contain more than the proteins of interest. Lab reagents, cell culture supplements and microbes end up in the samples too. They will make quantification less accurate and when the cell culture is infected, it will change the biology we measure. Most of these peptides are never seen because database searching, which is one of the most used methods, only can find peptides which are already in the database, but de novo peptide sequencing reads the amino acid sequences directly from the MS2 spectrum, so it does not depend on database.

In the GLEAMS dark proteome, almost 40 million clustered spectra from 216 public human proteomics datasets in MassIVE-KB are still unidentified. Each cluster is the same peptide used again and again in different experiments, so we ran Casanovo, a de novo peptide sequencing tool, on the data. After filtering on confidence and peptide length, 2 million high confidence matches remained and about 61% matched the human proteome: human peptides that clustering and library searching previously missed. The remaining 814,117 peptides were screened with Unipept and matched to reference proteomes. Most

fall into one of these groups: laboratory reagents such as fetal bovine serum and digestion enzymes; immunoaffinity reagents from immunoprecipitation; environmental material such as pet hair; and microbial contamination by *Mesomycoplasma* or yeast.

Metadata from the associated manuscripts was extracted automatically with LLM-based text mining, providing complementary information at the study level. This links each spectrum back to the protocol that produced it: digestion enzymes appeared in studies reporting LysC and immunoaffinity reagents in studies reporting immunoprecipitation. Saliva studies were enriched for the oral microbiome taxa their authors also reported, and one brain tissue dataset contained *Serratia* peptides confirmed by spectral validation. The *Mesomycoplasma* and yeast infections, in contrast, appear nowhere in the metadata, so these published results may be affected without anyone knowing. Only part of these contaminants is covered by current databases, so we propose a longer list available for inclusion in standard search workflows.

This work shows that the unidentified fraction of public proteomics data is largely interpretable and can be traced back to its experimental origin at repository scale, and that contaminant filtering as practised today misses much of what is really in the data.

16:10–16:25 *Poster prize & closing remarks by Gabriel Mazzucchelli (local organiser) & An Staes (BePA President) — Exèdre Dick Annegarn*

08 Poster abstracts

Posters P1–P12. The abstracts of posters P13–P30 are printed with the corresponding talks in the detailed programme.

P1 POSTER

Evaluation of Protein Module Detection Analysis for Single Cell Proteomics

Enes Sefa Ayar — CBIO, de Duve Institute, UCLouvain

Correlated protein modules, groups of proteins that cooperate to execute biological functions, provide critical insights into cellular mechanisms. Many computational approaches have been developed to detect protein modules. However, most were developed for transcriptomic data and rely on the assumption that gene expression levels can be used to identify functionally related protein groups. Proteomics directly measures protein levels, eliminating this assumption and offering a more accurate view of functional protein relationships. Bulk measurements also obscure cell-to-cell variability by averaging signals across heterogeneous populations. Single-cell proteomics (SCP) quantifies protein levels at single-cell resolution and thus preserves cellular heterogeneity, enabling the discovery of dynamic and context-specific protein modules that are often masked in bulk measurements. While SCP has great potential, module detection in SCP is challenged by substantial batch effects, high missingness, and a lack of standardized computational workflows. Here, we systematically evaluated the impact of data pre-processing, module detection algorithms, and parameter settings using seven diverse SCP datasets. We demonstrate that early-stage analysis decisions, particularly pre-processing, exert a more profound influence on biological interpretation than the choice of detection method itself. To identify optimal workflows, we developed a benchmarking framework using the Biological Homogeneity Index (BHI) and empirical Z-scores validated against randomized module sets. Our results reveal that specialized SCP pre-processing strategies, specifically scplainer and omicsGMF, consistently yield higher functional coherence than traditional methods. Among detection algorithms, spectral clustering, and self-organizing maps (SOM) emerged as the most robust for capturing specific biological themes. This comprehensive evaluation highlights the inherent variability of protein module detection analysis and provides a critical view for distinguishing true biological signals from technical artifacts in SCP.

P2 POSTER

Genome-wide characterization of aberrantly expressed tumor antigens through proteogenomics

Gabriele Carriglio — Laboratory of Hematology, GIGA, University of Liège

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Cytotoxic CD8⁺ T cells are essential for anticancer immunity. Recognition of tumor cells is mediated through the interaction between their T-cell receptors and class I MHC-associated peptides (MAPs). While mutated MAPs are often considered the main source of tumor recognition, the contribution of non-mutated aberrantly-expressed antigens to the set of MAPs (i.e. immunopeptidome) and therefore to tumor recognition is misunderstood. In particular, the contribution of non-canonical genomic regions such as introns or endogenous retroelements to the cancer immunopeptidome is unknown.

We are developing a proteogenomic (i.e. genomic-informed proteomics) approach to identify all genomic regions (mutated or not, from coding exons or not) able to generate tumor antigens (TAs).

We first generate a virtual peptidome of 30 medullary thymic epithelial cell (mTEC) and dendritic cell (DC) samples by translating in silico all their RNA-seq reads to generate a reference catalog of non-immunogenic peptides likely to be expressed in healthy tissues. We then compare this peptidome with virtual peptidomes derived from RNA-seq data across eight cancer types to identify candidate tumor antigens based on their recurrence across tumors and differential expression between malignant and mTECs/DCs.

This identified approximately 336 million candidate TAs. Their amino acid sequences were used to interrogate mass spectrometry (MS) data and identify candidate TAs effectively presented by cancer cells. Depending on tumor type, between 500 and 3,600 TAs were detected by MS. Among these, 845 were shared by at least two cancer types, including 21 detected in more than half of cancer types analyzed.

These broadly shared TAs represent promising targets for the development of immunotherapies applicable across multiple malignancies.

Finally, we will use computational approaches to correlate the expression of MS-verified TAs with the infiltration of T cells in cancer RNA-seq data to determine which TAs contribute to tumor recognition. The top candidates will be validated via functional in vitro assays. Overall, our study will establish a database of TAs to help understand the mechanisms of tumor recognition by T cells.

P3 POSTER

Step-by-step method optimization with standard proteins for structural characterization of therapeutic megadalton virus-like particles

Charles Delvaux — *MSLab, University of Liège*

INTRODUCTION. ADDomers are self-assembling dodecahedral virus-like particles (VLPs) derived from adenovirus, that represent a promising new synthetic antivenom platform to solve issues of snakebite envenomation (a neglected tropical disease¹) due to their high stability, multivalency, and cost-efficiency. Their structural characterization remains challenging. This work introduces a native Mass Spectrometry (MS) and Ion Mobility (IM-MS) workflow to monitor the assembly kinetics and conformational stability of such 3.5 MDa complexes.

METHODS. A modified Synapt G2-S (Waters) for high mass capabilities and native MS and Collision-Induced Unfolding (CIU) experiments was used on model proteins (Myoglobin, Insulin, and bovine serum albumin as BSA) in non-denaturing and denaturing conditions. Energy-resolved collision induced dissociation (or breakdown curves survival yield (SY) experiments) were acquired to determine the relative stability of the molecular assemblies (V50 values as voltage where 50% of SY of the assemblies).

MAIN RESULTS. Training and validation using Holo-Myoglobin [M+9H]⁹⁺ demonstrated stable ion beam in non-denaturing MS conditions. CIU heatmaps showed three specific gas-phase population of conformation. Breakdown curves experiments and survival yield of insulin were successfully determined. Additionally, BSA native mass spectra in reduced and Oxidized forms identified overalkylation because of a carbamidomethylation patterns of +2 kDa (Corresponding to the 35 residues submitted to alkylation for 35 cysteines in BSA sequence). IM-MS and CIU will be applied to protein models of increasing mass before working with ADDomers for mapping their supramolecular assembly and avidity for toxins.

P4 POSTER

Understand the lack of immune response to mRNA vaccine for haemodialyzed patients

Lise Demulies — *ProtMic, UMONS*

L. Demulies¹, B. Chazarin¹, A. Delacuvellerie¹, N. Gemander^{2,3}, S. Depickère⁴, A. Waegemans², A. Marchant^{5,2}, M. Bizet⁵, S. Goriely⁵, R. Wattiez¹

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Patients with kidney dysfunction go through haemodialysis and demonstrated poor to no response to COVID mRNA vaccination represented by significantly reduced levels of anti-RBD. The goal of this study is to highlight regulations predicting the immune response to vaccination for non- and responsive haemodialyzed patients compare to healthy individuals.

Plasma samples prepared in heparin in 2021 were selected for proteome analysis by LC-MS but contained white flocculates. Multiple tests were performed as (i) removal by centrifugation and (ii) dispersion by pretreatments. Following, plasmas from 14 individuals from two pathologic (haemodialyzed patients before (NEPHRO-VAC) and after vaccination (COVICO)) and a

healthy group of individuals (PICOV-VAC) were analysed.

Flocculates are challenging due to various quantity across the samples and interfere with colorimetric assays. Pelleting them by centrifugation and decomplexifying on SDS-PAGE, (as well as clear (i.e. supernatant) and non-treated plasma (NP), demonstrates (i) overestimation of protein quantity in NP and (ii) similar protein profiles between the fractions and NP. Thus, centrifugation remove a part of the plasma proteome and 9 dispersion methods were explored to finally select sonication.

Plasmas were prepared with an adapted FASP protocol, prior analysis on 6600 MS instrument (Sciex) allowing identification of 229 proteins. 11 significantly regulated proteins were identified by statistics between pathologic groups or between pathologic and healthy groups. DAVID Enrichment determined 9 significantly enriched pathways (FDR $\geq$ 5%), including “Complement and coagulation cascades” and “Cholesterol metabolism”.

In conclusion, flocculates require an additional step of sonication before the sample preparation and proteome characterization led to potential biomarkers and to pathways which could reflect underlying mechanisms in the response to vaccination in haemodialyzed patients.

Fundings: FEDER, ERDF and Walloon Region (2022-2027 - project 167 (WAL IMAGIN) and 259 (SYST IMM UMONS)).

P5 POSTER

Optimized FFPE Tissue Processing: Complete workflow for in-depth proteome analysis of multiple FFPE formats

Adam Hughes — PreOmics GmbH – Biognosys Group

INTRODUCTION. Formalin-fixed paraffin-embedded (FFPE) tissues are essential for biomarker discovery due to their availability, long-term stability, and associated clinical metadata. However, proteomics laboratories receive FFPE material in diverse formats, requiring simple, standardized workflows. Although the BeatBox-iST FFPE workflow enables non-toxic, high-throughput processing without deparaffinization, it is currently restricted to curl formats and requires additional handling steps. Here, we present an end-to-end workflow supporting both FFPE curls and punches, integrating streamlined sample preparation with LC-MS and data analysis.

GOALS. Develop and evaluate a robust, reproducible, and flexible proteomics workflow for non-deparaffinized FFPE curls and punches, enabling standardized processing across sample types with high proteome depth and quantitative precision.

MATERIALS & METHODS. Quadruplicates of FFPE curls (2–5 × 10 µm) and 1 mm punches from mouse liver and heart were processed without deparaffinization. Samples were homogenized using BeatBox (24-tube format) and incubated at 95 °C for 1 h for simultaneous de-crosslinking, extraction, reduction, and alkylation. The iST workflow included tryptic digestion and optimized peptide cleanup. LC-MS analysis was performed on a nanoElute2 system with PepSep Advanced or integrated-emitter columns (25 × 75 cm, 30-min gradient) coupled to a timsTOF HT in dia-PASEF mode. Data were analyzed using Spectronaut with directDIA+.

RESULTS. The workflow enabled efficient processing of both FFPE formats with high proteome coverage (>5000 proteins in heart, >6000 in liver). Quantitative reproducibility was high across all conditions, with lower median CVs using PepSep Advanced compared to a competitor column (proteins: 7.0–9.9% vs. 8.1–11.5%; peptides: 11.9–15.8% vs. 15.7–19.9%). Minimal differences between sampling formats were observed in liver, while heart samples showed sampling-dependent effects. Punch-derived proteins were enriched in nuclear and chromosomal components, whereas curl-derived proteins were associated with membrane and peripheral compartments, indicating tissue-dependent heterogeneity.

CONCLUSION. We established a reproducible and flexible BeatBox-iST-based end-to-end proteomics workflow for FFPE curls and punches, combining efficient sample preparation, robust LC-MS analysis, and streamlined data processing.

P6 POSTER**Dissection and modulation of mitochondrial pathways during activation and transdifferentiation of cardiac fibroblasts into cardiomyocytes**

Guillaume Paulissen — URBC, NARILIS, University of Namur

G. Paulissen, J. Houssemmand, T. Arnould, L. Bertrand, M. Dieu, P. Renard, D. Detraux

Cardiovascular diseases cause nearly 20 million deaths annually, with myocardial infarction leading to irreversible cardiomyocyte (CM) loss and poor regenerative capacity. Direct reprogramming of cardiac fibroblasts (CFs) into induced cardiomyocytes (iCMs) offers a promising regenerative approach by bypassing pluripotency.

In this study, human iPSC-derived CFs are first activated into a myofibroblast-like state, then transdifferentiated using a doxycycline-inducible MEF2C-GATA4-TBX5 (MGT) construct for controlled gene expression. Comparative transcriptional, structural, and metabolic analyses between converted and non-converted cells, alongside hiPSC-CMs, aim to uncover barriers to efficient reprogramming.

Given the crucial role of mitochondria in lineage conversion, the study emphasizes mitochondrial remodeling as a key determinant of success. Quantitative proteomics reveal profound mitochondrial changes in activated CFs, correlating with network morphology. To enhance iCM maturation and function, metabolic regulators and small molecules are tested to promote mitochondrial biogenesis, oxidative phosphorylation, and the metabolic transition from glycolysis to fatty acid oxidation, hallmarks of mature CMs. Finally, 3D spheroids combining CFs and hiPSC-CMs provide a physiologically relevant platform to model direct conversion. Future work will extend the model to activated and matrifibrotic CF states, offering a physiologically relevant system to dissect and therapeutically target the metabolic and epigenetic barriers that restrict reprogramming in fibrotic cardiac tissue.

Altogether, this integrative strategy advances understanding of mitochondrial dynamics in reprogramming and supports the development of improved in vitro cardiac repair models.

Price : Best poster award at BeSSCR November 2025

P7 POSTER**A living proteomics benchmark for comprehensive evaluation of deep learning-based de novo peptide sequencing tools**

Marina Pominova — Bittremieux Lab, University of Antwerp

De novo peptide sequencing identifies peptides from MS/MS data without relying on a reference proteome database. It is particularly valuable for discovering novel peptides and in specialized applications where sequence database searching is less effective, such as immunopeptidomics and metaproteomics.

Recent advances in deep learning for sequential data have led to the emergence of multiple new de novo sequencing tools. However, their evaluation and comparison remain challenging due to the lack of standardized metrics and universal test datasets. To address this gap, we present a comprehensive, community-driven benchmark of 17 de novo sequencing tools evaluated on a collection of 29 MS/MS datasets spanning diverse organisms, experimental conditions, post-translational modifications, and proteomics applications.

The evaluated tools achieved high accuracy across the benchmark, particularly under favorable experimental conditions, with a median peptide average precision (AP) of 0.714. However, the performance varied substantially between experimental settings, with particularly strong reductions under several forms of domain shift, such as unfamiliar acquisition platforms and unsupported peptide modifications.

Shifting from Orbitrap to timsTOF or low-resolution platforms caused a notable performance decline, reducing precision by up to 50%. Similarly, non-tryptic proteases reduced peptide precision by 3–30% depending on the protease. The presence of TMT labeling or unsupported PTMs also resulted in near-complete performance loss for the corresponding peptides.

In contrast, sequence novelty had a limited effect on performance. On non-natural sequences, median peptide AP decreased by only 0.051 compared with standard human peptides, and performance also did not decline across non-human species with increasing taxonomic distance from humans. These results indicate that current models generalize well to unfamiliar

peptide sequences when the experimental conditions remain similar to those represented during training.

Overall, our results suggest that current methods have already reached a level of accuracy that makes them practically useful across many proteomics applications, while identifying specific areas where further methodological development is required. The benchmark is accessible through a continuously updated online dashboard and provides a resource for both users and tool developers.

P8 POSTER

Inhibitors of Tax1-PDZ Interactions Block HTLV-1 Viral Transmission by Changing EV Composition

Jedidja Puttemans — *Viral Interactomes Network Lab, GIGA, University of Liège*

Extracellular vesicles (EVs) are known to facilitate infection by enveloped RNA viruses including the Human T-cell leukemia virus type-1 (HTLV-1). HTLV-1-encoded proteins, like the transactivator and oncoprotein Tax-1, are loaded into EVs but their precise impact on EV cargos is not yet known. Here, we report a comprehensive interaction map between Tax-1 and the human PDZ (PSD)95/DLG/ZO-1 proteins that regulate EVs formation and composition. We show that Tax-1 interacts with more than one-third of hPDZome components, including proteins involved in cell cycle, cell-cell junctions, cytoskeleton organization and membrane complex assembly. We extensively characterized Tax-1 interaction with syntenin-1, an evolutionary conserved PDZ hub that controls EV biogenesis. Using nuclear magnetic resonance (NMR) spectroscopy, we have determined the structural basis of the interaction between the C-terminal PDZ binding motif of Tax-1, and two PDZ domains of syntenin-1. Importantly, we show that a small molecule able to inhibit HTLV-1 cell-to-cell transmission breaks the Tax-1/syntenin-1 interaction, impacts the levels of syntenin-1 and viral proteins in EVs, and shifts the EV composition toward cellular antiviral proteins and microRNAs, including the miR-320 family. Consequently, we demonstrate that mimics of miR-320c, encapsulated into EVs, have antiviral activities with a potential to be used against HTLV-1 induced diseases.

P9 POSTER

Scop3P-Toolkit: executable structure-aware workflows linking PTMs, peptides, and mutations to protein function

Natalia Tichshenko — *CompOmics, VIB – Ghent University*

Post-translational modifications (PTMs) and genetic variants regulate protein function, signalling, and disease, but their interpretation requires integration of sequence annotations with structural, interaction, and biophysical context. Although resources such as Scop3P, UniProt, the Protein Data Bank, and AlphaFold provide extensive annotations and structural information, integrating these data into reproducible structure-aware analyses still requires custom scripting and manual coordination between multiple independent tools. To address this challenge, we developed Scop3P-Toolkit, an open-source executable analytical environment for interactive analysis of PTMs, mutations, and proteomics-derived peptides in their structural context. The toolkit integrates protein annotation retrieval with structural mapping, residue interaction network analysis, comparative structural analysis, and residue-level biophysical profiling within a unified framework. Experimentally supported phosphosites, phosphopeptides, and phosphoproteomics evidence are provided for human proteins through Scop3P, with optional integration of curated UniProt PTM annotations. UniProt-derived PTMs, sequence features, and genetic variants are available for proteins from any species, extending the framework beyond the human phosphoproteome. Scop3P-Toolkit supports structure-centric analyses including interpretation of PTMs and disease-associated variants, analysis of residue interaction networks and their rewiring across alternative conformations, structural localisation of peptides, and exploration of protein-protein, protein-ligand, and host-pathogen interfaces. Interactive visualisation links sequence annotations, three-dimensional structures, residue interaction networks, and biophysical profiles, enabling coordinated exploration across multiple molecular representations. The toolkit is distributed as Jupyter notebooks, browser-based Voilà applications, and a Galaxy interactive tool, providing transparent, accessible, and reproducible workflows for both computational and experimental researchers. By integrating biological annotation resources into executable, structure-aware workflows, Scop3P-Toolkit enables reproducible interpretation of PTMs, mutations, and proteomics data.

P10 POSTER**Advancing Plasma Proteomics Through a Next-Generation Single-Particle Enrichment Workflow for Deeper and More Quantitative Biomarker Discovery**Karin Yeoh — *PreOmics GmbH – Biognosys Group*

PURPOSE. Human plasma represents an exceptional yet analytically demanding matrix for proteomic biomarker discovery. Its extensive dynamic range and compositional heterogeneity limit the detection of low-abundance proteins, which often convey critical pathophysiological insights. To address these challenges, we present a workflow that integrates P2 plasma enrichment technology with iST sample preparation and advanced Spectronaut® 20 data processing. The combined platform leverages the selective enrichment power of P2 and the reproducibility of iST-based digestion and cleanup, enabling deep proteome coverage from human EDTA plasma samples.

METHODS. Human EDTA-plasma samples from a pilot colorectal cancer cohort (n=6 per group) were processed using the P2 single-particle enrichment workflow (Biognosys Group), employing proprietary nanoparticles that form transient protein coronas to selectively capture low-abundance proteins while excluding high-abundance proteins. Enriched fractions were subsequently digested using the optimized iST technology (Biognosys Group), ensuring maximal recovery and standardized peptide generation. Peptides were analyzed on a timsTOF HT (Bruker) in dia-PASEF® mode in a library-free DIA framework for deep, quantitative profiling.

RESULTS. Compared to conventional direct digestion preparations, the P2-iST workflow achieves significantly deeper coverage of the plasma proteome with substantially higher identification of protein groups and greater quantitative precision (CV <15%). Nearly 6,000 proteins were identified in 12 samples, demonstrating a high data completeness of more than 90% for the P2-iST technology. Pathway enrichment analyses show an emerging biological separation between disease and control groups. In addition, more cytokines, interleukins, and other biomarkers were identified, demonstrating the workflow's potential to uncover new insights into disease biology and biomarker discovery.

CONCLUSION. The integration of P2 enrichment with streamlined iST technology and Spectronaut 20 data analysis defines a next-generation, high-performance platform for deep, precise, and reproducible plasma proteomics. This synergistic approach holds significant promise for advancing biomarker discovery and clinical translational research.

P11 POSTER**Biological Relevance of Measuring Low Abundant Proteins in Human Plasma**Rajendra Kumar Chauhan — *Illumina*

INTRODUCTION. Large-scale affinity proteomic platforms enable biological discovery beyond traditional mass spectrometry (MS) methods. As these assays increasingly detect low-abundance plasma proteins in healthy individuals, the biological basis of those rarely observed remains unclear. We aimed to determine whether low-abundance proteins measured by the SomaScan™ Assay exhibit clinically meaningful, biologically coherent associations across diverse routine phenotypes.

METHODS. We selected Olink Explore HT proteins below the estimated limit of detection (LoD) across all three dilutions in at least one-third of a healthy reference cohort1, (n=78). Proteins (n=3,298) were mapped by UniProt identifiers to analytes on the SomaScan 11K Assay, yielding 2,123 SOMAmer™ Reagents. This subset was evaluated in plasma from 1,015 participants in a separate healthy cohort2. Associations between log10-transformed, center-scaled relative fluorescence units and 75 clinical endpoints (48 continuous, 27 categorical) were tested using Spearman correlation or Wilcoxon rank-sum tests with Benjamini-Hochberg FDR control (FDR<0.05). Analyses were unadjusted for covariates.

RESULTS. Despite low expected abundance, these analytes showed extensive signal across all endpoints, with a mean of 398 significant proteins per endpoint. Overall, 2,118/2,123 analytes were significantly associated with at least one clinical variable, and most associated with multiple endpoints; 675/2,123 also signaled above LoD by MS1. Representative associations were biologically coherent with known healthy-expression patterns: FBP1 strongly tracked with ALT, consistent with hepatocyte-enriched liver expression; PZP showed a marked sex association, in line with estrogen-responsive plasma expression; IL1RN correlated with BMI, consistent with adipose-linked inflammation; MYL11 tracked with creatinine, reflecting skeletal muscle expression; and DEFB104A showed sex-specific patterns consistent with male reproductive tract expression.

CONCLUSIONS. Low-abundance plasma proteins measured by the SomaScan Assay show widespread, robust associations with common clinical variables in a general-population cohort, demonstrating that expanded proteome coverage, with high sensitivity, yields deeper biological insight and that many such signals reflect underlying biology rather than assay noise.

1. Kirsher DY, et al. *Commun Chem*. 2025.

2. Williams SA, et al. *Nat Med*. 2019.

P12 POSTER

Smarter Libraries for Faster DIA: A Sequential Digestion Strategy to Enhance Proteome Coverage in DDA-based Spectral Libraries

Alia Gillet — MSLab Omics, University of Liège

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Large-cohort studies are increasingly required in multifactorial proteomics, demanding high-throughput and scalable workflows. Sample preparation automation and fast LC-MS instrumentation, including short-gradient chromatography combined with Data Independent Acquisition (DIA), have enabled rapid data generation. However, DIA data processing needs high-quality spectral libraries, which is a current bottleneck. While AI-generated libraries offer comprehensive coverage, their large size leads to time-consuming data searches. In contrast, DDA-based libraries reduce search space but limit peptide identifications to those observed in DDA runs. Here, we propose a novel strategy combining sequential protease digestion, peptide fractionation and DDA acquisitions on the timsTOF SCP. In this approach, three replicate samples are separately digested with trypsin, Arg-C, or Lys-C, followed by peptide fractionation and a final digestion with trypsin. This yields tryptic peptides distributed differently across fractions based on the initial protease, enhancing orthogonality between fractionation and LC separation.

Compared to conventional post-trypsin fractionation, our method identifies nearly 50% more peptides. Applied to 10-minute DIA runs, libraries from sequential digestion yield 10% more protein IDs without notably increasing processing time. This strategy enhances peptide coverage and search efficiency, making it ideal for large-scale DIA proteomics requiring both speed and depth.

09 Index of authors

All 77 presenting authors and co-authors, with the contributions in which they appear. **Bold**: presenting author. Codes: Keynote A–D2, talks A1–D3 (with their poster number), posters P1–P12; small figures give the page.

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10 Venue, access & accommodation

CONFERENCE VENUE

Building B8 – Maison des Étudiants & Exèdre Dick Annegarn

Campus du Sart Tilman – Quartier Agora, L'Agora 1, B-4000 Liège, Belgium · GPS 50.5847 N, 5.5705 E

From Liège-Guillemins station, bus B2 « Sart-Tilman-CHU-Botanique » reaches the campus in about 20–25 minutes (stop « Sart-Tilman Amphithéâtres », 175 m from B8). From the city centre, take tram T1 to « SCLESSIN Standard » then bus 8 « Sart-Tilman CHU » (about 30–37 minutes). By car, parkings B, C and D on the campus are free (12–18 minutes from the city centre or the station).

ACCESS & ACCOMMODATION GUIDE

The following pages reproduce the full Access & Accommodation Guide: train and bus connections, campus plan and parkings, walking route from the bus stop, the historical centre of Liège and the list of hotels.



UNIVERSITY OF LIÈGE · SART-TILMAN CAMPUS

B8 – Maison des Étudiants et Exèdre Dick Annegarn

Conference venue — Access & accommodation guide

ADDRESS

B8 – Maison des Étudiants et Exèdre Dick Annegarn

B4000 (Sart-Tilman) – Liège – BELGIUM

GPS: 50.5847 N, 5.5705 E

CONTACT PERSONS

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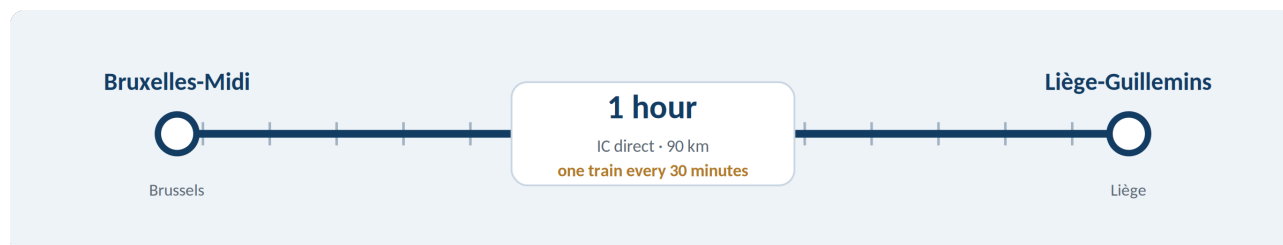
Dominique Baiwir

Tel: (32)-4-366.34.48



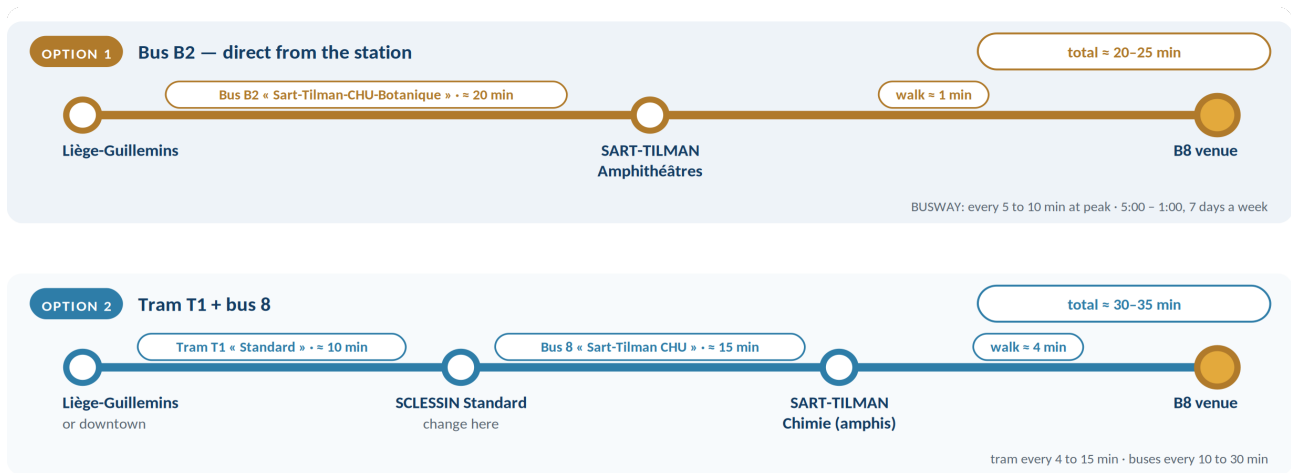
Liège, in the east of Belgium — 1 hour by train from Brussels

1 GETTING TO LIÈGE BY TRAIN



- **1 hour** between Bruxelles-Midi and Liège Guillemin in train (90 km, direct IC)
- **One train each 30 minutes**
- Liège-Guillemins is also the hub for the tram T1 and the bus B2 to the campus.

2 FROM LIÈGE-GUILLEMINS TO THE VENUE BY PUBLIC TRANSPORT



Indicative journey times on the TEC network (letec.be) — the B2 became a BUSWAY line in September 2025

Option 1 — Bus B2 (direct)

From Liège-Guillemins, take the bus B2 « **Sart-Tilman-CHU-Botanique** » until « **SART-TILMAN Amphithéâtres** » stop, then walk around 1 minute to **B8 – Maison des Étudiants et Exèdre Dick Annegarn**.

Total: about 20 to 25 minutes (bus ≈ 20 min, walk ≈ 1 min).

Option 2 — Tram T1 + bus 8

From downtown or Liège-Guillemins: Tram T1 « **Standard** » to « **SCLESSIN Standard** » stop, then bus 8 « **Sart-Tilman CHU** » to « **SART-TILMAN Chimie (amphis)** » stop, and then walk around 4 minutes to **B8 – Maison des Étudiants et Exèdre Dick Annegarn**.

Total: about 30 to 35 minutes (tram ≈ 10 min, bus ≈ 15 min, walk ≈ 4 min).

Since 15 September 2025 the B2 is a BUSWAY line: 100% electric, mostly on its own lane, every 5 to 10 minutes at peak, from 5:00 to 1:00, seven days a week. The tram T1 opened in April 2025 and runs every 4 to 15 minutes; from Sclessin Standard it serves Guillemins, Pont d'Avroy, Sauvenière, Opéra and Place Saint-Lambert, then follows Féronstrée and the quai Saint-Léonard (Pont Maghin, Marengo, Pont Atlas), where the line splits into two branches: Parc Reine Astrid – Coronmeuse, and Droixhe – Liège Expo (Bressoux). 23 stations over 11.7 km. In the historical centre the line runs on a single track in each street: towards Coronmeuse it uses rue Léopold and the quai de la Batte (stops La Batte and Curtius), towards Sclessin it uses Féronstrée (stops Féronstrée and Pont Maghin). Journey times are indicative — check letec.be for live timetables.

Key facts

- **Nearest stop:** « SART-TILMAN Amphithéâtres » (bus B2), 175 m — 2 minutes on foot.
- **Second stop:** « SART-TILMAN Chimie (amphis) » (bus 8), 302 m — 4 minutes.
- **From Liège-Guillemins:** bus B2 ≈ 20–25 min, or 12 min by car (8.6 km).
- **Parkings B, C and D:** free, open every day 7:00–22:30, 2 to 3 minutes on foot.
- **From the city centre:** ≈ 30–37 min by bus, 14–18 min by car.
- **From Brussels:** 1 h by train, then 20–35 min across Liège.

3 THE NETWORK AT A GLANCE

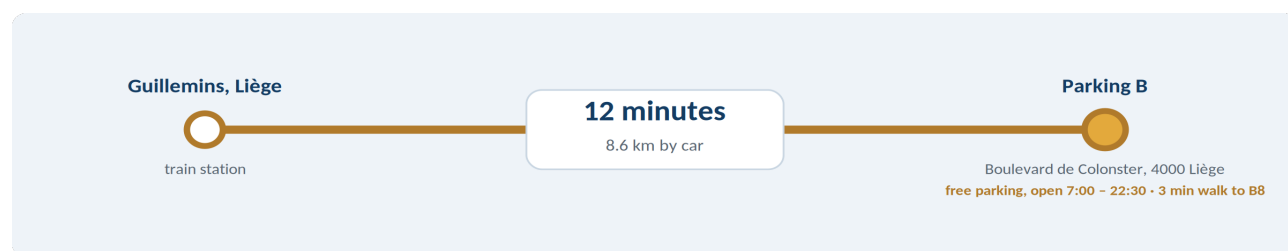
Tram T1, bus B2 and bus 8 between the city, the station and the Sart-Tilman campus. Every stop is placed on its exact Google Maps coordinates; the lines between stops are simplified.



Liège: tram T1 with its two northern branches (Coronmeuse and Liège Expo), bus B2, bus 8 and the conference venue

4 COMING BY CAR

From Liège-Guillemins to Parking B, near the conference venue (12 minutes).



5 PARKINGS AND CAMPUS PLAN

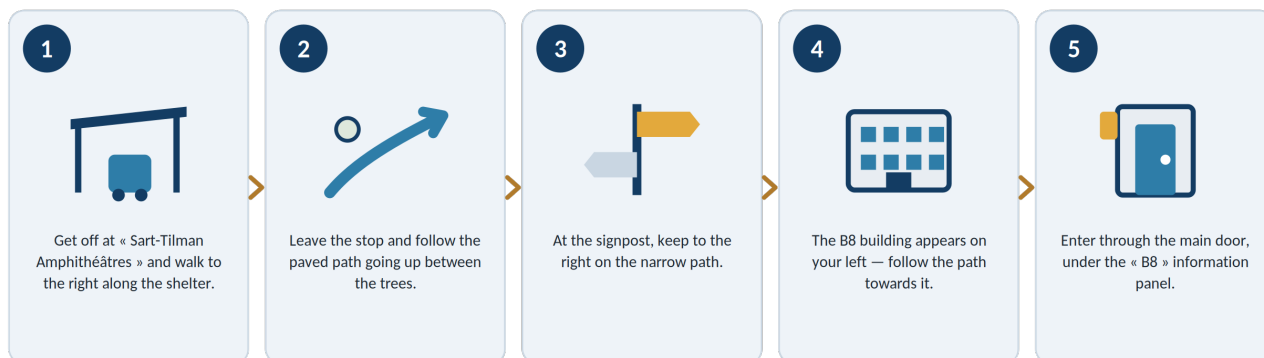


Sart-Tilman campus: parkings B, C and D, the two bus stops and the walking routes to the B8 building

- Cars can park freely in the parkings **B, C and D** (open every day 7:00–22:30).
- Walking distances to B8: Parking D **160 m**, Parking C **156 m**, Parking B **216 m** — 2 to 3 minutes.
- From the Sart-Tilman Amphithéâtres stop (**TEC** on the plan), follow the dotted route to the "**B8 building**".
- **Parking B** — Boulevard de Colonster, 4000 Liège.

6 WALKING MAP: FROM THE BUS STOP TO THE VENUE

From the « Sart-Tilman Amphithéâtres » stop to the B8 – Maison des Étudiants et Exèdre Dick Annegarn: 175 m, 1 to 2 minutes on foot.



The same five points, on site



1

Sart-Tilman Amphithéâtres stop



2

The path going up



3

Keep right at the signpost



4

The B8 building on your left



5

The B8 entrance

7 THE HISTORICAL CENTRE OF LIÈGE

Where the hotels are, and what is worth seeing around them. Note that the tram splits at Place Saint-Lambert: northbound trams follow rue Léopold and the quai de la Batte, southbound trams come back through Féronstrée. From the centre, count about 30 to 37 minutes by bus, or 14 to 18 minutes by car, to reach the conference venue.



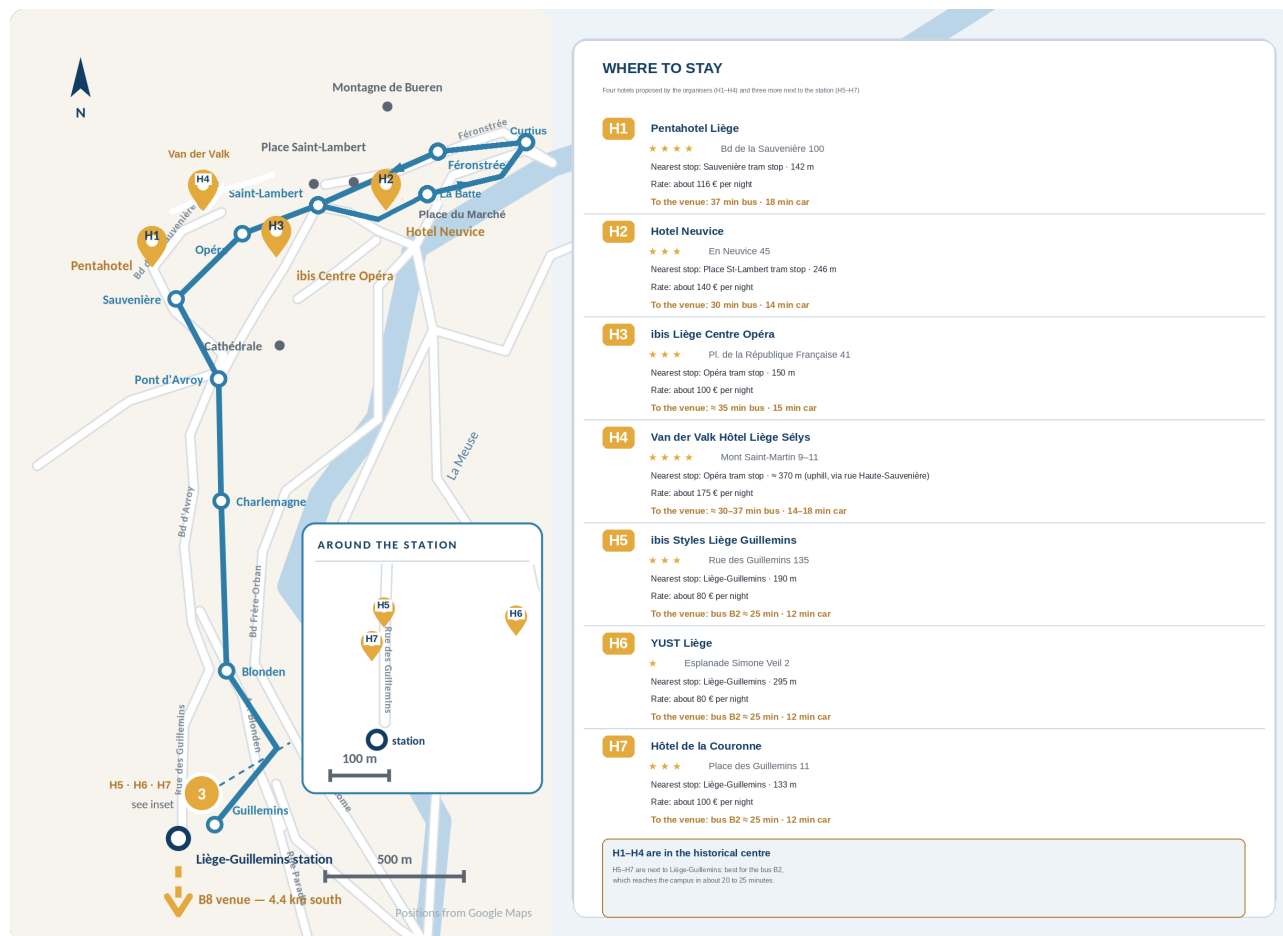
Liège city centre: main sights, the four hotels (H1–H4) and the way back to Liège-Guillemins

From your hotel to the conference venue

- From downtown, take the tram T1 « **Standard** » to « **SCLESSIN Standard** », then bus 8 « **Sart-Tilman CHU** » to « **SART-TILMAN Chimie (amphis)** » — about 30 to 37 minutes door to door, including a 4-minute walk.
- From Liège-Guillemins, the bus B2 « **Sart-Tilman-CHU-Botanique** » is the fastest option: about 20 to 25 minutes to the venue.
- By car, count 14 to 18 minutes from the centre; parkings B, C and D on the campus are free.

8 LIST OF HOTELS

Rates and conditions as communicated by the hotels for the first three (H1–H3). H4 to H7 are added for information, with an indicative average rate per night.



The seven hotels, their nearest tram or train stop and the way to the conference venue — inset: the three hotels around the station

Staying in the centre (H1–H4)

- Restaurants, museums and « Le Carré » on the doorstep.
- Tram T1 to Guillemins, then bus B2 — or tram T1 to Sclessin Standard and bus 8.
- Count 30 to 37 minutes by bus to the venue, 14 to 18 minutes by car.

Staying by the station (H5–H7)

- Under 300 m from Liège-Guillemins, where the bus B2 to the campus starts.
- About 20 to 25 minutes to the venue, the shortest option in the morning.
- The historical centre is 8 minutes away by tram T1.

Pentahotel Liège ★★★★★**About 116 € per night**

ADDRESS	Boulevard de la Sauvenière 100, 4000 Liège
BOOKING	Valerie.Ruytinx@pentahotels.com
PHONE	T: +32 (0) 4 221 77 20 · M: +32 (0) 493 10 07 00
WEBSITE	https://www.pentahotels.com/hotels/belgium/liege
ACCESS	37 minutes by bus (18 minutes by car) from the conference location
NOTE	Formerly the Mercure hotel

Hotel Neuvise ★★★★★**About 140 € per night**

ADDRESS	En Neuvise 45, 4000 Liège
BOOKING	info@hotelneuvise.be
PHONE	+32 (0)4 375 97 40
WEBSITE	https://reservations.cubilis.eu/hotel-neuvise-luik?Language=en-GB
CANCELLATION	Free of charge if min. 48 h before the arrival date
ACCESS	In the historical heart of Liège, near Market Square. 30 minutes by bus (14 min by car) from the conference location

ibis Liège Centre Opéra ★★★★★**About 100 € per night**

ADDRESS	Place de la République Française 41, 4000 Liège
NOTE	Listed as “Hotel IBIS” in the original document
BOOKING	H0864@accor.com
PHONE	+32 4 230 33 33
WEBSITE	https://all.accor.com/hotel/0864/index.en.shtml
CANCELLATION	Free of charge till max. 24 h before the arrival date

Van der Valk Hôtel Liège Séllys ★★★★★**About 175 € per night**

ADDRESS	Mont Saint-Martin 9–11, 4000 Liège
BOOKING	info@hotelselys.be
PHONE	+32 (0)4 222 94 94
WEBSITE	https://www.hotelselys.be/en
ACCESS	West of Place Saint-Lambert, ≈ 370 m uphill from the Opéra tram stop via rue Haute-Sauvenière. ≈ 30–37 min by bus (14–18 min by car) to the venue
NOTE	125 rooms, spa, indoor pool, 2 restaurants; formerly Les Comtes de Méan

ibis Styles Liège Guillemins ★★★**About 80 € per night**

ADDRESS	Rue des Guillemins 135, 4000 Liège
BOOKING	https://all.accor.com/hotel/B6D9/index.en.shtml
PHONE	+32 4 221 69 00
ACCESS	190 m from Liège-Guillemins station — bus B2 about 25 min to the venue, 12 min by car
NOTE	Comic-themed rooms, bar, private parking. Check-in from 14:00, check-out 12:00

YUST Liège ★**About 80 € per night**

ADDRESS	Esplanade Simone Veil 2, 4000 Liège
BOOKING	liege@yust.com
WEBSITE	https://www.yust.com/fr/liege/short/
PHONE	+32 4 295 57 50
ACCESS	295 m from Liège-Guillemins station — bus B2 about 25 min to the venue, 12 min by car
NOTE	Hybrid hotel, hostel and coworking space; 31 rooms; reception 7:00–23:00

Hôtel de la Couronne ★★★**About 100 € per night**

ADDRESS	Place des Guillemins 11, 4000 Liège
BOOKING	info@hdlc.be
WEBSITE	https://www.hoteldelacouronne.be/fr/
PHONE	+32 4 340 30 00
ACCESS	133 m from Liège-Guillemins station, right opposite the station — bus B2 about 25 min to the venue, 12 min by car
NOTE	77 rooms, 24-hour reception, covered terrace, meeting room. Breakfast 7:00–10:00 (Sun. 8:00–11:00)



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