



# GBM Compact :

Focus on Proteomics

SEPTEMBER 5 - 6, 2023 / FRANKFURT AM MAIN

PROGRAM

# Scientific Board

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# Welcome



Christian Münch



Volker Haucke



Albert Sickmann

Dear Friends and Colleagues,

We warmly welcome you to the GBM Compact Conference 2023 in Frankfurt.

Our meeting will cover different areas of proteomics – from intact to bottom-up proteomics and from basic to clinical research questions. We aim at providing a solid overview of proteomics methods, how to use them and in which way they have contributed to new scientific insight.

Main topics of the conference are

- General proteomics
- Structural proteomics
- Clinical proteomics
- Bioinformatics/Systems biology
- Methods development

Cutting-edge technologies are increasingly important for basic and applied research. This year's conference aims at providing a broad overview over proteomics and offering an opportunity for participants to discover how to use proteomics for their own research.

We are fortunate to have world-leading experts who will introduce a broad range of proteomics methods and how they used them to address biological and clinical questions.

We sincerely hope that the upcoming meeting will offer interesting opportunities to learn about proteomics, spark in-depth discussions, initiate new friendships, collaborations, and joint projects.

We wish you an exciting conference!

Christian Münch / Albert Sickmann / Volker Haucke

# Invited Speakers



Pedro Beltrao



Tami Geiger



Kathryn Lilley



Matthias Mann



Nina Morgner



Jesper Olsen



Matthias Selbach



Charlotte Uetrecht



Bettina Warscheid

# Program

September 5

11:00 | Arrival and registration

13:00 | Welcome

(by the organizers)

13:15 | Keynote Lecture:  
**Matthias Mann** /Martinsried [DE]  
Advances in Mass spectrometry-  
based proteomics for body fluid  
and single cell type-resolved tissue  
proteomics

14:15 | **Charlotte Uetrecht** /Hamburg [DE]  
Flying viruses - mass spectrometry  
meets X-rays

14:45 | Short talk 1:  
**Julia Hesselbarth** /Mainz [DE]  
SNARE complex regulation by  
Complexin-1 - a structural mass  
spectrometry study

15:00 | Short talk 2:  
**Marc van Oostrum** /Frankfurt [DE]  
The proteomic landscape of syn-  
aptic diversity across brain regions  
and cell types



Frankfurt Skyline



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15:15 Coffee break

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15:45 Short talk 3:  
**John Weir** /Tübingen [DE]  
Insights into Meiosis: Elucidating DNA Repair  
Modulation via Mass Spectrometry

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16:00 **Nina Morgner** /Frankfurt [DE]  
Native mass spectrometry: How to probe mole-  
cular principles of assembly and interactions of  
protein complexes

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16:30 **Jesper Olsen** /Copenhagen [DK]  
Narrow-window DIA for ultra-fast quantitative  
analysis of comprehensive proteomes with high  
sequencing depth

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17:00 Poster Teasers:  
**Ashley Bourke** /Frankfurt am Main [DE]  
**Maximilian Gerwien** /Berlin [DE]  
**Daniel Hofacker** /Tübingen [DE]  
**David Mick** /Homburg [DE]  
**Sylvia Oimage** /Jena [DE]  
**Luisa Schwarzmüller** /Heidelberg [DE]  
**Tilman Werner** /Freiburg [DE]

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17:30 Panel Discussion:  
**The future of Proteomics**  
(Chair: Christian Münch)

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17:30 Workshops:  
5-6 short presentations on **how to use proteo-  
mics in your own research project** with an over-  
view of methods, followed by 1:1 discussions  
with participants

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18:30 **Get together & Poster session**  
with fingerfood & drinks

# Program

September 6

09:00

**Tami Geiger** /Rehovot [IL]

Understanding the tumor microenvironment through high-sensitivity MS-based proteomics

09:30

Short talk 4:

**Emma Fenech** /Rehovot [IL]

A toolbox for systematic discovery of stable and transient protein interactors in baker's yeast



Frankfurt University Hospital



Frankfurt Römer

09:45	<b>Pedro Beltrao</b> /Zürich [CH] Towards a structurally resolved and tissue specific human protein interaction network
10:15	Short talk 5: <b>Dhriti Arora</b> /Bonn [DE] Investigation of the human lysosomal proteome by targeted proteomics
10:30	<b>Bettina Warscheid</b> /Würzburg [DE] Multifaceted Proteomics to Comprehend Mitochondrial Function and Dysfunction
11:00	Coffee break
11:30	Short talk 6: <b>Florian Meier-Rosar</b> /Jena [DE] μPhos: a scalable and sensitive platform for functional phosphoproteomics
11:45	<b>Matthias Selbach</b> /Berlin [DE] An Integrated Landscape of mRNA and Protein Isoforms
12:15	Keynote lecture: <b>Kathryn Lilley</b> /Cambridge [UK] Capturing the spatial re-localization of RNA and protein in response to the unfolded protein response
13:15	Poster prizes & closing remarks

## Conference Office

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Opening hours are

Sept. 5: 11:00 - 18:30

Sept. 6: 08:15 - 13:30

Phone: +49 69 660567-0

## Internet

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There will be a wireless LAN access point on the campus.

SSID: ukfguest

Key: ukfguest

## Meals & Drinks

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Coffee, tea and mineral water will be provided for free during the coffee breaks.

Lunch is available at your own expense nearby the conference building:  
Cafeteria in house 20 (opposite the venue, open from 8 a.m. to 4 p.m.), Mensa in house 35 (see campus map)

During the poster session on Tuesday we will provide drinks and finger food.

## Poster

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Poster session: Tuesday, Sept. 5  
18:30 - 20:30

During the poster sessions the presenting authors are requested to stay near their posters. Posters should be presented throughout the whole meeting.

All poster abstracts are available as pdf-file for download on the meeting homepage.

Please see the poster list on page 16 for poster numbers.

The best two posters will be awarded (with certificate and 300 € each).

The winners will be announced at the end of the meeting on Wednesday. To receive the price, personal attendance is required.

## Venue

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University Hospital Frankfurt  
Haus 22  
Theodor-Stern-Kai 7  
60598 Frankfurt am Main

Please see the campus map on page 15 or on the meeting homepage.

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# MAP OF SITE



Conference Venue  
University Hospital Frankfurt  
Theodor-Stern-Kai 7  
60590 Frankfurt /Germany  
Building 22

M 05

Aerts, Jordan

Comparison of HPLC and Capillary Electrophoresis for Hydrogen Exchange Mass Spectrometry

G 11

Astorga, Jose

Protein Synthesis in Autism Spectrum Disorder

G 04

Bender, Julian

Autoprot: A Modular Package for Processing, Analysis and Visualization of Complex Proteomics Data in Python

G 14

Bourke, Ashley

Using quantitative proteomics to uncover ribosome heterogeneity in neurons

G 18

Bozkurt, Süleyman

The Hidden Role of Reactive Oxygen Species in Modulating Mitochondrial-Processing Peptidase

M 11

Cabrera-Orefice, Alfredo

Let's make it clear: systematic exploration of mitochondrial DNA-/RNA-protein complexes by complexome profiling

G 13

Cavalcanti Franco, Pedro Henrique

A study on small proteins present in terminal cytochrome oxidases

G 25

Chakraborty, Rahul

Investigating novel functions of Rab24 in mitochondrial fission and protein secretion



G 24

Desch, Kristina

Proteomic profiling of sex- and oestrus-cycle specific changes in the midbrain

O 01

Ecker, Anna-Lena

Why do mitochondria still contain a genome? Mechanistic insights from allotopically expressed proteins

G 02

Eirich, Juergen

The interplay of posttranslational protein modifications in Arabidopsis leaves during photosynthesis induction

O 05

Farges, Frederic

Analysis of 3CL Protease inhibitors: an automated assay for rapid screening of compounds

G 22

Fehmer, Martin

Quantitative Secretome Kinetics

M 09

Gerwien, Maximilian

Combining Data Independent Acquisition with Spike-in SILAC (DIA-SiS)

G 12

Gupta, Nikita

Nuclear localization of non-imported mitochondrial proteins modulates epigenetic landscape

C 01

Hamed, Mohamed Ismail

Loss of nuclear pore complex function and cellular compartmentalization in the steroid resistant nephrotic syndrome

S 04

Hesselbarth, Julia

SNARE complex regulation by Complexin-1 - a structural mass spectrometry study

M 12

Hofacker, Daniel

De novo Protein Interactome Profiling of Small Molecule and Antisense Oligonucleotide Drugs

G 03

Höhlschen, Julia

Gliflozin drug class and its effect on the proteome of cardiomyocytes

O 04

Jooyeh, Bahareh

Akt isoforms differentially affect Rho signaling pathways in H23 non-small cell lung carcinoma cells

M 04

Kaspar-Schoenefeld, Stephanie

Improved dia-PASEF isolation window schemes for proteomics measurements

G 15

Kohli, Aneesha

Using proteomics to characterize RNF213- a unique AAA+ ATPase and E3 ligase

G 17

Kokoli, Marianna

Single-cell multiomics on brain organoid models of autism spectrum disorder

G 09

Kotnik, Florian

Investigating the role of Arabidopsis HISTONE DEACETYLASE 14 in chloroplasts

M 03

Kühl, Toni

Edman degradation relaunched for unequivocal analysis of disulfide-rich peptides

G 05

Lenhard, Svenja

Establishing a cytosolic version of the mitochondrial processing peptidase to study mitochondrial protein import

G 29

Lenz, Thomas

The natural small molecule compound prodigiosin targets the Golgi stacking protein GRASP55/GORASP2

S 01

Lermyte, Frederik

Bridging top-down proteomics and native mass spectrometry: A consortium-based study

M 02

Li, Chengkang

Nano-flow HILIC-MS-based site-specific assessment of RNA modifications

G 08

Li, Mujia

Secretome Analysis Revealing Effects of Kallikrein-related Peptidase 6 (KLK6) in Pancreatic Ductal Adenocarcinoma

G 21

Lichtner, Simone

Proteomics-based evaluation of different cell culture models for the development of treatments for psoriasis

M 06

Link, Martin

Assessment of cellular redox regulation via proteomics: Establishment of an appropriate sulfenic acid labeling procedure in human bronchial epithelial cells

G 26

Lucht, Max Thomas

Bio genesis of the presynaptic compartment

G 28

Meier-Credo, Jakob

Detection of known and novel small proteins in *Pseudomonas stutzeri* using a combination of bottom-up and digest-free proteomics and proteogenomics

M 08

Mick, David

APEX-based proximity labeling for time-resolved, subcellular proteomics of primary cilia to study proteome dynamics during active signaling

G 16

Mohseni, Farbod

Identification of mitotic DNA-protein complexes formed after replication stress by ChIP-MS analysis

G 10

Müller, Torsten

Single cell proteome analysis with ultra-high sensitivity using a timsTOF mass spectrometer

M 01

Omage, Sylvia

Identification of novel cellular targets of  $\alpha$ -13'-COOH and garcinoic acid using a compound-centric chemoproteomic method

O 03

Pandrea, Maria

Coordination of DNA damage and aging by ubiquitin signaling and the ubiquitin-proteasome system

C 04

Pauls, Stella

Proteome analysis of precursor lesions from pancreaticobiliary cancer to improve early cancer diagnostic

B 01

Rrustemi, Trendelina

Exploring Pathogenic Mutations on Phosphorylation Sites: Unraveling Disease Mechanisms via Interactome Studies

G 06

Russo, David A.

In-depth exploration of the cyanobacterial secretome with trapped ion mobility spectrometry coupled to dia-PASEF

M 10

Schmidt, Andreas

ENRICH-iST technology provides deeper coverage of the plasma proteome

G 23

Schmidt, Jonas

Characterizing mitochondrial protein import in senescence

M 13

Schroda, Michael

TurboID reveals the proximiomes of VIPP1 and VIPP2 in *Chlamydomonas reinhardtii* and confirms VPL2 and PGRL1 in the VIPP1 proximiome

C 03

Schwarz Müller, Luisa

Proteomic Characterization of Colorectal Cancer Patients for Precision Oncology

O 02

Simakin, Pavel

A modular cloning (MoClo) toolkit for reliable intracellular protein targeting in the yeast *Saccharomyces cerevisiae*

M 07

Tascher, Georg

Quantitative Translation and Import Proteomics using mePROD

G 19

van der Laan, Martin

Structural & Functional Analysis of MICOS & the Mitochondrial Intermembrane Space Bridging Complex (MIB)

G 30

van Oostrum, Marc

The proteomic landscape of synaptic diversity across brain regions and cell types

G 01

Vu, Van Loi

The electrophilic immunometabolite itaconate causes an acid stress response as well as S-bacillithiolation and S-itaconation in the thiol proteome of *Staphylococcus aureus*

G 20

Waselenchuk, Quinn

Unraveling the Link between Neuronal Activity Patterns and Proteome Remodeling through Optogenetic Stimulation and Mass Spectrometry Analysis

S 03

Weir, John

Insights into Meiosis: Elucidating DNA Repair Modulation via Mass Spectrometry

M 09

Welter, Anna Sophie

Combining Data Independent Acquisition with Spike-in SILAC (DIA-SiS)

C 02

Werner, Tilman

Proteomic subtypes of intrahepatic cholangiocarcinoma are linked to patient's time-to-recurrence

S 02

Wittig, Ilka

Maintenance on mitochondrial complexes ensures bioenergetic function in differentiated cells

G 27

Wohlgemuth, Ingo

Learning from errors: Deducing the action of aminoglycoside antibiotics from error landscapes

G 07

Wolfgramm, Hannes

N-terminomics identifies substrates of the secreted *Staphylococcus aureus* protease Jep previously missed by classical label-free proteomics

O 05

Zöller, Jonathan

Analysis of 3CL Protease inhibitors: an automated assay for rapid screening of compounds P 01

Ade, Jens

A scalable method for identifying the protein interactomes of individual RNAs by quantitative mass spectrometry