

# BIOMEMBRANE DAYS 2025



SEPT. 29  
TO OCT. 1,  
2025



## BOOK OF ABSTRACTS



**LOCATION:** Harnack-Haus Berlin

**REGISTRATION:** <https://biomembrane-days-2025.mpikg.mpg.de>

**ORGANIZERS:** Rumiana Dimova, Helge Ewers, and Thomas Weikl

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## Organization

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**Additional support:** Mila Dimova Tietze, Berlin silhouette drawing on program book cover

## We thank our sponsors:

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## 1. Code of conduct

This Code of Conduct outlines the principles and expected behaviour for all participants of the Biomembrane Days 2025 to be held at Harnack Haus, Berlin, from September 19 to October 1.

**Core Values and Respect:** All participants shall treat one another with respect and dignity, free from any form of discrimination based on race, ethnicity, gender, gender identity or expression, sexual orientation, age, disability, religion, or any other status unrelated to scientific merit. Diversity is a source of strength, creativity, and innovation.

- Treat all participants respectfully and professionally.
- Avoid discriminatory language, behaviour, or exclusionary practices.
- Embrace diversity as a driver for creativity and innovation.

**Scientific Integrity:** We uphold the highest standards of scientific integrity, prioritizing quality over quantity. All research discussions should be conducted openly and constructively, acknowledging the contributions of others and providing feedback in a professional manner.

- Present research honestly and transparently.
- Give proper credit to the contributions of others.
- Provide constructive, respectful feedback.

**Anti-Harassment Policy:** Harassment of any kind will not be tolerated. Harassment includes, but is not limited to: unwelcome verbal, written, or physical conduct relating to race, gender, sexual orientation, religion, disability, or other protected characteristics. Sexual harassment, including unwelcome sexual advances and explicit jokes or imagery, is prohibited.

- Refrain from offensive, derogatory, or discriminatory remarks or behaviour.
- Avoid physical contact without consent.
- Report harassment immediately to conference organizers.
- Cooperate fully in investigations.

**Responsibility and Sustainability:** We recognize our responsibility toward colleagues, the public, and the environment. The conference will be organized with a commitment to ecological sustainability.

- Reduce printed materials by prioritizing digital resources.
- Encourage public transport, cycling, or walking.
- Minimize single-use plastics; use reusable/compostable materials.
- Recycle and manage waste responsibly.

**Open Communication:** We communicate openly and transparently, both within the conference and with the public. Participants are encouraged to share knowledge responsibly through talks, posters, and social media, respecting confidentiality where required.

- Communicate clearly and respectfully in all formats.
- Respect confidentiality agreements and unpublished work.
- Promote conference activities responsibly on public platforms.

**Enforcement and Accountability:** Conference organizers are responsible for ensuring this Code of Conduct is upheld. Violations will be addressed promptly and fairly, with measures ranging from informal resolution to removal from the event.

- Report any violations immediately to designated contacts.
- Participate in resolution processes when called upon.
- Accept and comply with disciplinary actions when warranted.

By participating in this conference, all attendees agree to abide by this Code of Conduct. Our collective responsibility is to foster a safe, inclusive, and inspiring environment for scientific exchange.

## 2. General information

### Location and Badge Pickup

The conference location is the Harnack Haus in Berlin (Address: Ihnestrasse 16-20, 14195 Berlin, [GoogleMap](#)). The Harnack Haus is located close to the station 'U Freie Universität (Thielplatz)' of the subway line U3.

Your name tag and meeting materials will be available for pickup in the Planck lobby starting Monday, September 29, at 8:00h. All sessions will take place in the Hahn-Hörsaal room.

### Guideline for Presentations

A. **Talks:** Invited speakers will have a total of 30 minutes, including 5 minutes for questions. Contributed speakers will have 20 minutes in total, including 5 minutes for questions.

B. **Posters:** The poster session will take place on Goethe-Saal and Meitner-Saal I + II. Poster boards have usable dimensions of 144 cm (height) × 116.5 cm (width). Standard A0 posters (118.9 cm × 84.1 cm) fit comfortably in portrait (vertical) orientation, but can also be displayed in landscape (horizontal) orientation.

We are pleased to announce that **poster prizes for the three best posters** will be awarded, generously sponsored by Lipotype GmbH. Poster presenters are required to stay in the allotted time slot for evaluation. The posters will be displayed through the whole conference.

Posters should be taken down on Oct 1 by 18:00h. All posters left uncollected at the end of the meeting will be discarded.

### Coffee Break, Lunch and Dinner

Coffee breaks will take place in the Planck-Lobby. Lunch and the conference dinner will take place in the Harnack-Haus restaurant.

### Social Media & Group Picture

Pictures may be taken during the conference for use on social media. If you do not consent to your picture being used on social media, please inform us at the registration desk.

Please do not photograph posters unless you have received prior approval from the presenter.

A group picture will be taken on Monday, September 29 at 17:30. We warmly encourage everyone to join!

### Contact Information

In case of any questions, please send an email to biomembrane-days [at] mpikg.mpg.de.

### 3. Program schedule

#### Monday, September 29

**09:05 - 10:15 | Session 1 | Chair: Andreas Janshoff**

09:00 - 09:05 | [Welcome](#)

09:05 - 09:35 | **Reinhard Lipowsky** - *The fluid architecture of biomembranes and vesicles*

09:35 - 09:55 | **Yifan Ge** - *Three-phase prewetting by TFAM at the mitochondrial inner membrane drives nucleoid assembly*

09:55 - 10:15 | **Claudia Contini** - *Synthetic cells: from soft matter to cell-like behaviours*

**10:15 - 10:45 | [Coffee Break, Poster Mounting & Viewing](#)**

**10:45 - 12:25 | Session 2 | Chair: Tom Robinson**

10:45 - 11:15 | **Erdinc Sezgin** - *Biophysical properties of cells and nanoscale bioparticles as new biomarkers in health and disease*

11:15 - 11:45 | **Jeanne Stachowiak** - *Intrinsic disorder as an organizing principle for membrane bending*

11:45 - 12:05 | **Eva Sevcsik** - *Probing the nanoscopic environment of transmembrane proteins in living cells reveals the absence of tightly associated boundary lipids*

12:05 - 12:25 | **Carla Kirschbaum** - *Characterising lipid transfer proteins and their cargo by native mass spectrometry*

**12:30 - 14:00 | [Lunch](#)**

**14:00 - 15:10 | Session 3 | Chair: Claudia Contini**

14:00 - 14:30 | **Zheng Shi** - *A genuine fluorescent sensor for membrane tension*

14:30 - 14:50 | **Agata Witkowska** - *Membrane tension control of neurotransmission via the disordered domain of an endocytic protein*

14:50 - 15:10 | **Javier Montenegro** - *Supramolecular dynamic chemistry for membrane transport and biomimetic systems*

**15:10 - 15:40 | [Coffee Break and Poster Viewing](#)**

**15:40 - 17:30 | Session 4 | Chair: Saša Svetina**

15:40 - 16:10 | **Patricia Bassereau** - *A minimal human ESCRT-III system to mimic HIV-1 detachment*

16:10 - 16:30 | **Bert Poolman** - *Structural and functional implications of in vivo phase separation of membrane protein in Escherichia coli*

16:30 - 16:50 | **Dragomir Milovanovic** - *Contact sites at the interface of membraneless organelles and membranes*

16:50 - 17:10 | **Charu Sharma** - *From curvature sensing to membrane scission: real time visualization reveals mechanistic insights into DynaminA mediated synthetic cell-division*

17:10 - 17:30 | **Janett Göhring** - *CD4+ T-cells create a stable mechanical environment for force-sensitive TCR:pMHC interactions*

**18:00 | [Poster Viewing and Snacks Dinner](#)**

## Tuesday, September 30

### 08:30 - 10:00 | Session 5 | Chair: Andreas Heuer

- 08:30 - 09:00 | **Roland Wedlich-Söldner** - *Adaptation of plasma membrane domains to metabolic stress*
- 09:00 - 09:20 | **Claudia Steinem** - *Dynamics of ordered domains in pore-spanning membranes: comparing artificial bilayers with plasma membranes*
- 09:20 - 09:40 | **Frederick Heberle** - *Investigating the influence of membrane dipole potential on liquid-ordered/liquid-disordered phase separation in model membranes*
- 09:40 - 10:00 | **Tiemei Lu** - *Dynamic interactions between coacervates and membranes: from endocytosis to penetration*

### 10:15 - 10:45 | Coffee Break and Poster Viewing

### 10:45 - 12:25 | Session 6 | Chair: Karin Riske

- 10:45 - 11:15 | **Ewa Paluch** - *The nanoscale regulation of cell surface mechanics in cell and tissue morphogenesis*
- 11:15 - 11:35 | **Oliver Rocks** - *Formation of giant membrane rods through lipid unmixing and segregation of ER-shaping proteins under thermal stress*
- 11:35 - 11:55 | **Christian Eggeling** - *Zooming in into lipid membrane structure and dynamics with super-resolution MINFLUX microscopy*
- 11:55 - 12:25 | **Rumiana Dimova** - *When a droplet meets a membrane: membrane remodeling by bimolecular condensates*

### 12:30 - 14:00 | Lunch

### 14:00 - 15:10 | Session 7 | Chair: Aleš Iglič

- 14:00 - 14:30 | **Omer Dushek** - *Optimising CAR-T cell sensitivity by engineering extracellular receptor/ligand sizes*
- 14:30 - 14:50 | **Harsha Bajaj** - *Dynamic duos: coacervate-lipid membrane interactions in regulating membrane transformation and condensate size*
- 14:50 - 15:10 | **Gerald Hammond** - *Balancing the membrane: feedback and feedforward regulation of plasma membrane PI(4,5)P<sub>2</sub>*

### 15:10 - 15:40 | Coffee Break and Poster Viewing

### 15:40 - 17:30 | Session 8 | Chair: Daxiao Sun

- 15:40 - 16:10 | **Markus Deserno** - *On the thermodynamics of ternary asymmetric lipid membranes*
- 16:10 - 16:30 | **Seraphine Wegner** - *Light based communication between cells across membranes*
- 16:30 - 16:50 | **Ludger Johannes** - *GlycoSwitch — a novel signaling circuit to control endocytosis*
- 16:50 - 17:10 | **Petia Vlahovska** - *Curvature dynamics of biomembranes: role of membrane viscosity and interleaflet friction*
- 17:10 - 17:30 | **Tanmoy Ghosh** - *Elevated actin contractility combined with cargo-loaded clathrin pits decisively shapes midplane-peaked apico-basal tension profiles in HeLa cells*

### 18:00 | Conference Dinner and Poster Session

## Wednesday, October 1

### 08:30 - 10:00 | Session 9 | Chair: James Saenz

08:30 - 09:00 | **Jay Groves** - *Protein condensation and signal transduction on the membrane*

09:00 - 09:20 | **Yuka Sakuma** - *Long-range viscosity of *C. elegans* plasma membrane*

09:20 - 09:40 | **Jan Steinkühler** - *Reconstitution of electrically excitable membranes and lipid nanotubes*

09:40 - 10:00 | **Giacomo Fiorin** - *Simulating membrane remodeling under asymmetric and symmetric membrane tensions*

### 10:05 - 10:35 | Coffee Break and Poster Viewing

### 08:30 - 10:00 | Session 10 | Chair: Jelger Risselada

10:35 - 11:05 | **Padmini Rangamani** - *Biophysical modeling of membrane curvature generation by the glycocalyx*

11:05 - 11:35 | **Alf Honigsmann** - *Role of adhesion protein size on segregation of epithelial cell junctions*

11:35 - 11:55 | **Kandice Levental** - *Nanoscale organization of living membranes by protein paralipidomes*

11:55 - 12:15 | **Rainer Böckmann** - *Unraveling the stability, dynamics, and mechanics of cellular model membranes through multiscale simulations*

### 12:30 - 14:00 | Lunch

### 14:00 - 15:10 | Session 11 | Chair: Kandice Levental

14:00 - 14:30 | **Michael Kozlov** - *Model for tension propagation in crumpled compartmentalised cell membranes*

14:30 - 15:00 | **Helge Ewers** - *Membrane compartmentation by submembrane actin rings*

15:00 - 15:30 | **Georg Pabst** - *Can lipid asymmetry allosterically modulate integral membrane protein function?*

### 15:30 - 16:00 | Coffee Break (please remove posters from boards)

### 16:00 - 17:50 | Session 12 | Chair: Antonio Stocco

16:00 - 16:30 | **Petra Schwille** - *Protein-driven membrane remodeling for synthetic cell division*

16:30 - 17:00 | **Ilya Levental** - *Lipid number asymmetry: The hidden dimension of mammalian plasma membranes*

17:00 - 17:20 | **Thomas Weikl** - *Excess area and elasticity of the Piezo protein-membrane nanodome*

### 17:20 - 17:50 | Closing Remarks & Best Poster Awards

## 4. Speaker Abstracts

The speaker abstracts are arranged by presentation order.

### **Reinhard Lipowsky: “The Fluid Architecture of Biomembranes and Vesicles” – Max Planck Institute of Colloids and Interfaces, Germany**

(Monday, September 29, Session 1, 09:05 - 09:35)

All biomembranes around cells and organelles consist of fluid bilayers of lipid molecules and membrane-bound proteins. Because of their fluidity, biomembranes can easily remodel their shape, topology, and composition. To a large extent, our physical understanding of these processes is based on biomimetic model membranes such as nanovesicles, with a size of a few tens of nanometers, and giant unilamellar vesicles, with a size that exceeds many hundreds of nanometers. This talk will focus on recent insights into the multiscale nature of membrane tension [1], the remodeling of vesicles by condensate droplets [2-4], and the fascinating membrane architecture of the endoplasmic reticulum [5].

[1] R. Lipowsky: The many faces of membrane tension for biomembranes and vesicles.

Faraday Discuss. (in press) DOI: 10.1039/d4fd00184b

[2] R. Ghosh et al: Different pathways for engulfment and endocytosis of liquid droplets by nanovesicles.

Nature Commun. 14, 615 (2023) DOI: 10.1038/s41467-023-35847-z

[3] A. Mangiarotti et al: Wetting and complex remodeling of membranes by biomolecular condensates. Nature Commun. 14, 2809 (2023) DOI: 10.1038/s41467-023-37955-2

[4] Z. Zhao et al: Membrane nanotubes transform into double-membrane sheets at condensate droplets. PNAS 121, e2321579121 (2024) DOI: 10.1073/pnas.2321579121

[5] R. Lipowsky et al: Elucidating the Morphology of the Endoplasmic Reticulum: Puzzles and Perspectives. ACS Nano 17, 11957–11968 (2023) DOI: 10.1021/acsnano.3c01338

### **Yifan Ge: “Three-Phase Prewetting by TFAM at the Mitochondrial Inner Membrane Drives Nucleoid Assembly” – Shanghai Institute of Organic Chemistry, Chinese Academy of Sciences, China**

(Monday, September 29, Session 1, 09:35 - 09:55)

The organization of genetic material within membrane-bound organelles represents a fundamental challenge in cellular biology, yet the physical principles governing this process remain unknown. Here, using *in vitro* reconstitution assays combined with live cell STED-FLIM analysis and cryo-electron tomography, we discover that three-phase prewetting—a thermodynamic phenomenon previously observed only in non-biological systems—controls mitochondrial genome assembly. Using the mitochondrial transcription factor Tfam, we demonstrate experimentally that membrane forms distinctive curvature-dependent transient domains and trigger Tfam prewetting, coordinating mtDNA molecules into nucleoid structures. Such observation was also confirmed using super-resolution microscopy in living cells and cryo-electron tomography *in situ* by modulating inner membrane structures through different biochemical cues. Considering membrane curvature is a universal feature of organellar architecture, our data proved membrane-driven phase transitions as a new paradigm for functional structure organization.

**Claudia Contini: “Synthetic Cells: From Soft Matter to Cell-like Behaviours” – Imperial College London, UK**

(Monday, September 29, Session 1, 09:55 - 10:15)

Synthetic cells offer a versatile platform to investigate how life-like behaviours can emerge from soft, self-assembled systems. In our work, we develop polymeric and hybrid vesicles with programmable mechanical and chemical properties that enable dynamic behaviours such as fusion, deformation, contraction, and stimulus-responsive structural transitions. By tuning membrane composition and responsiveness, we recreate essential features of biological membranes in fully synthetic constructs. Our approach integrates tools from membrane biophysics, synthetic biology, and soft matter chemistry, contributing to the growing effort to build synthetic systems that mimic or interface with biological structures.

**Erdinc Sezgin: “Biophysical properties of cells and nanoscale bioparticles as new bi-omarkers in health and disease” – Karolinska Institutet, Sweden**

(Monday, September 29, Session 2, 10:45 - 11:15)

Remodeling of our cells as response to environmental changes is essential for their survival and function. Although numerous studies aimed at finding protein markers during such cellular processes, there is a major gap in our understanding of how collective biophysical properties of the cells (such as stiffness, membrane fluidity, viscosity etc) alter during these crucial biological processes. Similarly, our understanding of how biophysical properties of cells change in diseases is also limited. To gain a thorough mechanistic perception of cellular processes and diseases, it is essential to fill this gap and have a clear and quantitative picture of biophysical remodeling of the cells. We and others have made extensive effort to unravel the biophysical aspects of cells in a quantitative manner. To achieve this, we developed advanced imaging approaches that could reveal the molecular details with very high spatiotemporal resolution. These technologies allowed us to see how biophysical properties of cells play crucial roles for signaling from molecular to cellular level. Although these technologies were extremely useful to study biophysical aspects of cellular life at the molecular level, their low sampling (one cell at a time) has been a major obstacle to apply them to medical problems that require measuring thousands of cells. This can be overcome with high throughput methodologies that can robustly report on the ensemble biophysical properties of cells which require reliable reporters and instruments. Thus, while developing advanced instrumentation, we also develop reliable probes to quantify different biophysical properties of cells. Here, I will discuss our approach from probe development to high throughput biophysical analysis.

**Jeanne Stachowiak: “Intrinsic disorder as an organizing principle for membrane bending” – University of Texas at Austin, USA**

(Monday, September 29, Session 2, 11:15 - 11:45)

As the gateway for cellular entry and communication, the surface of the cell holds the answers to critical questions in biology and medicine, while simultaneously providing inspiration for engineered materials and systems. Membranes have a remarkable ability to precisely and rapidly organize themselves in an environment of staggering complexity. Thousands of distinct protein species reside on cellular membranes, yet functional membrane protein complexes can form within seconds in response to diverse stimuli. Traditionally, structured protein assemblies such as vesicular coats and cytoskeletal

filaments have been thought to organize membrane surfaces. In contrast, recent work illustrates that networks composed of proteins with a high degree of intrinsic disorder may provide the necessary flexibility to facilitate efficient assembly of functional protein complexes at membrane surfaces. Our recent work has illustrated that a flexible network of disordered proteins helps to catalyze the assembly of endocytic structures at the plasma membrane. Specifically, we find that an intermediate strength of interaction between these proteins, which leads to liquid-like properties at the macro-scale, maximizes the efficiency of endocytic vesicle assembly. This understanding provides new insight into the optimal design of therapeutic carriers that harness endocytosis for entry into cells. More broadly, our lab seeks to understand and mimic the ability of biological membranes to spontaneously reorganize in response to diverse cues. This remarkable capacity for self-organization, which is largely absent in man-made materials, holds great promise for the design of responsive, cell-like therapeutic systems. Specific areas of our ongoing work include the role of disordered protein networks in organizing the cytoskeleton, and transmembrane coupling of protein condensates as a novel mechanism of information transfer across biological interfaces.

**Eva Sevcsik: “Probing the nanoscopic environment of transmembrane proteins in living cells reveals the absence of tightly associated boundary lipids” – Vienna University of Technology, Austria**

(Monday, September 29, Session, 11:45 - 12:05)

Weak and transient lipid-protein interactions likely shape plasma membrane organization and function but have largely eluded experimental characterization. While model systems can only reproduce certain aspects of these interactions, extraction of unambiguous data from live cell experiments is challenging. We here ask a simple question directed at a fundamental aspect of plasma membrane organization: To what extent does a transmembrane protein influence, by its mere presence, the fluidity of its immediate lipid nano-environment? By specifically immobilizing proteins of interest at various densities in the live cell plasma membrane, we were able to determine its apparent in-plane radius via quantification of the mobility reduction of lipid tracer molecules. In this assay, tight adhesion of lipid layers with reduced fluidity would be detectable as an increased radius of the protein of interest. To characterize putative lipid nano-environments, we compared the determined protein sizes with corresponding data from structural biology. Simulations allowed us to map the parameter space for possible nano-environment architectures around four different transmembrane proteins. For three of the four proteins, our data rule out the presence of tightly associated boundary lipids, suggesting that boundary lipids are not a fundamental element of plasma membrane organization.

**Carla Kirschbaum: “Characterising lipid transfer proteins and their cargo by native mass spectrometry” – University of Oxford, UK**

(Monday, September 29, Session 2, 12:05 - 12:25)

The lipid composition of biomembranes is unique to each cell type and organelle, and is tailored to support their respective functions. Eukaryotes fine-tune their lipid distribution by lipid transfer proteins (LTPs), which mediate intracellular lipid transport from the endoplasmic reticulum to the target organelle or plasma membrane. This directed transport relies on the high selectivity of LTPs for their target lipids and often exploits lipid gradients

between membranes as a driving force. To date, more than a hundred LTPs have been identified in humans. For many of them, the lipid cargo, site of action and membrane recognition mechanism are not fully understood. Here we use native mass spectrometry to identify natural ligands and post-translational modifications of human LTPs. This approach maintains the native protein conformation and protein-lipid interactions of LTPs intact from the cell to the final analysis step. We characterised the endogenous ligands of the human phosphatidylcholine transporters STARD2, STARD7 and STARD10 and related them to lipid binding preferences in vitro. While the three proteins overlap in function, we found that they vary in their lipid preferences. Further, to investigate the phosphorylation-modulated membrane association and dissociation of these soluble proteins, we profiled phosphorylation states using native mass spectrometry and proteomics. We thus obtained a comprehensive snapshot of the LTPs as they were pulled out of their native environment, including their endogenous ligands, loading state, and post-translational modifications.

### **Zheng Shi: “A Genuine Fluorescent Sensor for Membrane Tension” – The State University of New Jersey, USA**

(Monday, September 29, Session 3, 14:00 - 14:30)

The surface of a cell experiences frequent stretching and poking forces. The resulting membrane tension governs a wide range of cellular processes, often through modulating the subcellular behavior of mechanosensitive membrane proteins. However, mapping the spatiotemporal heterogeneity of cell membrane tension remains technically challenging. In this talk, I will present our current efforts towards developing fluorescent sensors that directly report changes in lipid membrane tension. Combined with recent understandings of cell membrane mechanics and mechanosensitive membrane proteins, we aim to decode mechanical signaling pathways at the cell surface and shed light on various mechanobiological processes.

### **Agata Witkowska: “Membrane tension control of neurotransmission via the disordered domain of an endocytic protein” – Leibniz-Forschungsinstitut für Molekulare Pharmakologie (FMP), Germany**

(Monday, September 29, Session 3, 14:30 - 14:50)

Synaptic vesicle (SV) exo- and endocytosis are tightly coupled to maintain neurotransmission fidelity. We demonstrate that dynamic membrane tension fluctuations at synapses directly coordinate these processes and unravel a novel molecular mechanism responsible. Using a combination of in vitro reconstitution of SV exo/endocytosis, optical tension measurements, and advanced neurotransmission characterization, we identify FBP17, an endocytic protein, as a presynaptic membrane tension sensor. We show that its intrinsically disordered domain undergoes a tension-dependent conformational change, triggering SV endocytosis and suppressing spontaneous exocytosis – a process crucial for high-fidelity neurotransmission. This biomolecular-condensation-to-ordered-assembly transition-based mechanism links exocytosis to rapid, local endocytosis, ensuring synaptic integrity. Our findings reveal membrane tension is not merely a passive biophysical property, but an active regulator of neurotransmission, highlighting the critical role of membrane biophysical properties in neuronal signaling. This work suggests that similar tension-sensing mechanisms may operate at other membrane remodeling sites including exo-endocytosis in exocrine and

endocrine cells, during immunological synapse formation, or in endosomal membrane scission.

### **Javier Montenegro: “Supramolecular Dynamic Chemistry for membrane transport and Biomimetic Systems” – Universidade de Santiago de Compostela, CIQUS, Spain**

(Monday, September 29, Session 3, 14:50 - 15:10)

Our research group is interested in the application of supramolecular chemistry to understand and manipulate biology. [1,2] Our work philosophy is based in the importance of weak and non-covalent forces to control the shape and the topology of biomolecules, which are governed by the principles described by supramolecular chemistry. These supramolecular lessons can then be applied to control the properties and function of biomolecules. We believe that by modulating the shape we can mimic, control and improve functional behaviour. With focus in supramolecular interactions for artificial membranes and tubular composites, we investigate the construction of synthetic systems for controlling and emulating biology and life-like soft systems. [3-4]

[1] Fuertes, A.; Juanes, M.; Granja, J.R.; Montenegro, J.; Chem. Commun. 2017, 53, 7861–7871.

[2] Lostalé-Seijo, I.; Montenegro, J.; Nat. Rev. Chem. 2018, 2, 258–277.

[3] Priegue, J.M.; Crisan, D.N.; Martínez-Costas, J.; Granja, J.R.; Fernandez-Trillo, F.; Montenegro, J.; Angew. Chem. Int. Ed. 2016, 55, 7492–7495. b) Lostalé-Seijo, I.; Louzao, I.; Juanes, M.; Montenegro, J.; Chem. Sci. 2017, 8, 7923–7931. c) Barba-Bon, A. et al. Nature, 2022, 603, 637–642.

[4] Insua, I.; Montenegro, J.; J. Am. Chem. Soc. 2020, 142, 1, 300-307, b) Méndez-Ardoy, A.; Granja, J.R.; Montenegro, J.; Nanoscale Horizons, 2018, 3, 391-396. c) Méndez-Ardoy, A. et al. Angew. Chem. Int. Ed. 2020, 59, 6902–6908. d) Booth, R., Insua, I., Ahmed, S., Rioboo, A. & Montenegro, J.; Nat Commun. 2021, 12, 6421.

### **Patricia Bassereau: “A minimal human ESCRT-III system to mimic HIV-1 detachment” – Institut Curie, France**

(Monday, September 29, Session 4, 15:40 - 16:10)

ESCRT-III complexes mediate membrane remodeling and scission in various cellular processes. In human cells, scission typically involves a subset of 12 ESCRT-III proteins. Notably, HIV-1 budding requires only a minimal set—CHMP4B, CHMP2A, CHMP3, and the ATPase Vps4B—for viral release. Previous studies have shown that membrane scission can be inhibited and HIV-1 budding stalled when the bud neck is too wide, such as in the absence of the I-BAR protein IRSp53, even though ESCRT proteins are still recruited. Inspired by this, we reconstituted scission in vitro using the minimal human ESCRT-III machinery. Using GUVs and purified proteins, we induced membrane buds by osmotic deflation or by adding IRSp53 to generate inward tubules. In some case, CHMP4B recruitment to bud necks was enhanced via dimeric Alix. In these conditions, by fluorescence microscopy, we always observed membrane scission, even without ATP and when using C-terminally truncated CHMP4B- $\Delta$ C and CHMP2A- $\Delta$ C constructs. Scission was comparatively more efficient when adding Vps4B/ATP, in particular for the full-length proteins. In contrast, scission failed when forming a bud neck by wrapping GUV membranes around colloidal beads, even when pulling on the beads with optical tweezers, a setup previously successful using a larger set of yeast ESCRT-III (A.-K. Pfitzner et al. Cell (2020)). In this geometry, strong membrane-bead interactions likely constrain neck shape, preventing efficient scission. Our results suggest that the minimal ESCRT-III set used by HIV-1 can mediate scission, but with a strong dependence on membrane geometry. The broader diversity of ESCRT-III proteins in human cells may serve to ensure robust scission across a wider range of physical contexts.

**Bert Poolman: “Structural and functional implications of *in vivo* phase separation of membrane protein in *Escherichia coli*” – University of Groningen, Netherlands**

(Tuesday, September 30, Session 6, 11:35 - 11:55)

Liquid-liquid phase-separation (LLPS) controls protein activity and dynamically organizes (macro)molecules in living systems without the need for membrane-bound compartments. Biomolecular condensates of water-soluble proteins have extensively been studied, but LLPS of membrane proteins is uncharted territory. In this work we induce *in vivo* condensation of lactose permease (LacY), a widely-studied model monomeric inner membrane protein in *Escherichia coli*, and evaluate how it affects LacY function. We fused LacY with engineered, condensate-forming protein PopTag. We observe major changes in the localization and mobility of LacY<sup>Pop</sup>. Molecular dynamics simulations show how the PopTag domain drives the condensate-like association dynamics of LacY<sup>Pop</sup> through hydrophobic sticker interactions. LacY<sup>Pop</sup> preserves native-level transport activity and outperforms the non-condensated LacY under mild hyperosmotic stress. Perturbation experiments suggest that membrane curvature drives the accumulation of LacY<sup>Pop</sup> at the poles of *E. coli*. Co-condensation of LacY and  $\beta$ -galactosidase LacZ slightly reduces their activity and results in remarkable cellular reorganization of the proteins. Our research shows the localization, dynamics, and function of phase-separated membrane proteins in bacteria and highlights the potential of LLPS for engineering complex metabolic networks *in vivo*.

**Dragomir Milovanovic: “Contact sites at the interface of membraneless organelles and membranes” – Institute of Biochemistry, Charité - Berlin University of Medicine, Germany**

(Monday, September 29, Session 4, 16:30 - 16:50)

Phase separation is a major mechanism for organizing macromolecules, particularly proteins with intrinsically disordered regions, in compartments not limited by a membrane or a scaffold. The cell can thus be viewed as a dynamic emulsion, composed of numerous biomolecular condensates alongside classical membrane-bound organelles. The condensate-membrane interfaces emerge as chemical microenvironments that couple diffusion and the material properties of condensates to biochemical processes occurring in the membranes. For example, synapsin/synaptic vesicle condensates – a membraneless organelle that is in fact packed with membranes – can harbor ion potential differences at their interfaces and may act as a charge center in synapses. Another prominent example of large membrane areas that are tightly juxtaposed in cells are mitochondria and ER. Our recent data show that PDZD8, the ER-resident protein identified as a tether between the ER and mitochondria, can undergo liquid-liquid phase separation via its intrinsically disordered region. Endogenously-labeled PDZD8 forms condensates on membranes both *in vitro* and *in vivo*. These observations highlight how phase separation at membrane interfaces can create adhesion zones that tether vesicle cohorts or stitch neighboring organelles, revealing new principles for mesoscale cellular organization.

**Charu Sharma: “From Curvature Sensing to Membrane Scission: Real time visualization reveals mechanistic insights into DynaminA mediated Synthetic Cell-Division”** – Delft University of Technology, Netherlands

(Monday, September 29, Session 4, 16:50 - 17:10)

Synthetic biology seeks to understand life by building synthetic cells from the bottom up. A major challenge is developing robust division machinery for precise content distribution. Existing strategies, from membrane mechanics to divisomes like actomyosin or FtsZ, remain insufficiently robust for complete division. The Dekker lab recently proposed DynaminA, a bacterial dynamin-like protein from *Bacillus subtilis*, as a simple one-component division system. When liposomes are reshaped into dumbbells, DynaminA self-assembles at the highly curved neck, inducing hemi-scission or full scission. However, the mechanistic understanding of DynaminA machinery is currently lacking. I will present cell-free expression of DynaminA in lipid vesicles, enabling real-time observation of membrane scission events via fluorescence microscopy. Towards this, I will also discuss the role of anionic lipids in the membrane composition in facilitating the correct folding of DynaminA and enabling functional protein to induce scission. Real-time imaging further revealed that DynaminA not only senses membrane curvature but can also locally induce spontaneous curvature—an unreported property of DynaminA. Finally, I will show how tuning membrane tension increases scission efficiency from previously reported 26% to an improved 76%, highlighting DynaminA a promising division module for synthetic cells.

**Janett Göhring: “CD4+ T-cells create a stable mechanical environment for force-sensitive TCR:pMHC interactions”** – University of Natural Resources and Life Sciences, Austria

(Monday, September 29, Session 4, 17:10 - 17:30)

Efficient scanning of tissues that T-cells encounter during their migratory life is pivotal for protective adaptive immunity. In fact, T-cells can detect the presence of even a single antigenic peptide/MHC complex (pMHC) among thousands of structurally similar yet non-stimulatory endogenous pMHCs on the surface of antigen-presenting cells (APCs) or target cells. Mechanical forces acting on ligand-engaged T-cell receptors (TCR) have previously been implicated in T-cell antigen recognition and ligand discrimination, yet their magnitude, frequency, and impact remain unclear. Here, we quantitatively assess forces across various TCR:pMHC pairs with different bond lifetimes at single-molecule resolution, both before and during T-cell activation, on platforms that either include or exclude tangential force registration. For this purpose, we use glass-supported lipid bilayers (SLBs) presenting pMHC conjugated to a molecular force sensor unit at its base, adhesion factors and costimulatory molecules to the approaching T-cells. Observed TCR-exerted molecular forces within the synaptic environment reached up to 6-7 pN for high-affinity TCR-pMHC pairs, but were substantially reduced, if not absent, for lower affinity receptor-ligand pairs. Notably, a large majority of monitored sensors did not experience forces. On gel-phase SLBs, the high-force fraction made up less than 14% of all measured single-molecule FRET events. This proportion was further reduced (less than 6%) on fluid-phase SLBs. Our results imply that CD4+ T-cell TCRs experience significantly lower forces than previously estimated, with only a small fraction of ligand-engaged TCRs being subjected to these forces during antigen scanning. These rare and minute mechanical forces do not impact the global lifetime distribution of the TCR:ligand bond. We propose that the immunological synapse is created

as biophysically stable environment to prevent pulling forces from disturbing antigen recognition.

### **Roland Wedlich-Söldner: “Adaptation of plasma membrane domains to metabolic stress” – University of Münster, Germany**

(Tuesday, September 30, Session 5, 08:30 - 09:00)

Saprophytic fungi evolved a large arsenal of membrane transporters to allow uptake of a wide range of organic materials as nutrients and energy source. These transporters are tightly regulated in their expression and turnover to allow adaptation to rapid environmental changes and stresses. We and others have previously shown that an additional level of cellular adaptation for transporters is their dynamic segregation into a patchwork of overlapping but distinct PM domains. Recent results from our lab on the PM proton pump Pma1 that demonstrate progressive clustering of the hexameric protein into characteristic hexagonal 2D crystals upon glucose starvation. This striking behaviour goes hand in hand with a strong reduction in overall protein density within the PM and is directly regulated by the 7 transmembrane protein Mrh1. Our results suggest that clustering is specifically mediated by sequestration of phosphatidylserine via the highly charged C-terminal tail of Mrh1. Interestingly, we were also able to block Pma1 relocation and clustering by overexpression of a tetraspanner that assembled into polymeric cages within the PM. Our live cell imaging experiments combined with super resolution microscopy and freeze fracture EM suggest a novel mechanism for formation of lateral micropatterns in the yeast PM as adaptation to acute nutrient stress.

### **Claudia Steinem: “Dynamics of ordered domains in pore-spanning membranes: comparing artificial bilayers with plasma membranes” – Georg-August University of Göttingen, Germany**

(Tuesday, September 30, Session 5, 09:00 - 09:20)

The biological membrane exhibits dynamic heterogeneity, with lipids and proteins capable of segregating into distinct micro- and nano-domains. These specialized domains, often termed “rafts”, are thought to play fundamental roles in regulating membrane functions by controlling the spatial organization of proteins and lipids. To better understand the organization and biophysical properties of biological membranes, various model membrane systems, such as giant unilamellar vesicles or supported lipid bilayers, have been developed. However, model membranes, typically made from only a few lipid species, cannot recapitulate the immense complexity of the native plasma membrane. Based on porous supports with micrometer-sized pores, we have established pore-spanning plasma membranes (PSPMs) derived from giant plasma membrane vesicles, which mirror the intricate lipid and protein heterogeneity in eukaryotic plasma membranes. Fluorescence microscopy has unequivocally demonstrated that these PSPMs phase-separate into liquid disordered (ld) and liquid ordered (lo) domains, a finding that was corroborated by cholesterol depletion using dimethyl- $\beta$ -cyclodextrin. Mobile lo-domains were observed in the freestanding membrane parts (f-PSPMs) experiencing confined diffusion. From the domains’ trajectories followed by an MSD-analysis, diffusion coefficients were extracted as a function of the lo domain sizes, which provided access to the plasma membrane’s surface viscosity. Recording the two-dimensional undulations of the lo domains further allowed us to determine the domains’ line tension. The obtained membrane surface viscosity and line

tension are compared to the values found for artificial liquid-liquid phase-separated pore-spanning membranes.

**Frederick Heberle: “Investigating the influence of membrane dipole potential on liquid-ordered/liquid-disordered phase separation in model membranes”**  
– Stockholm University, Sweden

(Tuesday, September 30, Session 5, 09:20 - 09:40)

Cells can dynamically alter the spatial organization of lipids and proteins in the plasma membrane (PM) to regulate processes including cell signaling. The size and morphology of membrane domains, and how these depend on lipid composition, have drawn attention as potentially important variables in these processes. Model membranes have proven to be useful tools for elucidating the influence of phospholipid chains and headgroups, as well as cholesterol concentration, on phase behavior. Following this approach, we have investigated simplified three- and four-component models that mimic the composition of the PM outer leaflet to understand the role of the lipid backbone. Replacing ester-linked DPPC and DOPC with their ether-linked counterparts allowed us to selectively change the membrane dipole potential of coexisting liquid-disordered (Ld) and liquid-ordered (Lo) phases, while replacing DOPC with POPC allowed us to change the line tension. We used confocal fluorescence imaging to gain insight into the macroscopic phase behavior of GUVs, and FRET and cryo-EM to probe nanoscale heterogeneity of LUVs. Our results can be understood in terms of a model in which the tendency toward micron-scale phase separation is counteracted by dipole repulsion, which lowers the miscibility transition temperature and can in some cases result in stable arrays of small domains or stripe phases. These findings suggest that relatively small changes in the structure of the lipid backbone can exert a large influence on domain formation and morphology in biomimetic membranes.

**Tiemei Lu: “Dynamic Interactions Between Coacervates and Membranes: From Endocytosis to Penetration”** – University of Oxford, UK

(Tuesday, September 30, Session 5, 09:40 - 10:00)

Recent studies have shown that the interactions between condensates and biological membranes are of functional importance, for example, in T-cell receptor signal transduction, RNA granule transport, autophagy, the formation of protein storage vacuoles, or size control of ribonucleoprotein granules. Wetting is thought to govern these interactions, yet its role in membrane deformation and endocytosis remains unclear. Using complex coacervates and liposomes as model systems, we show that varying interaction strengths lead to a spectrum of wetting behaviors—from non-wetting to engulfment (endocytosis) and complete wetting. Endocytosis of coacervates was found to be a general phenomenon: coacervates made from a wide range of components could be taken up by liposomes. A simple theory taking into account surface energies and coacervate sizes can explain the observed morphologies. We further examined the physical parameters that govern the penetration of oligo-arginine/RNA complex coacervates across phospholipid bilayers. Successful entry into liposomes was found to depend primarily on two factors: the  $\zeta$ -potential difference between the coacervates and liposomes, and the lipid partition coefficient into the coacervate phase. Guided by these principles, we identified several coacervates capable of crossing cellular membranes. Together, these results provide new

insights into condensate–membrane interactions and offer a foundation for designing coacervate-based systems for intracellular delivery of therapeutic agents.

**Ewa Paluch: “The nanoscale regulation of cell surface mechanics in cell and tissue morphogenesis” – University of Cambridge, UK**

(Tuesday, September 30, Session 6, 10:45 - 11:15)

Precise control of cell morphology is key for cell physiology, and cell shape deregulation is at the heart of many pathological disorders. Cell morphology is intrinsically controlled by mechanical forces acting on the cell surface, to understand shape it is thus essential to investigate the regulation of cell surface mechanics. I will discuss how the mechanical properties of the cell surface are regulated, with a focus on cortical tension and membrane-cortex interactions. I will then discuss how cortex and membrane mechanics affect morphogenesis at the cell and tissue level.

**Oliver Rocks: “Formation of giant membrane rods through lipid unmixing and segregation of ER-shaping proteins under thermal stress” – Charité -**

University Medicine Berlin, Germany

(Tuesday, September 30, Session 6, 11:15 - 11:35)

Maintenance of organelle plasticity through lipid homeostasis in response to environmental changes is essential for cellular fitness. Here, we report the rapid and reversible formation of cell-spanning tubular membrane structures at reduced temperatures. These ‘rods’ emerge from the endoplasmic reticulum, are remarkably rigid, have a multilamellar architecture and do not require ATP or structural support. Rod formation is driven by lipid-lipid phase separation, characterized by increased membrane packing and promoted by shifts towards saturated over unsaturated fatty acids. Proteins critical for maintaining tubular ER membranes are excluded from rods, suggesting that growing solid-like phases induce their segregation, allowing large-scale membrane flattening and, ultimately, multi-layered wrapping. Notably, tissue-derived alveolar type II cells, known for surfactant production and their elevated saturated lipid content, form rods even at 37°C. These findings provide a paradigm for the polymorphism of cellular membranes and offer fundamental insights into the spatial organization of lipid and protein domains on endomembranes in response to environmental and metabolic conditions.

**Christian Eggeling: “Zooming in into lipid membrane structure and dynamics with super-resolution MINFLUX microscopy” – Leibniz Institute of Photonic Technologies, Germany**

(Monday, September 29, Session 4, 16:10 - 16:30)

Molecular interactions are key in membrane-based cellular signalling. They are usually ruled by the organization and mobility of the involved molecules. However, the direct and non-invasive observation of the interactions in the living cell membrane is often impeded by principle limitations of conventional far-field optical microscopes, for example with respect to limited spatio-temporal resolution and information content. Here, we present an advanced optical microscopy study of lipid membrane dynamics involving optimized tools, especially employing single-molecule tracking on a super-resolution MINFLUX microscope. We highlight limitations and advantages and present how these approaches reveal novel

aspects of lipid membrane reorganizations and dynamics during endocytosis, viral infection or in neuronal axons.

**Rumiana Dimova: “When a droplet meets a membrane: membrane remodeling by bimolecular condensates”** – Max Planck Institute of Colloids and Interfaces, Germany

(Tuesday, September 29, Session 6, 11:55 - 12:25)

Bimolecular condensates are key organizers of cellular biochemistry, yet their interactions with membranes remain underexplored. Given the prevalence of membrane-bound compartments in cells, condensate–membrane encounters are inevitable and can profoundly influence cellular function and architecture. Using giant unilamellar vesicles (10–100  $\mu\text{m}$ ) as a minimal model, we investigate how condensates wet, reshape, and remodel membranes [1–3]. We show that condensates can induce striking morphological transformations [4], reorganize lipids [5], trigger endocytosis-like events [6], and even seal damaged membranes by patching pores [7]. Membranes, in turn, actively modulate these interactions: their lipid composition and packing determine condensate affinity and wetting behavior [8]. Notably, we find that affinity is governed not by the hydrophobicity of condensates but by the permittivity contrast between them and the dilute phase around them [9]. Together, these results reveal how fundamental physicochemical principles— independent of active processes or scaffolding proteins—can drive membrane interactions and remodeling. Our findings provide insight into the role of condensate-membrane interactions in cellular organization and offer design principles for engineering artificial cells.

[1] Mangiarotti & Dimova, *Annu. Rev. Biophys.* 53:319, 2024.

[2] Dimova & Lipowsky, *Adv. Mater. Interfaces* 4:1600451, 2017.

[3] Liu et al., *Front. Chem.* 7:213, 2019.

[4] Mangiarotti et al., *Nature Commun.* 14:2809, 2023.

[5] Mangiarotti et al., *Nature Commun.* 14:6081, 2023.

[6] Mangiarotti, Aleksanyan et al., *Adv. Sci.* 11:2309864, 2024.

[7] Bussi et al., *Nature* 623:1062, 2023.

[8] Mangiarotti et al., *Nature Commun.* 16:2756, 2025.

[9] Sabri et al., *bioRxiv*, doi:10.1101/2025.03.09.642144 (2025).

**Omer Dushek: “Optimising CAR-T cell sensitivity by engineering extracellular receptor/ligand sizes”** – University of Oxford, UK

(Tuesday, September 30, Session 7, 14:00 - 14:30)

Chimeric antigen receptors (CARs) are synthetic receptors that can re-direct immune cells to kill target cells that express their cognate antigen ligand. When expressed in T cells, CARs exhibit low antigen sensitivity, which restricts their therapeutic efficacy and leads to patient relapses when cancer cells downregulate antigen expression. Despite the pressing need to overcome this limitation, the underlying mechanisms remain poorly understood. Here, we demonstrate that enhancing CAR sensitivity to match the sensitivity of the native T-cell receptor (TCR) can be achieved by engineering matched extracellular sizes of CAR/antigen and CD2/CD58 complexes. We find that different CAR/antigen sizes, which are generated by different CAR architectures and different target antigens, require a different CD2/CD58 size to optimise sensitivity. This extracellular size-matching improves antigen engagement and co-localisation of CAR/antigen and CD2/CD58 complexes. We also find that size-matching controls co-inhibition of CARs by PD-1/PD-L1. These findings highlight the importance of

size-matching for signal integration by surface receptors at cell-cell interfaces and offers a new approach to tune CAR-T cell sensitivity by matching or mismatching extracellular sizes.

**Harsha Bajaj: “Dynamic Duos: Coacervate-Lipid Membrane Interactions in Regulating Membrane Transformation and Condensate Size”** – Council of Scientific & Industrial Research - National Institute for Interdisciplinary Science and Technology (CSIR – IIIST), India

(Tuesday, September 30, Session 7, 14:30 - 14:50)

Biomolecular condensates interfacing with lipid membranes is crucial for several key cellular functions. Despite this importance, the mechanisms by which lipid membranes influence condensate behavior within cells remain poorly understood. In this study, model systems mimicking cellular environments, such as giant unilamellar vesicles (GUVs), are utilized to investigate the detailed interactions between condensates and lipid membranes. The results uncover a significant role of coacervate size and electrostatic interactions in altering membrane characteristics and driving membrane deformation. Notably, it is shown that larger coacervates with weaker electrostatic attraction to membranes can induce budding at the interface. In contrast, strong charge-based interactions lead to the accumulation of coacervates at membrane surfaces, giving rise to a wrinkled vesicle morphology. Using fluorescence recovery after photobleaching (FRAP), lipid diffusion dynamics were observed to be altered at the condensate-membrane interface, thereby limiting coacervate coarsening. High-resolution imaging, including transmission electron microscopy (TEM), reveals that coacervate droplets become embedded within membrane folds and invaginations, which restrict droplet size and produce distributions similar to those seen in cellular contexts. Collectively, these findings offer valuable mechanistic insights into how lipid bilayers can modulate condensate size and organization, shedding light on the principles governing condensate nucleation and spatial localization in cells.

**Gerald Hammond: “Balancing the Membrane: Feedback and Feedforward Regulation of Plasma Membrane PI(4,5)P<sub>2</sub>”** – University of Pittsburgh, USA

(Tuesday, September 30, Session 7, 14:50 - 15:10)

Phosphoinositides, especially the most abundant PI(4,5)P<sub>2</sub> species, control most every facet of plasma membrane function and organization. From the cytosolic leaflet, they recruit or allosterically activate scores of peripheral and integral membrane proteins. In turn, these proteins facilitate the transport of molecules and information to, from, and across the membrane, and also anchor the cortical cytoskeleton. As a result, disrupted PI(4,5)P<sub>2</sub> levels cause a huge swathe of diseases, from lethal neurological defects to dysentery. Despite the vital need to maintain PI(4,5)P<sub>2</sub> levels, we still lack a detailed molecular understanding of how this is accomplished. We have been identifying homeostatic mechanisms that maintain global membrane PI(4,5)P<sub>2</sub> levels. We identified PIP4K enzymes as receptors and control centers for PI(4,5)P<sub>2</sub> homeostasis, and now describe a detailed molecular mechanism for how these proteins disrupt the activity of their effector, PIP5K, capping PI(4,5)P<sub>2</sub> levels. We also describe how a feed-forward mechanism augments PIP5K activity during phospholipase-C-mediated PI(4,5)P<sub>2</sub> hydrolysis. Collectively, our experiments begin to build a picture for how cells maintain PI(4,5)P<sub>2</sub> levels to support all membrane functions in the face of multiple functional and metabolic demands.

**Markus Deserno: “On the thermodynamics of ternary asymmetric lipid membranes” – Carnegie Mellon University, USA**

(Tuesday, September 30, Session 8, 15:40 - 16:10)

Ternary lipid membranes—comprising a high-melting species, a low-melting species, and cholesterol—have long served as minimal model systems for studying lipid organization. Despite their ostensible simplicity, they reproduce a surprising range of the complex mixing behavior observed in biological membranes, including fluid-fluid phase coexistence and its associated critical point. A longstanding motivation behind these studies has been the hope that ternary mixtures might help unravel the enduring mystery of lipid rafts. Extensive research on well-controlled model systems has indeed revealed many of the physical principles that govern ternary lipid phase behavior, while complementary discoveries in living cells have added both support and intrigue. Yet the physiological reality remains perplexing. Recent findings from multiple groups suggest that further progress will likely require addressing a second fundamental feature of biomembranes: their pronounced asymmetry across the two leaflets. This asymmetry is not limited to composition (i.e., the presence of distinct ternary mixtures in each leaflet) but likely extends to mechanical properties as well. There is growing evidence that the two leaflets may experience very different lateral tensions, resulting in a differential stress that strongly influences cholesterol partitioning—arguably one of the central players in membrane organization. In this talk, I will examine these two intertwined aspects of biomembrane complexity—compositional and mechanical asymmetry—and propose a generic (though not yet very predictive) thermodynamic framework for describing their interplay. I will also present initial coarse-grained simulation results that begin to elucidate the cross-talk between asymmetry and lipid mixing thermodynamics.

**Seraphine Wegner: “Light based communication between cells across membranes” – University of Münster, Germany**

(Tuesday, September 30, Session 8, 16:10 - 16:30)

Cells commonly communicate through diffusible molecules, yet nonchemical modes of communication remain underexplored. While bioluminescent organisms use light for signaling at the macroscale, it remains an open question whether light-based signaling is feasible at the scale of cells. We demonstrate that intercellular communication via light is possible within synthetic cell communities constructed from biomimetic vesicles. In our design, sender cells generate an intracellular light signal, which induces a functional response in receiver cells. Unlike chemical messengers, light signals propagate rapidly, do not rely on diffusion, and bypass the need for membrane transport. This framework offers a new modality for signaling in both synthetic and living cells, providing a foundation for engineering light-mediated interactions in complex cellular systems.

**Ludger Johannes: “GlycoSwitch — a novel signaling circuit to control endocytosis” – Institut Curie, France**

(Tuesday, September 30, Session 8, 16:30 - 16:50)

It is commonly assumed that the glycan makeup of glycoproteins is final and static once these have reached the cell surface. Here, we challenge this notion by the discovery of a molecular switch — termed GlycoSwitch — that at the plasma membrane induces acute and reversible changes of glycan structure and arrangement in space. This leads to the binding

and oligomerization of galectins that in interaction with glycosphingolipids drive the formation of tubular endocytic pits from which clathrin-independent endocytic carriers emerge for uptake and retrograde trafficking of the glycoproteins to the Golgi apparatus. Here, the glycoproteins are resialylated and secreted in a polarized manner to specialized areas of the cells, such as the leading edge in migrating cells. We are now exploring the structural, molecular, and pathophysiological aspects of the GlycoSwitch in polarized trafficking in epithelial cells and in epithelial-mesenchymal transition.

MacDonald E, (...), and Johannes L. Growth factor-triggered desialylation controls glycolipid-lectin driven endocytosis. *Nat Cell Biol* 27: 449-463, 2025.

Shafaq-Zadah M, (...), and Johannes L. Spatial N-glycan rearrangement on  $\alpha 5 \beta 1$  integrin nucleates galectin-3 oligomers to determine endocytic fate.

Initial version at: <https://biorxiv.org/cgi/content/short/2023.10.27.564026v1>

## **Petia Vlahovska: “Curvature dynamics of biomembranes: role of membrane viscosity and interleaflet friction” – Northwestern University, USA**

(Tuesday, September 30, Session 8, 16:50 - 17:10)

Lipid bilayers are the main structural component of the membranes that shape and compartmentalize cells. Cell architecture is highly dynamic and membranes' conformation changes dramatically in processes such as movement, division, and vesicle trafficking. Fluidity plays essential role in the structural malleability and diversity of static shapes of membranes. However, its importance in the dynamics of membrane deformations is less appreciated. Membrane bending by thermal or active forces is commonly assumed to be damped by viscous losses in the surrounding medium. In this talk, I will present our recent experimental and theoretical work where we demonstrated that dissipation within the membrane controls the undulation dynamics of nonplanar membranes with a radius of curvature smaller than the Saffman-Delbruck length. Using flickering spectroscopy of giant vesicles made of DPPC:Cholesterol and pure diblock-copolymer bilayer membranes, the signature of membrane dissipation was detected in curvature fluctuations [1]. We extend the theoretical analysis to submicron liposomes, where lipid density fluctuations, which arise from the stretching and compression of the monolayer leaflets, and intermonolayer friction become important. The results highlight the crucial role of intramembrane dissipation in cellular membrane remodeling and in the thermally driven curvature fluctuations of submicron liposomes.

[1] HA Faizi, R Granek, PM Vlahovska “Curvature fluctuations of fluid vesicles reveal hydrodynamic dissipation within the bilayer”, *PNAS*, 121 (44), e2413557121 (2024)".

## **Tanmoy Ghosh: “Elevated actin contractility combined with cargo-loaded clathrin pits decisively shapes midplane-peaked apico-basal tension profiles in HeLa cells” – Indian Institute of Science Education and Research Kolkata, India**

(Tuesday, September 30, Session 8, 17:10 - 17:30)

The slow equilibration of tension results in inhomogeneities in cellular membrane tension, yet few studies have linked these mechanical heterogeneities to a cell's functional state. Mapping membrane mechanics at the cell surface is essential. Our study focuses on measuring membrane tension using tether force measurement, membrane fluctuations, and lipid compaction techniques. The plasma membrane of cells is closely associated with the actin cytoskeleton, which is critical for the flow of tension. To investigate variations in

this tension, we combined Interference Reflection Microscopy (IRM) to examine basal membrane fluctuations and tension, with Optical Trapping (OT) to assess apical region tension by extracting tethers. We also utilized Flip-TR lifetime measurements to evaluate membrane compaction. Our study quantified optical trap tension at two levels in the apical region, revealing a gradient of tension that depends on an intact actin cytoskeleton. Super-resolution (STED) image analysis of the motor protein myosin and the actin linker ezrin demonstrated that cytoskeletal contractility, mediated by myosin, creates this tension pattern. While Flip-TR measurements confirmed the existence of the tension gradient, they could not isolate the specific role of the actin cytoskeleton due to the dual effects of tension on lifetime. Furthermore, probing the membrane's functional state through endocytosis using fluorescently tagged transferrin (Tf) revealed that high-tension regions accumulated more Tf at clathrin sites, leading to an increase in cargo-loaded endocytic pits at the cell surface. Our findings show that tension at the apical surface of the membrane is lower than at the midplane, linked to the functional state of the cell's membrane during endocytosis. Overall, this research demonstrates how cells maintain a specific pattern of tension linked to cytoskeletal structure and membrane functions, utilizing a combination of correlative and multi-technique approaches.

**Jay Groves: “Protein condensation and signal transduction on the membrane” – University of California Berkley, USA**

(Wednesday, October 1, Session 9, 08:30 - 09:00)

I will discuss recent insights into the mechanisms by which protein condensates on the membrane regulate signal transduction processes. Many of our recent experimental observations have been made on the T cell signaling system, and the role of protein condensation involving the membrane-associated scaffold protein LAT. However, many parallels exist between this system and the EGFR signaling system. We will analyze common features between LAT and EGFR condensates as well as several distinct ways in which they differ, which illustrate the diversity of physical mechanism that can be deployed within protein condensates to regulate signaling.

**Yuka Sakuma: “Long-range viscosity of *C. elegans* plasma membrane” – Tohoku University, Japan**

(Wednesday, October 1, Session 9, 09:00 - 09:20)

The viscosity of the plasma membrane in living cells is a crucial biophysical parameter that regulates cellular functions. We categorize membrane viscosity into short- and long-range viscosities based on the spatial scale of membrane-associated processes. Short-range viscosity arises from nanometer-scale diffusion of membrane molecules and regulates signal transduction and transport. We measured the short-range viscosity in *C. elegans* early embryo as  $\sim 10^{-9}$  Pa·s·m using fluorescence recovery after photobleaching. In contrast, micrometer-scale membrane flow, which is driven by actin cytoskeleton, occurs in processes such as migration and division. We refer to the resistance to this flow as long-range viscosity. While transmembrane proteins anchored to the cytoskeleton have minimal impact on short-range viscosity, they may strongly affect long-range viscosity. Thus, these two viscosities likely differ significantly. In this study, we measured long-range viscosity by applying a local point force to the plasma membrane of *C. elegans* early embryos via

microinjection. In intact embryos, no membrane flow was observed. However, when actin polymerization was inhibited, the point force induced a pair of vortex flow. By comparing the vortex pattern with a hydrodynamic model, we found that the long-range viscosity was  $\sim 10^3$  times greater than the short-range viscosity in *C. elegans* embryos. This large increase is attributed to actin filaments that remain attached to transmembrane proteins even after polymerization inhibition. We conclude that the residual actin cytoskeleton and its associated proteins significantly contribute to the increased long-range viscosity.

**Jan Steinkühler: “Reconstitution of electrically excitable membranes and lipid nanotubes”** – Kiel University, Germany

(Wednesday, October 1, Session 9, 09:20 - 09:40)

Voltage-sensitive ion channels form the molecular basis for electrical spiking activity in neuronal networks. However, the spatial propagation of spikes is not a property inherent to individual ion channels but rather emerges from the arrangement of ion channels along a tubular lipid membrane. While the reconstitution of functional ion channels in model membranes is well established, the propagation of an action potential along a lipid bilayer nanotube has not yet been demonstrated. In this work, I discuss our lab's efforts toward achieving this goal through automated cell-free expression of ion channels and data-driven modelling of membrane excitability. I will also present initial results from electro-optical measurements on force-induced lipid nanotubes and memory effects by an interplay of electrical field induced lipid migration and ionic nanochannel conductance.

**Giacomo Fiorin: “Simulating membrane remodeling under asymmetric and symmetric membrane tensions”** – National Institutes of Health, USA

(Wednesday, October 1, Session 9, 09:40 - 10:00)

The propensity of a membrane to alter its morphology is a key factor in regulating organelle trafficking and molecular transport. However, the individual chemical characteristics of the plasma membrane influence its mechanical properties in distinct ways, and quantifying their combined effects remains challenging. To address this, molecular dynamics simulations offer a valuable complement to experimental data obtained from synthetic membrane models. By deriving the energy landscape of membrane remodeling directly from atomic forces, we examine the effects of different types of tension on membrane mechanics. Our results show that the differential tension arising from leaflet asymmetry can cause small bilayers to stiffen, although to a lesser extent than observed in giant vesicle experiments. In contrast, the mechanics of bilayers under symmetrically applied tension are very well explained by geometric factors such as exposed surface area and local curvature. Together, these findings provide deeper insight into the membrane's physical properties that most strongly influence various biological processes.

**Padmini Rangamani: “Biophysical modeling of membrane curvature generation by the glycocalyx”** – University of California San Diego, USA

(Wednesday, October 1, Session 10, 10:35 - 11:05)

The glycocalyx is a dense layer of glycosylated transmembrane proteins and lipids distributed on the extracellular surface of eukaryotic cells. It is known to mediate cell-cell interactions and protect cells from invasion by pathogens. We developed a polymer brush theory-based model, which suggests that the interplay between glycocalyx polymers and

membrane bending captures the wide variety of membrane shapes from spherical buds to elongated pearl-like shapes found in previously published experiments. We predicted that the physical properties of glycocalyx polymers and membrane properties play significant roles in regulating membrane morphologies. We then extended the model to consider the energy of a glycocalyx-membrane-actin cortex composite to investigate the effects of glycocalyx and membrane-cortex adhesion on the formation of outward budding extracellular vesicles. We showed that modulating the mechanical feedback among the glycocalyx, membrane-cortex attachment, and membrane curvature can give rise to two types of instabilities: a conserved Turing-type instability and a Cahn-Hilliard-type instability. Next, we identified the critical conditions for the formation of extracellular: an initial detachment of the membrane from the underlying cortex and then a sufficient driving force to induce membrane deformation. Finally, we used our model to predict that a heterogeneous size distribution of these vesicles can be generated through the regulation of glycocalyx properties, shedding insight into how extracellular vesicles of different radii may be generated.

**Alf Honigmann: “Role of adhesion protein size on segregation of epithelial cell junctions”** – Technische Universität Dresden, Germany

(Wednesday, October 1, Session 10, 11:05 - 11:35)

Epithelial cells control tissue shape and permeability via cell-cell adhesion complexes such as adherens junctions, desmosomes and tight junctions. Each junction type is comprised of distinct adhesion and scaffold proteins that assemble into separated functional units. How the sorting and segregation of junctional molecules happens is not well understood. Here we test the hypothesis that junctional segregation is driven by minimization of membrane bending induced by size differences of the ecto-domains of adhesion proteins. Combining bottom-up reconstitutions and genetic engineering of cell-cell interfaces of short and long adhesion proteins (JAM-A, Nectin-1 and E-Cadherin), we discovered spontaneous segregation of proteins into distinct junctional domains. Segregations dependents indeed on protein size differences and is modulated by the adhesion strength of the proteins. We confirm that size differences drive segregation in heterologous junctions reconstituted in HEK293 cells and using CRISPR we show that this mechanism is required to assemble functional tight and adherens junctions in epithelial cells. Our results provide a self-organizing mechanism how epithelial cells sort their junctional components at the mesoscale to assemble functional adhesion complexes.

**Kandice Levental: “Nanoscale organization of living membranes by protein paralipidomes”** – University of Virginia, USA

(Tuesday, September 30, Session 10, 11:35 - 11:55)

Membrane proteins reside in complex lipid environments composed of hundreds of lipid species. The function of these proteins depends on both their surrounding lipid composition and the biophysical properties of the lipid collectives. While some proteins bind specific lipid species, the distinct local membrane environments – termed paralipidomes – assembled by specific membrane proteins remain poorly defined. Here, we apply two complementary technologies to define protein paralipidomes. To probe local biophysical environments, we use HaloTags to covalently label membrane proteins with membrane-sensitive fluorescent probes, enabling in situ measurements of lipid packing in live cells. Using this strategy, we

quantify differences in packing between the inner and outer plasma membrane leaflets and directly observe nanoscopic heterogeneities associated with raft versus non-raft proteins. To determine paralipidome composition, we use synthetic amphipathic copolymers to solubilize membrane proteins from native membranes without detergents, preserving a solvating lipid bilayer. We then performed MS-MS to quantify the lipidome surrounding a given protein as compared to the bulk lipidome of the cell. Using this approach, we characterized the paralipidome of the G-protein coupled receptor adenosine 2A receptor (A2AR). Distinct lipid profiles were identified for apo-, agonist-, and antagonist-bound A2AR, suggesting conformation-dependent lipid selection. We are currently investigating how lipid composition affects ligand binding and receptor activation and integrating both approaches to comprehensively map biophysical and compositional paralipidomes. Together, these methods define a methodological framework for studying how the function of membrane proteins is regulated by their local lipid nano-environment.

**Rainer Böckmann: “Unraveling the stability, dynamics, and mechanics of cellular model membranes through multiscale simulations”** – Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Germany

(Tuesday, September 30, Session 10, 11:55 - 12:15)

Cellular membranes are complex, dynamic interfaces that orchestrate a wide range of biological functions. In this work, we combine all-atom and coarse-grained molecular dynamics (MD) simulations, along with constant-pH MD simulations and Brownian dynamics, to explore the lateral organization, mechanical behavior, and dynamic properties of both simplified and plasma membrane-like lipid bilayers. We focus on how membrane asymmetry shapes lipid mobility, domain formation, and thermal membrane bending. Our results challenge traditional paradigms of membrane structure by demonstrating that the dynamic local cholesterol distribution and thermal fluctuations can cooperatively soften membranes – despite cholesterol's well-established role in membrane stiffening and decreased permeability. Furthermore, we uncover how the length of the glycan chains of glycolipids modulates membrane behavior: longer oligosaccharides promote the formation of larger domains while simultaneously enhancing lipid diffusivity. These findings offer new perspectives on the principles underlying membrane organization and function.

**Michael Kozlov: “Model for tension propagation in crumpled compartmentalised cell membranes”** – Tel Aviv University, Israel

(Wednesday, October 1, Session 11, 14:00 - 14:30)

Propagation of membrane tension mediates mechanical signal transduction along surfaces of live cells and sets the time scale of mechanical equilibration of cell membranes. In stark contrast to the earlier expectations, studies in several cell types and under different conditions revealed a strikingly wide variation range of the tension propagation speeds including extremely low ones. The latter suggests a possibility of long-living inhomogeneities of membrane tension crucially affecting mechano-sensitive membrane processes. Here, we propose a general principle of tension propagation in cell membranes which are compartmentalised by the underlying cortical cytoskeleton and crumpled within each compartment. We suggest that the tension propagation is mediated by the 2D membrane flow between the compartments. We predict the pace of the tension propagation to be controlled by the relationship between the compartment's membrane tension and the

excess area stored in the crumples. We consider the realization of this principle for several specific mechanisms of the membrane crumpling.

**Helge Ewers: “Membrane compartmentation by submembrane actin rings” – Freie Universität Berlin, Germany**

(Wednesday, October 1, Session 11, 14:30 - 15:00)

The compartmentalization of the plasma membrane (PM) is a fundamental feature of cells. The diffusivity of membrane proteins is significantly lower in biological than in artificial membranes. This is likely due to actin filaments, but assays to prove a direct dependence remain elusive. We recently showed that periodic actin rings in the neuronal axon initial segment (AIS) confine membrane protein motion between them. Still, the local enrichment of ion channels offers an alternative explanation. Here we show, using computational modelling, that in contrast to actin rings, ion channels in the AIS cannot mediate confinement. Furthermore, we show, employing a combinatorial approach of single particle tracking and super-resolution microscopy, that actin rings are close to the PM and that they confine membrane proteins in several neuronal cell types. Finally, we show that actin disruption leads to loss of compartmentalization. Taken together, we here develop a system for the investigation of membrane compartmentalization and show that actin rings compartmentalize the PM.

**Georg Pabst: “Can Lipid Asymmetry Allosterically Modulate Integral Membrane Protein Function?” – University of Graz, Austria**

(Wednesday, October 1, Session 11, 15:00 - 15:30)

Lipid asymmetry is a defining feature of plasma membranes, yet its impact on integral membrane protein function remains incompletely understood [1]. One proposed mechanism involves asymmetric lateral stress between membrane leaflets influencing protein conformational equilibria. To explore this, we employed bottom-up strategies to construct synthetic asymmetric lipid bilayers and reconstituted the outer membrane phospholipase A (OmpLA) into these model systems. Using bilayers composed of phosphatidylcholine, phosphatidylethanolamine, and phosphatidylglycerol, we quantified OmpLA activity under defined compositional asymmetries. We found that lipid asymmetry significantly modulates OmpLA function: enzymatic activity was reduced in charge-neutral asymmetric membranes but enhanced in charged asymmetric environments. Remarkably, monovalent ions—traditionally not considered protein cofactors—further influenced the enzyme’s activity [2, 3]. These observations are consistent with allosteric modulation arising from differences in spontaneous monolayer curvatures between membrane leaflets and its regulation by ionic conditions. Our findings point to a general mechanism by which lipid asymmetry and ion–lipid interactions dynamically regulate membrane protein function, with broad implications for understanding membrane physiology and signaling.

[1] G. Pabst, and S. Keller, *Trends Biochem Sci*, 49: 333 -345 (2024).

[2] P. Piller, E.F. Semeraro, G. N. Rechberger, S. Keller, and G. Pabst, *PNAS Nexus* 2: 1 – 7 (2023).

[3] P. Piller, P., P. Reiterer, E.F. Semeraro, and G. Pabst, *RSC App Interf* 2: 69 – 73 (2025).

**Petra Schwille: “Protein-Driven Membrane Remodeling for Synthetic Cell Division” – Max Planck Institute of Biochemistry, Germany**

(Wednesday, October 1, Session 12, 16:00 - 16:30)

A notorious challenge in building synthetic cells is to achieve controlled, large-scale transformations of membrane vesicles, especially those required for division. Here, we explore how minimal protein systems can self-organize on and within membranes to produce such mechanical effects. Combining cytoskeletal contractility with spatial protein patterning, and coupling protein dynamics to lipid phase behavior, we observe furrowing, budding, and domain rearrangement in giant vesicles. These results demonstrate how physical principles of protein-membrane interaction can be harnessed to emulate core aspects of cytokinesis and advance bottom-up synthetic biology toward autonomous cellular reproduction.

**Ilya Levental: “Lipid number asymmetry: The hidden dimension of mammalian plasma membranes” – University of Virginia, USA**

(Wednesday, October 1, Session 12, 16:30 - 14:30)

The transbilayer distribution of lipids in mammalian plasma membranes (PMs) is functionally important and incompletely understood. It is generally assumed that the two leaflets of lipid bilayers must contain similar numbers of phospholipids (PLs) due to the constraint that their areas must be evenly matched. Contrary to this assumption, our recent detailed lipidomics analysis of live human erythrocytes reveals a large phospholipid imbalance between PM leaflets, with the cytoplasmic leaflet possessing almost 2-fold more PLs than the exoplasmic one. This surprising finding challenges our understanding of living membrane organization and structure. Extensive atomistic simulations guided by the lipidomics data reveals that a large PL imbalance between PM leaflets can be sustained via highly asymmetric distribution of cholesterol. We confirm that cholesterol increases membrane tolerance for PL imbalances in model membranes and cells. Driven by preferential interactions with saturated lipids and its tendency to ‘fill gaps’, we show that cholesterol is poised for enrichment in the PM exoplasmic leaflet and confirm this prediction in live red blood cells using a novel FRET-based assay. The resulting lipid number asymmetries give rise to unique PM biophysical properties including differential permeability of the two bilayer leaflets and substantial differential stress. Thus, lipid number asymmetry of major membrane constituents presents a largely unexplored dimension of membrane organization.

**Thomas Weikl: “Excess area and elasticity of the Piezo protein-membrane nanodome” – Max Planck Institute of Colloids and Interfaces, Germany**

(Wednesday, October 1, Session 12, 17:00 - 17:20)

The mechanosensitive ion channels Piezo 1 and 2 induce a curved protein-membrane nanodome that flattens with increasing membrane tension  $\gamma$ . The tension-induced flattening of the nanodome is associated with Piezo activation and driven by the energy  $\gamma \Delta A$  where  $\Delta A$  is the excess area of the curved nanodome relative to its planar projected area. From extensive coarse-grained and atomistic simulations of membrane-embedded Piezo 1 and 2 proteins, we obtained an excess area  $\Delta A$  for the Piezo protein-membrane nanodome of about 40 nm<sup>2</sup> in tensionless membranes, and a half-maximal reduction of  $\Delta A$  at tension values of about 3 to 4 mN/m, which is within the range of experimentally determined values

for the half-maximal activation of Piezo 1. In line with recent experimental investigations of Piezo proteins in cell membranes and membrane vesicles, the membrane-embedded Piezo proteins adopt conformations in our simulations that are significantly less curved than the protein conformations in the detergent micelles of cryo-EM structures. An elasticity analysis of the nanodome shapes and protein conformations obtained from our simulations leads to an elastic model for Piezo activation that distinguishes the different energy components of the protein and the membrane in the tension-induced flattening of the nanodome. According to this model, the Piezo proteins resist flattening with a force constant of about 60 pN/nm.

## 6. Posters

The number (1 – 120) indicates the poster board where the poster will be displayed.

1. Tom F. Aarts, Jan Gumathi Bormin, Megan V. Farrell, Linde Meyaard, Michiel van der Vlist, and Kristina A. Ganzinger: ***Visualizing inhibitory signaling of immunoreceptor LAIR-1 at the plasma membrane***
2. Matilde Accorsi, Teimuraz Gochitashvili, Ivan Ivanov, Rumiana Dimova: ***Branching membranes and far-reaching nanotubes : a journey to lipid networks***
3. Uliana Afonina, Parashara Shamapras, Edward Lymann, Ulrike Endesfelder and James Saenz: ***Studying the membrane of the haloarchaeon Haloferax volcanii***
4. Mina Aleksanyan, Agustín Mangiarotti, Naresh Yandrapalli, Andrea Grafmüller, Fucsia Crea Vasil N. Georgiev, Antreas Vorkas, Macarena Siri, Tsu-Wang Sun, Stephan Block Ramona Schlesinger, Reinhard Lipowsky, Joachim Heberle, Rumiana Dimova: ***Photomanipulation of membrane properties, shape and transport***
5. Özgün Doğa Aşık, Katia Cosentino: ***Correlative structural and functional investigation of Gasdermin D oligomers at the plasma membrane***
6. Sakshi Barhai, Elias Sabri, Agustin Mangiarotti, Rumiana Dimova: ***Exploring the impact of protein condensates on membrane resilience and repair mechanisms***
7. Subhadip Basu, Oded Farago: ***Lattice simulation of mixture of proteins and lipids***
8. Elda Bauda, Andreas Boland and Robbie Loewith: ***Structural study of yeast plasma membrane domains using cryo FIB-ET***
9. Matilde Becheroni, Tsu-Wang Sun, Rumiana Dimova: ***Light-responsive asymmetric membranes***
10. Thomas Bissing, Laura Heinen: ***From liquid condensates to synthetic cells: Controlled membranization of coacervates***
11. Leonard de Boer, Arthur Champain, Cenk Gurdap, Luca Andronico, Erdinc Sezgin: ***The role of membrane fluidity in immune cell migration***
12. Andrea Eisenreichova, Jana Humpolickova, Bartosz Różycki, Evzen Boura: ***Lipid transport by the ORP8 protein***
13. Mert Bozoflu, Jan A. Stevens, Siewert J. Marrink: ***Modeling the minimal cell envelope***
14. Christoph Trenzinger and Mario Brameshuber: ***Addressing T-cell sensitivity under confined conditions***
15. Adrià Bravo Vidal, Weria Pezeshkian: ***Multi-body Fluctuation-Induced Forces Between Membrane Proteins: Insights from Mesoscale Simulations***
16. Gresy Bregu, L. Wong-Dilworth, S. Restel, C. Rodilla-Ramirez, and F. Bottanelli: ***A GTPase cascade drives the maturation of ERES into cis-Golgi cisternae***
17. Eric Bumüller, Lori van de Cauter, Kristina Ganzinger: ***Functionalizing GUVs with modular transmembrane peptides***
18. Bastian Bundschuh, Wibke Schumann, Jennifer Loschwitz, Birgit Strodel: ***The interplay between the dynamics, polymerization and membrane binding of guanylate-binding proteins***

19. Ece Büber, Marta Tena-Solsona, Job Boekhoven: ***Engineering Compartments for Synthetic Evolution***
20. Giorgia Carai, Luis Wong-Dilworth, Eleanor Fox, Francesca Bottanelli: ***Regulation of intracellular trafficking during establishment and maintenance of cell polarity in epithelial cells***
21. Yorgos Chatziantoniou, Matej Kanduč, H  l  ne Berthoumieux: ***Characterizing the mechanical properties of the mitochondrial crista membrane using MD simulations***
22. Ainhoa Collada, Antonio Cruz and Jes  s P  rez Gil: ***Transient exposure to hyaluronic acid restores the structure and performance of pulmonary surfactant membrane complexes***
23. Leo Corne, Apostolos Vagias, Bruno Dem  , Philipp Gutfreund, Nicolo Paracini, Judith Peters, Carlos M. Marques: ***Study of Polystyrene Presence in Membranes Using Neutron Diffraction and Reflectometry***
24. Tomasz Czerniak, James P. Saenz, Erdinc Sezgin: ***Towards a molecular understanding of RNA–Lipid interactions in biological systems***
25. Lara Dohmen, Hendrik K  hl, Claudia Steinem, Andreas Janshoff: ***Oligomerization Matters: Investigating Gephyrin–NL2 Interactions in an In-Vitro Synapse Model***
26. Joris Dommissie, Marileen Dogterom, Gijsje Koenderink: ***Establishing a robust FtsZ-based divisome for synthetic cell constriction***
27. Andrea Eisenreichova, Jana Humpolickova, Bartosz R  zycki, Evzen Boura, Alena Koukalova: ***Effects of biophysical membrane properties on recognition of phosphatidylserine, or phosphatidylinositol 4-phosphate by lipid biosensors LactC2, or P4M***
28. Megan V. Farrell, Linde Meyaard, Michiel van der Vlist, Kristina Ganzinger: ***Investigating inhibitory receptor activation criteria using DNA origami***
29. Carla Kirschbaum, Jack L. Bennett, Sophie A. S. Lawrence, Carol V. Robinson: ***Native mass spectrometry: a powerful technique for studying protein-lipid interactions***
30. Christopher J. Garvey: ***Lamellar diffraction as a probe of packing of lipids and small molecules into biomembranes***
31. Beatrice J. Geiger, Weria Pezeshkian: ***Membrane necks’ split personality: how the nuclear envelope responds to osmotic pressure***
32. Cenk O. Gurdap, Dunya Aydos, G  bor T  th, Simon C. Rapp, Maria Tsiokou, Tugce Ceker, Yagmur B. Urem, Pablo Carravilla, Leonard L. de Boer, Sarantis Giatrellis, John Cowgill, Patrick A. Sandoz, Cagla A. Cinar, Jaromir Mikes, Andrey S. Klymchenko, Frances Platt, Federico Pietrocola, Anna K. Simon, Bj  rn   nfelt, Jonas Fris  n, Petter Brodin, Ingela Lanekoff, Luca A. Andronico, Verda C. Bitirim, Erdinc Sezgin: ***High-throughput biophysical measurements of cells in health and disease***
33. Eduard Haar, Kevin Tanzusch, Lars Langemeyer, Changjiang You, Christian Ungermann: ***Reconstitution of membrane tethering and fusion machineries on supported membranes***
34. Marco Halbeisen, Svetozar Gravrilovic, Dr. Yusuf Qutbuddin, Prof. Dr. Petra Schwille: ***Membrane-Anchored Hydrogels for Extracellular Matrix Mimicry Using Click Chemistry***

35. Caroline Haupt, Dmitry A. Semchonok, Ambroise Desfosses, Farzad Hamdi, Sebastian Daum, Sarah Neudorf, Panos L. Kastritis, Milton T. Stubbs and Kirsten Bacia: ***Fluorescence and electron microscopy study to elucidate the structure of Arf1-coated membrane tubules***
36. Larissa Henke, Christoph von Ballmoos: ***Engineering Out-of-Equilibrium Synthetic Cells for Targeted Drug Release***
37. Andreas Heuer, S. Kellers, F. Keller: ***Mapping microscopic simulations on a lattice model: new perspectives on domain formation in membranes***
38. Azeline Hilaire, Antonio Stocco, Jean Farago, Fabrice Thalmann: ***Cycles of buckling in gel phase giant unilamellar vesicles***
39. Alena Ballekova, Andrea Eisenreichova, Bartosz Różycki, Evzen Boura, Jana Humpolickova: ***Coordination of transporter, cargo, and membrane properties during non-vesicular lipid transport***
40. Aleš Igljič, Raj Kumar Sadhu, Luka Mesarec, Nir S. Gov, Veronika Kralj-Igljič: ***On the role of curved proteins and cytoskeleton forces in encapsulation of nanoparticles***
41. Emmanuel Joseph, Pavan Kumar B.V.V.S., Nicolas Martin: ***Coacervate droplet wetting of membrane domains in giant unilamellar vesicles***
42. Aditi Kakkad, Ilia Korobko, Amnon Horovitz: ***How are protein folding and stability affected by encapsulation in the GroEL cavity?***
43. Michael Kaltenecker, Robert Ernst, Gustav Oberdorfer, Georg Krainer, Sandro Keller, Georg Pabst: ***Impact of differential membrane curvature stress on integral membrane protein-protein interactions***
44. Selcan Karaz, Dr. Gaurav Gardi: ***Emergent motility of self-organized particle-giant unilamellar vesicle assembly***
45. Manpreet Kaur, Fabio Lolicato, Walter Nickel: ***Plasma membrane transbilayer asymmetry of PI(4,5)P2 facilitates FGF2 membrane translocation***
46. Caroline König, Dmitry Shvarev, Jieqiong Gao, Eduard Haar, Nicole Susan, Kathrin Auffarth, Lars Langemeyer, Arne Moeller and Christian Ungermann: ***Vps41 functions as a molecular ruler for HOPS tethering complex-mediated membrane fusion***
47. Varvara Kramkova, James P Saenz: ***How many lipids are enough?***
48. Maximilian Krebs, Herre Jelger Risselada: ***Evolutionary Optimization of a bacterial toy model membrane***
49. Jana Kroll, Uljana Kravčenko, Mohsen Sadeghi, Christoph A. Diebolder, Lia Ivanov, Małgorzata Lubas, Thiemo Sprink, Magdalena Schacherl, Mikhail Kudryashev, Christian Rosenmund: ***Dynamic nanoscale architecture of synaptic vesicle fusion in mouse hippocampal neurons***
50. Minoru Kurisu, Masayuki Imai: ***Osmotic spawning vesicle***
51. Anna Łągowska, Emilia Krok, Maria Domanska, Piotr Setny, Lukasz Piatkowski, Hanna Orlikowska-Rzeznik: ***Steroid-specific modulation of lipid membranes: progesterone acts through a mechanism distinct from cholesterol***
52. Tunde Lawal, Christian Ungermann and Lars Langemeyer: ***The Rab7-like GTPase Ypt7 hypervariable domain functions in GEF recognition and effector binding***

53. Pia Lazki-Hagenbach, Nina Heindorf, Miriam Herfort, Francesca Bottanelli: ***Studying secretory granule biogenesis and maturation in mast cells – a novel approach***
54. Špela Lemež, Xevi Casadevall i Solvas: ***Building Membranes for Division: A Minimal Model for Artificial Cell Fission***
55. Aisha Levina, Mojca Mally, Jure Derganc: ***High-Throughput Microfluidic Quantification of Cellular Membrane Reservoirs***
56. Yehonatan Levy, Dganit Danino, Daniel Harries: ***Drunk Membranes: Phospholipid Mesophase Transitions in the Presence of Ethanol and Methanol***
57. Ludovic Gardré, Swen Helstroffer, Pierre Muller, Giovanna Fragneto, Arnaud Hemmerle, Léo Henry, Fabrice Thalmann, Thierry Charitat, Laurent Joly, and Claire Loison: ***Nanoseparated charged lipid layers***
58. Mehaiarii Louis, Seraphine Wegner: ***Light triggered transport across lipid membranes***
59. Vincent Louis, Eli van der Sluis, Marileen Dogterom, Gijsje Koenderink: ***Force sensing in artificial cells***
60. Sebastian Lütge, Jelger Risselada: ***Artificial evolution of sterol-like molecules for optimizing membrane bending stress***
61. Jacek Lyskawa, Emilia Krok, Lukasz Piatkowski: ***Fluorescence lifetime of selected probes as an effective indicator of cell membrane hydration***
62. Mojca Mally, Nika Žibrat, Gregor Anderluh, Jure Derganc: ***Single-vesicle study on NLP toxins affecting model plant-cell membranes: microfluidic method***
63. Titas Mandal, Bastian Albrecht, Shorouk Abdelwahed, Peggy Jones, Salvatore Chiantia: ***Molecular determinants of Hepatitis C virus assembly on lipid membranes***
64. Mia Mönnig, Christoph Pollmann, Jacob Piehler: ***Oncogenic mutations differentially dysregulate stoichiometry and structural organization of G-CSFR signaling complexes in the plasma membrane***
65. Stephanie Monson, Sahil Kulkarni, Ravi Radhakrishnan: ***Patchy but Powerful: Percolation physics governs nanoparticle recognition by the innate immune system***
66. Abdelbasset Yabrag, Naeem Ullah, Aftab Nadeem: ***Mechanisms of Lipid Membrane Perturbation by Bacterial Pore-Forming Toxins***
67. Chikim Nguyen, Kristina Ganzinger: ***Real-Time Mapping of CAR T Cell Signaling at Molecular Resolution***
68. Thuy An Nguyen, Petra Schwill: ***Micropatterned membranes direct Min protein pattern formation***
69. Ha Ngoc Anh Nguyen, James P. Saenz, Edward R. Lyman, Liam M. Sharp: ***Tuning membrane properties with a tunable living membrane***
70. Ilona Opiełka, Anita Hryniewicz-Jankowska, Aleksander Czogalla: ***Plasma membrane biophysical remodeling during epithelial-to-mesenchymal transition in breast cancer model***
71. Hanna Orlikowska-Rzeźnik, Emilia Krok, Maria Domanska, Piotr Setny, Anna Łągowska, Madhurima Chattopadhyay, Jan Versluis, Huib J. Bakker, and Lukasz Piatkowski: ***Interplay between cholesterol and interfacial water in membrane heterogeneity and fusion***

72. Julia Pabisz, Aleksander Czogalla, Piotr Hinc: ***Interplay between mTOR and ceramide-1-phosphate - a molecular perspective***
73. Sivadas Palliyil, Anna Jose, Shabin Neeruttikkal Chathangad, Harini SureshKumar, Sovan Lal Das, Mintu Porel, Sushabhan Sadhukhan & Anand Srivastava: ***Small molecule-based sequence-defined oligomers as membrane disrupting antibacterial agents : A biophysical study***
74. Aviya Perlman Illouz, Ruth Meyer, Sarah Koester, Gonen Golani, Raya Sorkin: ***Investigating the Role of Tension in Non-Homogeneous Membrane Organization***
75. Sergio Alejandro Poveda-Cuevas, Kateryna Lohachova, Bornha Markusic, Adriana Covarrubias-Pinto, Andreas Kern, Gerhard Hummer, Ivan Dikic, and Ramachandra M. Bhaskara: ***Modelling receptor clustering, protein—protein, and protein—lipid interactions in autophagic membranes***
76. Annemarie Quas, Clara Rickhoff, Sarita Klügel, Andreas Heuer: ***Properties of long-chain lipid enriched regions in biological membranes: Insights from MD simulations***
77. Yusuf Qutbuddin, Ainoa Guinart, Svetozar Gavrilovic, Marco Halbeisen, Ben Feringa, Petra Schwille: ***The Dynamics of Enlightened Lipid Membranes***
78. Neda Rahmani, Ranjit Gulvady, Patricia Bassereau, Johannes Ludger, John Hjorth Ipsen, and Weria Pezeshkian: ***Novel DNA-based force sensor to measure membrane-mediated forces between proteins***
79. Neetu Rajendran, Anna Gaugutz, Gerhard J. Schütz: ***A Closer Look at the Dynamics of T Cell Receptor Microclusters***
80. Arun K. Rathod, Dhruvil Chavda and Moutusi Manna: ***Phase Transition and Phase Separation in Realistic Thylakoid Lipid Membrane of Marine Algae in All-Atom Simulations***
81. Mehdi Ravandeh, Alena Starikova, Jan Steinkühler: ***Electrical stimulation of lipid nanotubes***
82. Aoife Redlich, Raiza Maia, Constantin Flommersfeld, Antreas Vorkas, Kirsten Hoffmann, Ramona Schlesinger, Joachim Heberle: ***Tuning photocycles via light-responsive lipid nanodiscs***
83. Clara Rickhoff, Azadeh Alavizargar, Andreas Heuer: ***Comparison of imidazole-based cholesterol-analogs with native cholesterol via MD-Simulations***
84. Maria Clara A. Oliveira and Karin A. Riske: ***Properties of bilayers containing three classes of glycolipids***
85. Naresh Yandrapalli, Reinhard Lipowsky, and Tom Robinson: ***Synthetic cells with asymmetric and phase separated lipid membranes display budding and division events***
86. Midhun Mohan Anila, Rikhia Ghosh, Bartosz Rozycki: ***Membrane curvature sensing by model biomolecular condensates***
87. Theresa Rudd and James Saenz: ***Low Temperature Adaptation of the Minimal Cell JCVI-syn3B***
88. Elias Sabri, Agustín Mangiarotti, Rumiana Dimova: ***Understanding the complex interplay between biomolecular condensate micropolarity and protein hydration : implications in membrane-condensate mutual remodelling***

89. Atreyee Saha, Prof. Seraphine Wegner: ***Communication in tertiary communities of synthetic cells***
90. Kita V. Schmidt, Eric D.B. Foley, Manish S. Kushwah, Philipp Kukura, Rumiana Dimova, Helge Ewers: ***Dynamic assembly of septin complexes on supported lipid bilayers by mass photometry***
91. Lukas Schrangl, Florian Kellner, René Platzer, José L. Toca-Herrera, Gerhard J. Schütz, Johannes B. Huppa, Janett Göhring: ***Single-molecule FRET measurements of TCR-exerted mechanical forces and bond lifetime estimation within the immunological synapse***
92. Fabian Schuhmann, Jan A. Stevens, Neda Rahmani, Isabell Lindahl, Chelsea M. Brown, Christopher Brasnett, Dimitrios Anastasiou, Adrià Bravo Vidal, Beatrice Geiger, Siewert J. Marrink, Weria Pezeshkian: ***TS2CG 2.0 - the membrane builder***
93. Isabel Berg, Jasmin Penker, Vanessa Jerschabeck, Luisa Voigt, Felix Götze, Dariush Hinderberger, Sandro Keller, Christian Schwieger: ***Adsorption of Lipid Bilayers to Monolayers: A New Triple Layer System for Studying Membrane Proteins***
94. Pietro Sillano, Timon Idema, Siewert-Jan Marrink: ***A novel Coarse-Grained Membrane Model for Mesoscale systems***
95. Martin Berg Klenow, Anne Sofie Busk Heitmann, Sabina Elmi, Ellen J. Pørtner, Weria Pezeshkian, Michael Lomholt, Jesper Nylandsted, Adam C. Simonsen: ***Dissecting the mechanism of plasma membrane repair: Importance of membrane curvature and area expansion***
96. Keerti Singh, Thomas J. Pucadyil: ***Dissecting membrane remodeling by a Dynamin-like protein from Nostoc punctiforme***
97. Russell Spencer, Marcus Müller: ***How Dynamin Constriction Drives Membrane Tube Fission***
98. M. Ravendeh, Alena Starikova, J. Steinkühler: ***Electrical stimulation of lipid nanotubes***
99. Leonhard J. Starke, Kasparas Petkevicius, Anna L. Duncan: ***Heads vs. tails: is bmp deficiency linked to atp-synthase c-ring accumulation in lysosomes?***
100. Florent Fessler, Vaibhav Sharma, Antonio Stocco: ***Active Janus Colloids interacting with Giant Lipid Vesicles***
101. Robert Strutt, Petra Dittrich: ***Engineering biomimetic membrane systems for PK/PD analysis***
102. Tsu-Wang Sun, Elias Sabri, Mina Aleksanyan, Naresh Yandrapalli, Antreas Vorkas, Philip Stabler, Ramona Schlesinger, Joachim Heberle, Rumiana Dimova: ***Exploring the role of photoswitchable lipids in membrane shape, phase behavior and protein gating***
103. Daxiao Sun, Lennart Kleinschmidt, Tom Borianne, Saemi Lee, Cécilie Martin-Lemaitre, Alf Honigmann: ***Epithelial interface compartmentalisation by scaffold condensation and receptor size***
104. Saša Svetina and Bojan Božič: ***Piezo1 shape dependence on membrane curvature is a sign of its multi-conformational nature***

105. Taras Sych, Selim Tanriverdi, Jan Schlegel, Florian Weber, Hanna Barriga, Miina Ojansiivu, Daniel Fuerth, Leo Hanke, Andre Görgens, Samir El Andaloussi, Birgit Plochberger, Herbert Stangl, Aman Russom, Dunya Aydos, Ceylan Verda Bitirim, Erdinc Sezgin: ***High-Throughput analysis of the content and properties of nano-sized bioparticles with single-particle profiler***
106. Kevin Tanzusch, Eduard Haar, Arthur Felker, Nadia Füllbrunn, Rainer Kurre, Changjiang You, Christian Ungermann, Jacob Piehler: ***Ultrastructural organization and dynamics of the lysosomal HOPS tethering complex on membranes***
107. Megi Tinev, Luka Kristanc, Gregor Gomišček, Bojan Božič: ***Passage of the channel-forming agent nystatin through ergosterol-containing lipid membranes***
108. Yagmur Balim Urem, Helge Ewers: ***Single-Particle Tracking with Fluorescent Proteins: A Quantitative Study of mStayGold and mScarlet3-H***
109. Bas van Bommel, Benno Kuroopka, Barbara Zieger, Hauke B. Werner and Helge Ewers: ***Isoform-Specific Roles of Septin 8 in Brain Cells and Membrane Trafficking***
110. Stijn van der Ham, Alexander Brown, Halim Kusumaatmaja, Hanumantha Rao Vutukuri: ***How particle morphology and deformability control lipid membrane wrapping***
111. Sifre van Teeffelen, Habiba Hassani, Léo Corne, Yann Bretonnière, Carlos M. Marques: ***Solvatochromic dyes to probe the properties of hydroperoxidized lipid membranes***
112. Marco P.A. van Tilburg, Siewert J. Marrink, Melanie Koenig, Fabian Grunewald: ***Shocker - A molecular dynamics protocol and tool for accelerating and analyzing the effects of osmotic shock***
113. Nikhil Walani, Anabel-Lise Le Roux, Pere Roca Cusachs, Marino Arroyo: ***A mechano-sensing mechanism controls plasma membrane shape homeostasis at the nanoscale: Mathematical Model***
114. Eike Wienbeucker, Mia Mönnig, Marvin Wortmann, Steffen T. Harms, Eleonora Di Zanni, Alessio Accardi, Jacob Piehler: ***Spatiotemporal dynamics of plasma membrane lipid scrambling and its implications for cytokine receptor activation***
115. Maximilian Winkler, Katharina Overhoff, Nikolas K. Teiwes, Mark Skamrahl, Thanh Tan Huynh Huu, Nico Benten, Andreas Janshoff, Claudia Steinem: ***Membrane surface viscosity and line tension of artificial and natural liquid-liquid phase-separated pore-spanning membranes***
116. Marvin Wortmann, Arthur Felker, Bingshati Sarkar, Eike Wienbeucker, Emma Leder, Jacob Piehler: ***Spatial diffusion dynamics in plasma membrane nanodomains***
117. Ping Xiao, Stefan Moning, Amit V Pandey, Christoph von Ballmoos: ***Formate-Fueled Self-Sustained GUVs platform for CYP450-Mediated Drug Metabolism***
118. Qingrong Zhang, Ana J. García-Sáez: ***Annexin A6 Orchestrates Membrane Remodeling via Dynamic Ring Formation and Compression***
119. Yifan Zhou, Meng Diao, Yaqiang Liu, Kangmin He, Xiao Yang and Xun Huang: ***PS synthesis reduction disturbs IP3R-mediated ER Ca<sup>2+</sup> homeostasis***
120. Xiaohong Zhuang: ***Biomolecular condensation drive autophagosome formation for plant heat tolerance***

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