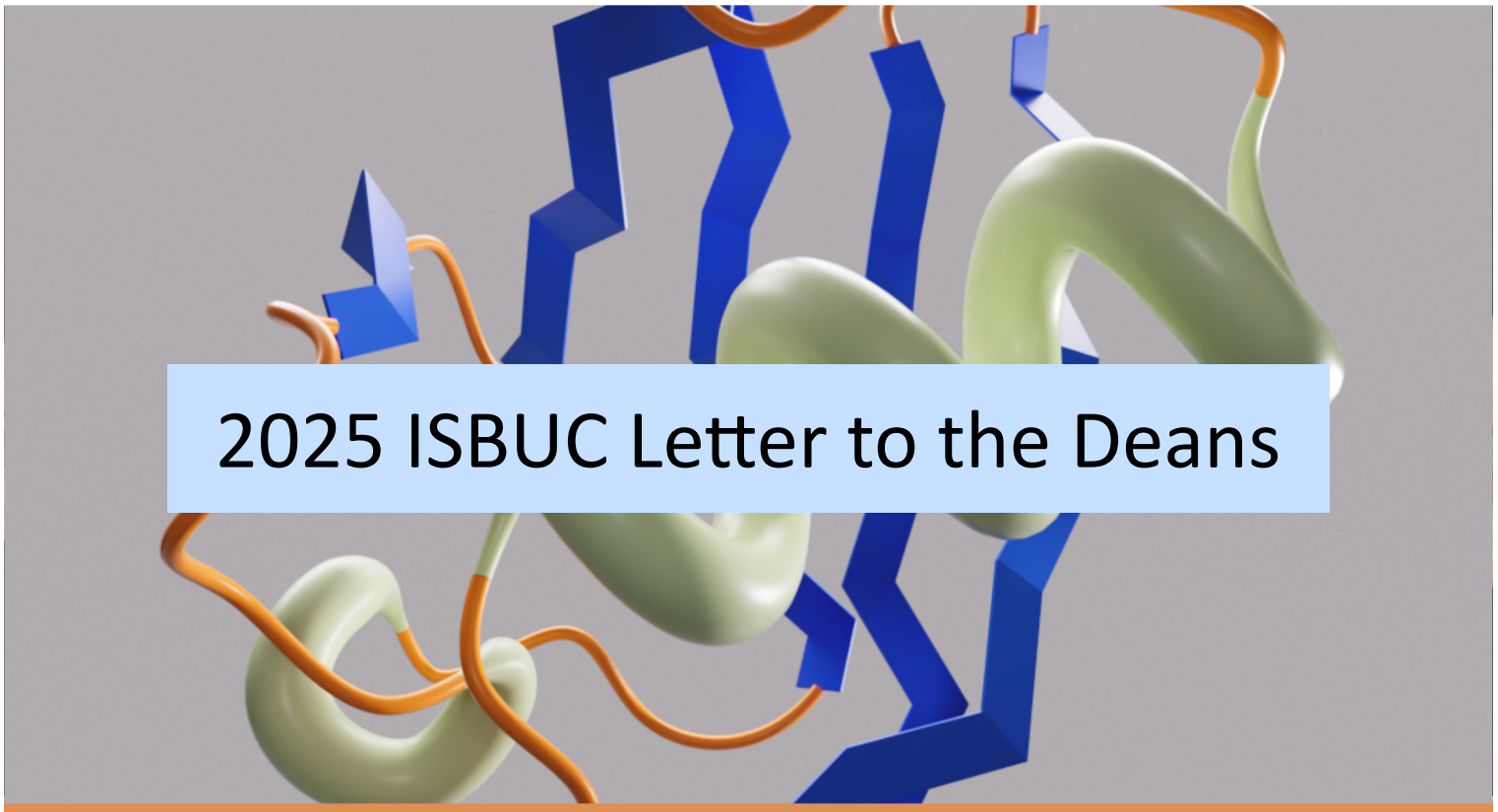
UNIVERSITY OF COPENHAGEN

INTEGRATIVE STRUCTURAL BIOLOGY CLUSTER



2025 ISBUC Letter to the Deans

Message from the ISBUC Steering Committee

In 2025, ISBUC announced itself as a leader within the Nordic structural biology landscape.

In the summer, we hosted the prestigious Chemical Solutions to Structural Biology symposium, organised in partnership with Professor Morten Meldal and the Department of Chemistry.

This symposium reflected all the best qualities of ISBUC. It brought together scientists from diverse disciplines pioneering new methods at the absolute forefront of scientific innovation. It dedicated significant time to networking, allowing new scientific collaborations to unfold. It shone a spotlight on the excellent science being done at UCPH by both young and senior scientists. A PhD course offered junior researchers the chance to learn from some of the world's most esteemed scientists. We leveraged the participation of editors from Nature, Nature Structural and Molecular Biology and Nature Methods, to organise one-on-one meetings with ISBUC scientists.

Praise for the symposium has been overwhelming, and we are now exploring a follow-up meeting which we hope to host in 2028 with a focus on Biophysical Solutions to Structural Biology.

In the winter, we established NordStruct, a collaborative network for structural biology across all five countries. NordStruct is supported by NordForsk via a research infrastructure hub grant and (sneak peek of the 2026 Letter to the Deans) we are extremely pleased to share that Novo Nordisk Foundation will provide further support.

The realisation of NordStruct follows four years of intensive partnership development between institutes, infrastructures and scientists, which has been driven by ISBUC. The initial grant from NordForsk includes funding opportunities for mobility, training and networking. These opportunities will have a significant impact on scientific excellence and collaboration across the Nordic region, with ISBUC placed firmly at the center. But our ambition for NordStruct goes far beyond the establishment of new funding opportunities.

Our aspiration is to create a thriving and engaged community for structural biology: forging new and meaningful relations between scientists and infrastructures across the Nordic region and creating the open, connected, creative and supportive spirit, which we benefit so much from here at UCPH. Achieving this will be challenging across such vast distances and varied disciplines and its realisation will require support and engagement abroad, but most importantly here at home: within ISBUC and from faculty at UCPH. We hope to count on all of you. NordStruct brings both opportunities and responsibilities for ISBUC. These will be managed by Chair Birthe B. Kragelund. As a result, Birthe will step down from the ISBUC Steering Committee and Claus Løland will take the helm as the ISBUC Chair. Birthe has played an instrumental role in both founding ISBUC and its ongoing success and we thank Birthe for the tremendous efforts she has made on behalf of the entire ISBUC community over the past nine years.

Putting together the ISBUC Letter to the Deans is always an inspiring process. In 2025, ISBUC scientists have continued to shine brightly, with an astonishing number of high-impact collaborative publications and new research projects.

These efforts are pushing forward break-through science within some of the most pressing areas within human health including virology, immunology, metabolism, microbial resistance, as well as drug discovery and delivery; further exciting science is having an impact within agriculture. Underpinning these breakthroughs, lies the development of new experimental approaches, nano-solutions, screening technologies, machine learning methods and quantum science.

It is this foundation of extraordinary science that allows ISBUC to take a leadership position within the Nordics and we are extremely honoured to be part of such an exciting scientific community.

Best regards,



Claus J. Løland
ISBUC Chair
Faculty of Health & Medical Sciences



Kresten Lindorff-Larsen
ISBUC Vice Chair
Faculty of Science



Karen Martinez
SCIENCE



Heloisa N. Bordallo
SCIENCE



Nikos Hatzakis
SCIENCE



Henriette E. Autzen
SUND



Céline Galvagnion-Büll
SUND

NordStruct: a new Nordic hub set to transform structural biology

There were some projects in 2025 that feel larger than a single grant or collaboration, and NordStruct is one of them. In 2025, an exciting new chapter for structural biology in the Nordic region began with support from NordForsk for the establishment of the NordStruct Research Infrastructure Hub for Structural Biology.

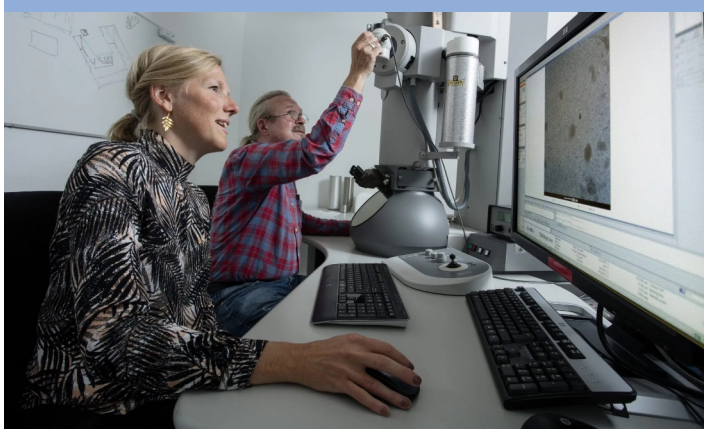
NordStruct

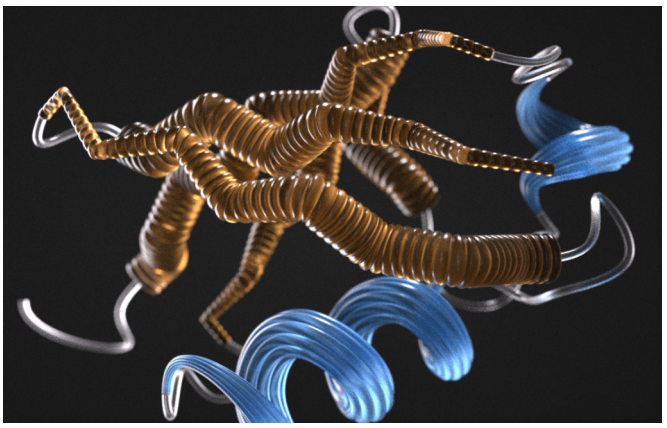
The initiative brings together an extraordinary network spanning 28 research institutions, more than 100 research infrastructures, and over 230 research groups across all five Nordic countries, creating one of the most comprehensive structural biology infrastructure networks anywhere in the world.

Although structural biology has undergone a remarkable technological revolution over recent decades and these technologies have transformed biological research, access to them has not been evenly distributed. Some institutions benefit from large infrastructure environments and established communities, while others operate with only a few groups and limited local resources. Therefore, ISBUC decided to create NordStruct, to address exactly this challenge.

The vision behind the initiative is not simply to connect instruments, but to connect people and communities. Through shared infrastructure access, coordinated training programs, methodological development, and stronger knowledge exchange, NordStruct will create a more connected and collaborative structural biology landscape across the Nordics.

The scale itself is one of the project's major strengths. No single university currently possesses the complete set of tools and expertise needed to fully exploit the possibilities of modern structural biology. By working together, the community gains access to a breadth that no individual institution could realistically build alone.

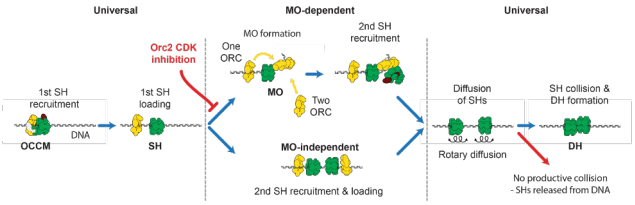




Training the next generation of researchers is also a major component of the initiative. Through PhD courses, thematic workshops, and mobility opportunities, junior scientists will gain access to methods and expertise far beyond what may exist in their local environments. NordStruct also establishes a network connecting infrastructure managers and technical experts across the region, allowing exchange of best practices and helping strengthen the long-term sustainability and development of advanced research facilities. The ambition is substantial: to lay the foundation for establishing the Nordic region as a globally leading environment for innovative structural biology research and training, not only during the funding period, but for many years afterward. For ISBUC, NordStruct represents a particularly exciting opportunity. We are investing significant effort into helping shape and strengthen this initiative and ensuring that our community can benefit fully from the collaborations, training activities, and scientific opportunities it creates. It is truly a unique opportunity for the Nordic structural biology, and it is difficult not to be excited about what will emerge when researchers, infrastructures, methods, and ideas are connected on this scale.

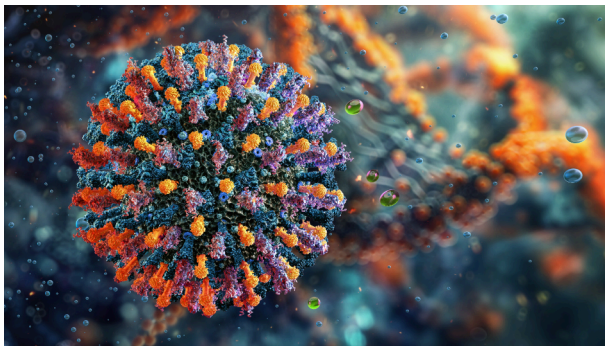


Thomas Miller reveals hidden flexibility in DNA replication control



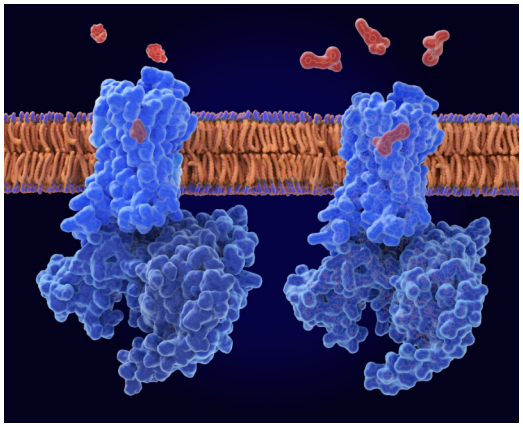
A study from Associate Professor Tom Miller (ICMM) and collaborators has been published in Nature Stuctural & Molecular Biology, addressing how DNA replication is regulated in budding yeast. The group showed how an intrinsically disordered region (IDR) in the Orc2 subunit of the origin recognition complex (ORC) plays a key role in initiating DNA replication. Specifically, they show that this region helps interact with the first loaded helicase complex (MCM), forming an intermediate step required the full replication machinery. This process was found to be tightly controlled by the cell cycle. The study demonstrates that cyclin-dependent kinase (CDK) can block replication initiation by phosphorylating this IDR, thereby preventing formation of the intermediate and ensuring DNA is only replicated once per cycle. Importantly, the work revealed plasticity in the mechanisms of MCM loading and showed that not all replication origins behave identically. Some “strong” origins, with high-affinity binding sites, can bypass this intermediate step and are less sensitive to CDK regulation, suggesting that cell cycle control mechanisms have influenced the evolution of replication origins in yeast.

A druggable ion channel identified in mumps virus



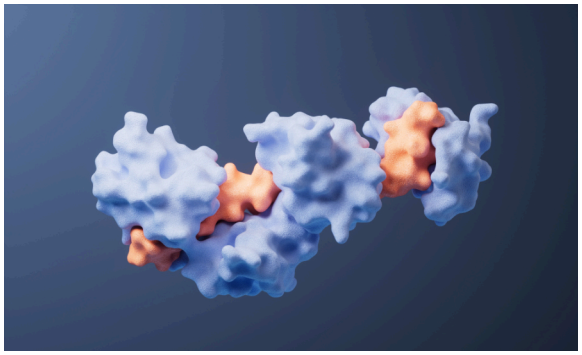
In a work led by PhD student Kira Devantier, Professor Mette Rosenkilde (BMI), Professor Birthe B. Kragelund (BIO) and coworkers have published a study in Science Advances identifying the small hydrophobic (SH) protein of mumps virus as a pentameric viroporin. Using biophysical data and structural modeling (HADDOCK), the study showed that the SH protein assembles into a five-unit membrane channel stabilized by its intracellular extended C-terminal region. Functional experiments demonstrate that SH acts as a chloride ion channel enabling transport across membranes. Importantly, this channel activity can be inhibited by the small molecule BIT225, highlighting SH as a potential antiviral drug target. Joint efforts from the groups of Birthe and Mette provided both structural and functional insights into a viral protein that was previously poorly understood, supporting broader efforts to target viroporins in antiviral therapy.

AI and massive virtual screening reveal new brain receptor drug candidates



Associate Professor Alexander Hauser (IFL) and collaborators have published a study in Nature Communications demonstrating how large-scale computational screening combined with high-resolution receptor structures can accelerate drug discovery. The work, led by first authors Israel Cabeza de Vaca, Boris Trapkov and Ling Shen, focused on GPR139, an orphan GPCR linked to neuropsychiatric disorders but still poorly understood biologically. Using structural information from the receptor, the team computationally screened 235 million compounds against the GPR139 binding site. Experimental testing of top-ranked candidates identified several new agonists, including compounds with nanomolar potency. Structure-guided optimization further improved activity, and cryo-electron microscopy structure confirmed the predicted receptor-ligand interactions. The study also evaluated whether AlphaFold could substitute for experimentally determined receptor structures in ligand discovery. The results showed that AI-based models currently have limited ability to accurately predict receptor-ligand interactions for understudied GPCRs.

Predicting protein condensates from sequence alone



Understanding how cells organize their molecular components remains one of the central challenges in biology. One mechanism increasingly recognized as critical for cellular organization is biomolecular phase separation, a process through which proteins and other biomolecules selectively concentrate into dynamic compartments without membrane boundaries, where these condensates play important roles in processes ranging from gene regulation and RNA metabolism to immune signaling. In a recent PNAS publication, Sören von Bülow from Professor Kresten Lindorff-Larsen's (BIO) group and collaborators developed and experimentally validated a machine learning model capable of predicting protein phase separation directly from amino-acid sequence. Phase separation is often driven by intrinsically disordered proteins and regions, whose flexible structures enable numerous weak interactions between molecules. However, predicting how strongly a specific sequence will undergo phase separation has remained a difficult task. To address this challenge, the research team combined coarse-grained molecular dynamics simulations with active learning to build a predictive framework capable of estimating key thermodynamic properties, including transfer free energies and saturation concentrations. The model was validated using existing experimental datasets alongside new measurements performed on six proteins. Applying the approach across the human proteome, the team analysed more than 27,000 intrinsically disordered regions and predicted that approximately 1,420 of these may undergo homotypic phase separation. Beyond prediction alone, the study also provided new insight into the molecular rules governing condensate formation, revealing how shifts between charge-driven and hydrophobic interactions influence the relationship between protein compaction and phase behaviour.

New model reveals how lipids drive Parkinson's protein aggregation

2025 was a standout year for Associate Professor Céline Galvagnion-Büll (ILF) with two major studies advancing understanding of how lipid interactions drive pathological protein aggregation in Parkinson's Disease.

Céline and collaborators have published a study in Proceedings of the National Academy of Sciences, presenting a quantitative model of protein aggregation linked to Parkinson's disease. The research focuses on alpha-synuclein, whose aggregation into amyloid fibrils is a defining feature of the disease. The study introduces a global kinetic model that captures how lipid membranes actively drive this aggregation process. The study showed that aggregation proceeds via a two-step primary nucleation mechanism, with lipids directly participating in both the formation and growth of fibrils, resulting in lipid-protein co-aggregates. What is more, the model also provides mechanistic insight into how small molecules can inhibit this process. The team demonstrated that squalamine reduces aggregation by specifically interfering with lipid-dependent nucleation, a critical early step. The study managed to establish a framework for design of therapeutics targeting protein aggregation, with direct relevance for Parkinson's disease and other neurodegenerative disorders.

In parallel, Galvagnion's group also published a study in Chemical Science showing that Ambroxol directly interferes with pathological α-synuclein-lipid interactions linked to Parkinson's Disease. The research demonstrates that Ambroxol not only affects lysosomal function through stabilization of glucocerebrosidase (GCase), but also directly inhibits early stages of alpha-synuclein aggregation. Specifically, the compound displaces



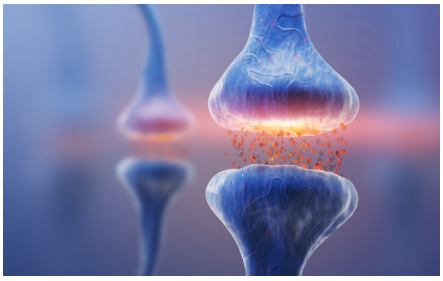
α-synuclein from negatively charged lipid membranes and prevents formation of early protein-lipid coaggregates involved in primary nucleation of amyloid fibrils. Because α-synuclein aggregation is a hallmark of several neurodegenerative disorders, including Parkinson's disease, multiple system atrophy, and dementia with Lewy bodies, the findings provide new mechanistic insight into how Ambroxol may exert therapeutic effects across multiple synucleinopathies.

Kristian Strømgaard advances peptide research across neuroscience, drug discovery, and metabolism

Professor Kristian Strømgaard's group (ILF) continued to expand peptide research in 2025, using polypeptide-based approaches to investigate and manipulate diverse biological systems.

One project introduced eSylites, small synthetic peptide-based probes for high-resolution imaging of excitatory synapses. By specifically targeting PSD-95, the probes enabled visualization of synaptic nanoscale organization and revealed that individual dendritic spines can contain distinct nanodomains enriched in PSD-95 or its homologues PSD-93 and SAP102.

A second study, led by Alexander Nielsen and Christian Bartling, addressed membrane permeability,



a major challenge in cyclic peptide drug development. Combining large-scale experimental screening with machine learning, the researchers identified design principles associated with cellular uptake. Cyclic peptides were more likely to enter cells when their molecular weight was below 800 Da, their polar surface area below 250 Å², or they contained fewer than six hydrogen-bond donors, providing a framework for designing peptide therapeutics with improved cellular permeability. The group also investigated naturally occurring polypeptides produced by the human gut microbiome. Two circulating peptides derived from Ruminococcus torques showed beneficial metabolic effects in preclinical models, including improved glucose tolerance, reduced fat mass, and increased expression of genes involved in thermogenesis and lipid metabolism. One peptide, RORDEP1, also affected hormones involved in appetite regulation and insulin signaling and improved hepatic glucose metabolism, highlighting its potential relevance for future therapies targeting obesity and metabolic disease.





Livestock bacteria may offer a new weapon against MRSA

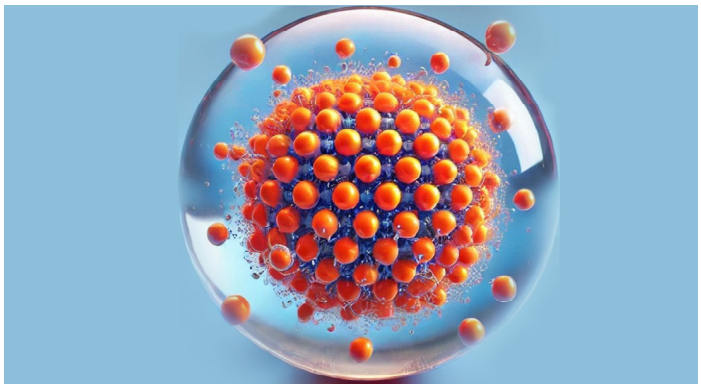
Professor Christian Adam Olsen (ILF) and postdoc Benjamin Svejdal Sereika-Bejder have demonstrated that signaling molecules produced by bacteria carried by livestock such as cows, goats, and horses can effectively treat infections caused by multi-resistant Staphylococcus aureus in an animal model. The study highlights the potential of these naturally occuring bacterial communication molecules as an alternative to conventional antibiotics in combating antibiotic-resistant infections, including MRSA. Researchers also investigated whether the bacteria could develop resistance to the treatment. In laboratory experiments, no resistance development was observed after 15 days of exposure, contrasting with the rapid resistance often seen for traditional antibiotics, suggesting a promising new strategy for addressing antibiotic resistance, although further validation in animal models and clinical systems will be required.

Thomas Hamelryck opens EURIPS Simbiochem workshop on physics-grounded machine learning

Professor Thomas Hamelryck (BIO/DIKU) delivered the opening keynote at the EURIPS Simbiochem workshop, which focused on bridging machine learning and physically grounded molecular simulation. The workshop addressed a key methodological gap in computational biology and chemistry where machine learning models have become highly effective across molecular sciences, but many approaches still rely on static structural representations and lack explicit physical constraints. In contrast, first-principles methods such as molecular dynamics provide a physically rigorous description of molecular systems but are computationally expensive and difficult to scale to large or complex systems. In order to address this gap, Simbiochem brought together researchers from machine learning, computational chemistry, biophysics, life sciences, and materials science with the aim of integrating scalable ML approaches with physically based simulation methods.

Microantibubbles could make medicines easier to take

Ph.D. student Charalampos Tsekeridis (NBI) has received a journal cover for his work on a novel encapsulation method for Ibuprofen, developed under the supervision of Associate Professor Heloisa Nunes Bordallo (NBI). The research introduces a Pickering-stabilized microantibubble system to encapsulate hydrophobic drugs. Using a solid-in-oil-in-water emulsion with hydrophobized silica particles, followed by freeze-drying, the team produced stable powder-form microantibubbles containing Ibuprofen. This approach addresses two key pharmaceutical challenges: taste masking, which is relevant for patient compliance, as well as enhanced solubility, which can improve drug absorption and reduce required dosage and associated side effects. The method represented a simple strategy for drug encapsulation, with ongoing work focused on further optimizing solubility by adjusting experimental parameters.



Nikos Hatzakis group publishes two AI-driven imaging frameworks in Nature journals

Professor Nikos Hatzakis (CHEM) and his group reported two methodological advances in 2025 with publications in Nature Methods and Nature Communications, both focused on applying machine learning to extract biological data from complex microscopy. In Nature Methods, the group introduced DeepSPT, which is a deep learning framework that rapidly interprets the intracellular movement patterns of molecules and identify their identity based exclusively on diffusion data alone. The tool allows for automated identification of biological processes and subcellular components, including events involved in viral infection and nucleic acid release, reducing analyses that previously required weeks to just seconds. In the paper published in Nature Communications, Hatzakis's group introduces SEMORE, a machine learning model designed to automate the analysis of super-resolution microscopy data. The tool combines density-based clustering with fingerprinting morphological structures to identify and quantify nanoscale assemblies. In this work, SEMORE enabled rapid and system-agnostic analysis, producing new insights into protein aggregation and allowing for the advances in diagnosing and treating complex diseases at the molecular level.

Henriette Autzen's group expands the structural biology toolbox for membrane proteins



Associate Professor Henriette Autzen's group continued to push the boundaries of membrane protein structural biology in 2025, with two studies highlighting new approaches for understanding membrane proteins in their native environments. One study has already been published, while a second was submitted in 2025.

Both studies address a common challenge of understanding membrane proteins while preserving the biological context that shapes their structure and function. Membrane proteins are among the most important classes of biomolecules in human health and disease, yet they remain among the most technically difficult to study.

In the first Nature Communications study, postdoctoral researcher Ciara Pugh and colleagues introduced MAASTY, a new copolymer that enables membrane proteins to be extracted directly from cellular membranes into native nanodiscs while preserving their natural lipid environment. The method supports high-resolution cryo-EM studies and proved effective across a broad range of mammalian membrane proteins, providing a powerful new platform for studying these challenging biological systems under near-native conditions. The second study focused on the human membrane transporter NHE6, an endosomal sodium/proton exchanger that plays a critical role in regulating intracellular pH and cellular trafficking processes in neurons. Mutations in NHE6 have been linked to severe neurological disorders, including Christianson syndrome, but the molecular basis of its function has remained poorly understood. By using single-particle cryo-electron microscopy, the researchers determined the first atomic structure of human NHE6 revealing details about ion

binding and transport regulation. Additionally, they performed functional studies in diverse lipid environments to elucidate the substrate and lipid preference. Their work revealed that NHE6 is capable of transporting a wide range of monovalent cations, including sodium and potassium, with a kinetic preference for potassium. Furthermore, the transport activity was regulated by specific lipids surrounding the protein and binding of lipid molecules might also regulate access to the ion-binding site. Together with complementary biophysical approaches, the researchers were able to generate an integrative structural model of the full-length protein. By providing the first detailed structural and functional characterization of human NHE6 function, the study offered new insight into how disease-associated mutations may disrupt transporter activity.

Structural biology provides new insights into autoimmunity and therapeutic antibodies







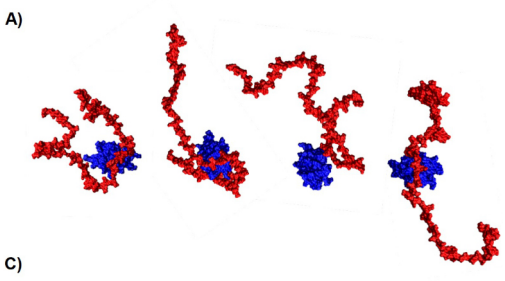
2025 has been a significant year for Kasper Rand's research group, with two publications highlighting how molecular structure and dynamics influence immune function.

The first study, published in Nature Communications and led by Susanne Ständer, Cyril Reboul, and Sarah Le, investigated why the enzyme GAD65, but not the closely related GAD67, is a major autoantigen in diseases such as type 1 diabetes. Using hydrogen-deuterium exchange mass spectrometry (HDX-MS), cryo-electron microscopy, X-ray crystallography, and computational modelling, the researchers showed that the two proteins differ primarily in their conformational dynamics rather than their amino-acid sequences. In particular, structural flexibility in GAD65 facilitates antibody recognition, including an interaction involving the 260PEVKEK265 motif and a long antibody CDRH3 loop bridging the GAD65 dimer. These findings provide a mechanistic explanation for GAD65 autoantigenicity. The group's second paper, published in Communications Biology with Assistant Professor Esben Trabjerg (ILF) as first author, examined the long circulation half-life of therapeutic IgG antibodies. IgG persistence is largely enabled by pH-dependent recycling through the neonatal Fc receptor (FcRn), traditionally thought to interact only with the antibody Fc region. Using HDX-MS and cross-linking mass spectrometry (XL-MS), the researchers confirmed Fc-mediated binding but also identified previously unrecognized interactions between the Fab regions and the α3-domain of FcRn. These findings may help explain why antibodies with identical Fc domains can nevertheless have different circulation half-lives.

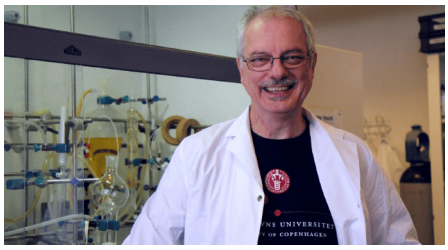
The group has also expanded its structural biology expertise with the arrival of Victor Yin (ILF) as a tenure-track Assistant Professor. Yin specializes in native mass spectrometry, which enables characterization of protein assemblies under near-native conditions.

Nature Communications study expands how dynamic proteins interact

Led by former Postdoc Katrine Bugge, Professor Birthe B. Kragelund (BIO) and collaborators have published a paper in Nature Communications examining how intrinsically disordered proteins (IDPs) interact with folded proteins while remaining fully disordered. The study demonstrated that the negatively charged IDP prothymosin α can bind to the positively charged globular domain of histone H1.0 through electrostatic interactions alone, without adopting a fixed structure or stable residue-specific contacts. Despite forming a functional complex, the IDP retains its dynamic and disordered nature throughout binding. By analyzing 25 charge variants of the folded domain, the researchers further demonstrated that both overall charge and charge distribution influence binding affinity, revealing a degree of selectivity in these highly dynamic and highly charged complexes. The findings significantly expand current understanding of protein interaction mechanisms and suggest that similar charge-driven, fully disordered complexes may be widespread in biology.



Morten Meldal's research continues to translate click chemistry into biomedical discovery



Professor Morten Meldal (CHEM) continues to apply click chemistry across chemistry and biomedicine, with notable studies in intracellular delivery and cancer biology.

One study addressed the challenge of transporting large biomolecules across cell membranes. Meldal and collaborators investigated cell-penetrating peptides (CPPs) and proposed that hydrophobic modifications in β-turn regions of cyclic CPPs could improve membrane permeability. By using a library of linear and click-cyclized peptides analyzed by flow cytometry and spinning-disk confocal microscopy, the researchers identified cyclic cell-penetrating peptide 15 (cCPP 15) as a particularly effective candidate. When linked to eGFP, cCPP 15 successfully transported the protein into MCF-7 and HeLa cells, demonstrating its potential for intracellular delivery of large biomolecular cargo. A second study examined the anticancer mechanism of parthenolide, a natural compound whose effects during cell division have remained unclear. Combining click chemistry, quantitative mass spectrometry, and cell biology, the researchers showed that parthenolide does not primarily act directly on microtubules, as previously proposed. Instead, it targets the kinetochore protein ZNF207, also known as BUGZ, which is required for proper chromosome organization during mitosis. Disruption of this protein impaired chromosome alignment at the spindle equator, revealing a previously unrecognized mechanism underlying parthenolide's anticancer activity.

New insights from neutron science: from water interfaces to bacterial genome

In 2025, Associate Professor Heloisa Nunes Bordallo (NBI) co-authored studies demonstrating how neutron-based methods can provide new insights into both bacterial genome organization and interface water dynamics. One study investigated Hfq, a nucleoid-associated protein involved in bacterial chromosome organization. Using transmission electron microscopy, neutron scattering, mutagenesis, and molecular modeling, the researchers identified an amyloid-like module in bridging and compacting six DNA strands. The findings showed that this structure contributes directly to chromosome organization and gene regulation, representing the first reported example of an amyloid with DNA-bridging functionality and expanding the biological roles attributed to amyloids beyond their association with disease. A second study used neutron spectroscopy to examine water behavior at silica particle interfaces in Pickering systems. Hydrophilic silica promoted a Wenzel-like wetting state with greater solid-water contact and reduced water mobility, whereas hydrophobic particles produced a Cassie-Baxter-like state with trapped air pockets and more bulk-like water dynamics. The work demonstrated for the first time that neutron spectroscopy can determine the wetting states of interfacially adsorbed Pickering particles in situ, providing a new approach for studying nanoscale hydration and colloidal interfaces.

Amelie Stein joins the new KIDnEx2 research project

Associate Professor Amelie Stein (BIO) has joined the KIDnEx2 research team, a 2025–2028 initiative focused on developing new drug-discovery strategies for kidney-related diseases.

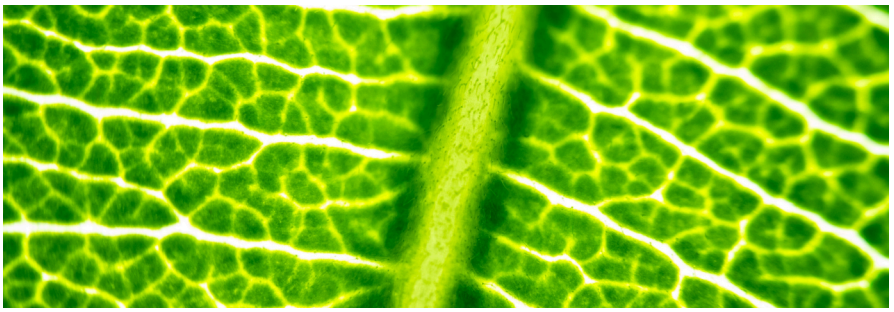
The project uses an inverse drug discovery approach based on electrophilic scout fragments to map the ligandable proteome of the kidney and identify previously uncharacterized protein targets relevant to cardiorenal and metabolic disease. By combining proteomics, computational biology, and in vitro models, the consortium will investigate proteins involved in podocyte function and metabolic regulation while developing a scalable discovery pipeline with potential applications beyond kidney disease. KIDnEx2 is organized through the Open Discovery Innovation Network (ODIN) at Aarhus University, supported by the Novo Nordisk Foundation. ODIN promotes precompetitive academic-industry collaboration with open sharing of data and methods.



Industrial partners include AstraZeneca, Danish software company Grit42, and Gubra, a Danish CRO and biotech company specializing in preclinical research and peptide-based drug discovery in metabolic and fibrotic diseases.

New insights into photosynthetic membrane dynamics and structural biology education

In 2025, Associate Professor Jacob J.K. Kirkensgaard (FOOD/NBI) contributed to both fundamental plant science and scientific infrastructure development, combining research output with efforts to broaden access to advanced structural biology methods.



A major research contribution, published in New Phytologist in collaboration with Warsaw University, uncovered a previously unrecognized regulatory mechanism in plant photosynthesis. The study investigated how thylakoid membranes respond structurally to transitions between dark and light conditions in Arabidopsis thaliana and Ficus elastica. Using a combination of transmission electron microscopy, confocal microscopy with 3D modeling, small-angle neutron scattering, and spectroscopic analyses, the researchers resolved long-standing contradictions in the literature regarding whether thylakoid membranes expand or contract under illumination. A meta-analysis of prior studies further supported experimental findings

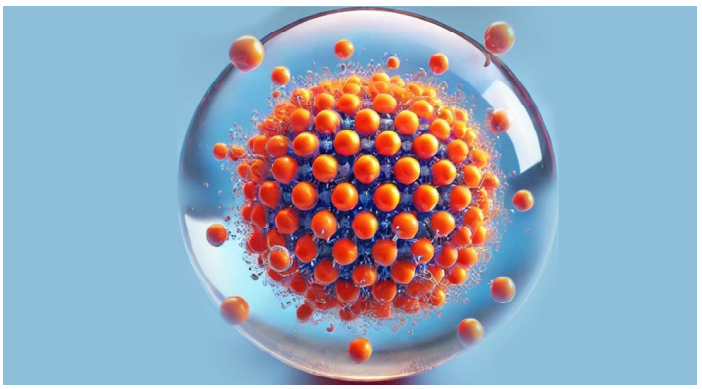
The work identified a three-phase structural response: an initial membrane shrinkage, followed by expansion, and finally relaxation toward a dark-state equilibrium. This dynamic sequence was shown to have functional significance, with the early shrinkage phase modulating the balance between cyclic and linear electron transport to provide rapid photoprotection. The results also demonstrated that growth conditions influence response kinetics, with plants adapted to constant light showing faster structural adjustments than those grown under glasshouse conditions.

In parallel, Kirkensgaard has also contributed to advancing scientific accessibility in structural biology.

Together with colleagues Associate Professor Martin C. Pedersen (NBI) and Assistant Professor Andreas H. Larsen (NBI), he has helped develop SAStutorials.org, a community-driven learning platform designed to support the analysis of small-angle X-ray and neutron scattering (SAXS/SANS) SAXS and SANS are widely used techniques for probing the structure of proteins, lipids, and complex soft-matter systems in situ, but data analysis often represents a significant barrier for both new and experienced users. The platform addresses this bottleneck and provides structured educational resources and practical guidance, and now serves more than 10,000 users annually.

Microantibubbles could make medicines easier to take

Ph.D. student Charalampos Tsekeridis (NBI) has received a journal cover for his work on a novel encapsulation method for Ibuprofen, developed under the supervision of Associate Professor Heloisa Nunes Bordallo (NBI). The research introduces a Pickering-stabilized microantibubble system to encapsulate hydrophobic drugs. Using a solid-in-oil-in-water emulsion with hydrophobized silica particles, followed by freeze-drying, the team produced stable powder-form microantibubbles containing Ibuprofen. This approach addresses two key pharmaceutical challenges: taste masking, which is relevant for patient compliance, as well as enhanced solubility, which can improve drug absorption and reduce required dosage and associated side effects. The method represented a simple strategy for drug encapsulation, with ongoing work focused on further optimizing solubility by adjusting experimental parameters.



GlycoScytale - Leveraging evolution to decipher the third language of life



A new research initiative led by Professor Thomas Hamelryck (BIO/DIKU) with Hiren Jitendra Joshi (ICMM) as co-principal investigator, aims to advance understanding of the so-called “third language of life”: complex carbohydrates on cell surfaces. The project has received 6 mil DKK in 2025 from the Independent Research Fund Denmark under the Technology and Production programme and represents the effort to bridge evolutionary biology and computational modelling to decode one of the least understood layers of biological information. The project focuses on glycan biology, where dense and structurally diverse sugar chains are present on all cell surfaces and encode biological information. These glycans are interpreted by sugar-binding proteins, that are often referred to as “readers” thattranslate glycan patterns into downstream biological signals. The central goal of the project is to uncover how such reader proteins evolve specificity for particular sugar structures. To achieve this, the team will combine evolutionary protein sequence analysis with machine learning methods and experimental validation, to systematically identify and characterize glycan-binding proteins. A key objective of the work is not only to understand natural protein-glycan recognition mechanisms, but also to use this knowledge to design new synthetic “readers” capable of decoding glycan information in controlled ways.

Leila Lo Leggio secures three grants supporting polysaccharide research

Associate Professor Leila Lo Leggio (CHEM) has secured three new research grants in 2025, strengthening her group's polysaccharide active enzymes research across applications ranging from agriculture to biotechnology and drug development. The largest of the awards is a DKK 6.2 million grant from the Independent Research Fund Denmark (DFF) for the project HIPPO: InHIbitors of Plant Pathogen’s Lytic Polysaccharide Mono Oxygenases. The HIPPO project focuses on lytic polysaccharide monooxygenases, enzymes used by plant pathogens to degrade structural polysaccharides in plant cell walls during infection. Because these enzymes enhance the ability of pathogens to invade plant tissue, they are considered important virulence factors and represent potential targets for new crop protection strategies. The project aims to develop inhibitors that interfere with these degradation mechanisms, with the broader goal of reducing agricultural losses and supporting more sustainable approaches to crop protection. The work brings together collaborators from Denmark, France, and Japan and combines expertise in chemistry, structural biology, and enzymology.

In addition, Lo Leggio was awarded a DFF Technology and Production Sciences grant as principal investigator for the project “Prodrug production through enzymatic glycosylation” (2025-2029, DKK 3.2 million). The project will investigate how enzymatic glycosylation can be used to generate modified drug molecules with improved properties and new therapeutic potential. What is more, Leila also received a Novo Nordisk Foundation project grant for “Time-resolved studies of the Lytic Polysaccharide MonoOxygenase reactions” (2025-2027, DKK 3 million). This project will examine the reaction mechanisms of LPMOs in greater detail by capturing the dynamic processes underlying enzyme activity.



Jacob Kirkensgaard secures NNF PREPARE grant



A new Novo Nordisk Foundation PREPARE grant has been awarded to a collaborative team at DTU and the University of Copenhagen, including Associate Professor Jacob J.K. Kirkensgaard (FOOD/NBI). The project aims to develop advanced educational resources that prepare students for experimental work with neutrons at large-scale facilities, in particular the European Spallation Source. The initiative focuses on strengthening conceptual understanding and practical readiness for neutron-based experiments, which become increasingly important in materials and soft-matter research.

New NNF grant supports alternative strategy against MRSA infections



Professor Christian Adam Olsen (ILF) has received significant support for two research initiatives focused on understanding and manipulating bacterial communication systems, with applications ranging from antibiotic resistance to gut microbiota biology. In 2025 Olsen was awarded a DKK 6.5 million collaborative grant through the Novo Nordisk Foundation Infectious Disease Catalyst program for the project "Targeting the accessory gene regulator (agr) System in Staphylococci as Alternative to Using Antibiotics." The project is carried out in collaboration with Professor Tom Muir at Princeton University and also includes ISBUC member Associate Professor Joseph Rogers (ILF). The project focuses on methicillin-resistant Staphylococcus aureus (MRSA), a major challenge in global healthcare due to its resistance to multipleantibiotics. Rather than directly targeting bacterial survival, the researchers aim to disrupt bacterial communication pathways that control virulence. By using protein engineering approaches, the team aims to develop novel cyclic peptide molecules designed to gene regulator (agr) system, a signaling network that enables bacteria to coordinate collective behavior through chemical communication. The Olsen laboratory will contribute expertise in the discovery, synthesis, and evaluation of cyclopeptide inhibitors, while the Princeton team will investigate their molecular mechanisms using biochemical model systems. In parallel, Olsen also received a Fulbright Scholar Award supporting a sabbatical at Scripps Research in California. During his stay, he is investigating bacterial communication mechanisms involving the secretion and sensing of peptides within the gut microbiota. This work aims to improve our understanding of how microbial communities communicate and influence host biology. In the longer term, insights into these signaling pathways may help identify strategies for modulating gut microbial communities toward healthier states and could open new therapeutic possibilities for microbiome-related diseases.

Stephan Pless and Joseph Rogers receive DFF Grant for therapeutic miniprotein design

Professor Stephan Pless (ILF) and Associate Professor Joseph Rogers (ILF) have received a grant from Independent Research Fund Denmark for a joint project on optimization of de novo designed miniproteins for therapeutic applications.

The project focuses on engineered miniprotein binders targeting Acid-sensing ion channel 1a (ASIC1a). While computationally designed miniproteins can achieve highly specific and potent protein binding, many current approaches lack systematic optimization for stability, affinity, and therapeutic performance. To address this, the researchers will combine computational protein diversification, mRNA display-guided mutational scanning, incorporation of canonical and non-canonical amino acids, and peptide cyclisation strategies to improve binder functionality and robustness. The project will support two postdoctoral researchers and aims



to establish a broadly applicable platform for developing optimized protein binders for mechanistic studies, biotechnology, and future therapeutic applications.

Joseph Rogers awarded Hallas-Møller Grant for peptide drug discovery

Associate Professor Joseph Rogers (ILF) has received a Novo Nordisk Foundation Hallas-Møller Ascending Investigator grant of DKK 11.4 million for the project "Breaking the Barrier: Engaging Intracellular Biology with New Macrocycle Chemistry." The five-year project addresses a major challenge in peptide therapeutics: developing molecules that not only bind strongly to disease-related proteins, but can also efficiently enter cells. While cyclic peptides are highly effective at targeting proteins that are difficult to reach with conventional small-molecule drugs, their limited cellular uptake has restricted broader therapeutic use. Rogers' group aims to overcome this by designing new macrocyclic peptide chemistries inspired by naturally occurring cyclic peptides with favorable cell-entry properties. The project will combine advanced synthetic and screening technologies capable of generating and testing extremely large molecular libraries to identify candidates with both strong binding and intracellular activity. The work has potential applications in both fundamental biology and the development of future therapeutics targeting previously inaccessible intracellular proteins.

Jannick Prentø awarded Lundbeck Experiment Grant for BBB research

Associate Professor Jannick Prentø (BMI) has received a Lundbeck Foundation Experiment grant (starting 2025) for a project aimed at resolving the molecular architecture of the blood-brain barrier. The project, "High-Resolution Blood-Brain-Barrier Structures by Claudin-Occludin Integration into Large Nanodiscs" focuses on the tight junction proteins claudin and occludin, which are central to BBB integrity and selective permeability. Using cryo-electron microscopy (cryo-EM) combined with large nanodisc membrane mimetics, the research aims to generate high-resolution structural models of these proteins in a native-like lipid environment. This approach is expected to provide mechanistic insight into BBB function and support BBB-targeted drug discovery, including strategies to enable therapeutics to cross into the central nervous system. What is more, the platform may also be adaptable to other tissues by incorporating different claudin isoforms, extending its relevance beyond the CNS. In 2025, Jannick was also awarded a DKK 6 million Lundbeck Ascending Investigator grant for the project "Building Cryo-EM High-Resolution Models of Claudin and Occludin CNS Assemblies," beginning in September 2026. The grant supports an ambitious effort to improve molecular understanding of the structural components that form the BBB. Despite tight junction barrier biological and clinical importance, many of the details underlying their organization and function remain poorly understood. Therefore, Prentø's project aims to address this challenge by generating high-resolution structural models of several key tight-junction proteins, including Claudins 1, 2, 3, 5, and 11, together with Occludin. Using cryo-electron microscopy and oligomeric nanodisc assemblies, the research will investigate how these proteins assemble and function within central nervous system barriers.



The resulting structural information is expected to provide a foundation for more rational development of therapeutics targeting the BBB and related systems. Beyond fundamental biological insight, the work also has broader translational potential. Detailed structural models may enable future identification of molecules that selectively bind tight-junction assemblies using computational design methods and screening approaches such as phage display.

DKK 40M funding boost for Kresten Lindorff-Larsen's research in IDPs and quantum methods



Professor Kresten Lindorff-Larsen (BIO) was part of two teams that received major grants from the Novo Nordisk Foundation supporting the group's work at the interface of molecular biophysics, cell biology and emerging quantum technologies. The first award is a DKK 20 million Data Science Collaborative grant, shared with Rasmus Hartmann-Petersen (BIO) and international collaborators, for the project «REWIRE: Reading, Writing and Interpreting the Rules of IDP Evolution». REWIRE will aim to uncover the underlying "rules" that govern IDP sequence-function relationships by combining molecular simulations, machine learning and biophysics. The goal is to develop predictive and generative models that can both interpret natural IDP evolution and design new functional sequences, thereby engineerig IDPs.

The project, FreeQuantum, focuses on developing quantum computing approaches for molecular interaction problems relevant to biology and chemistry. The core challenge addressed by FreeQuantum is the accurate and scalable calculation of molecular interactions, for example, for protein-ligand interactions. The goal is to develop a pipeline to integrate quantum computing quantum chemistry, molecular mechanics and machine learning to model complex systems across length- and timescales.

New funding supports Heloisa Bordallo's research in drug delivery and environmental analysis

Associate Professor Heloisa Nunes Bordallo (NBI) has received support for two new research initiatives in 2025, strengthening activities across both biomedical and environmental research.

One of the funded projects is "Nano Warriors: TCZ Takes Flight to Fight Inflammation," supported through a HALRIC grant and carried out in collaboration with Rasmus Hartmann-Petersen (BIO) and international partners. The project brings together researchers from MAX IV Laboratory, the European Spallation Source, the University of Copenhagen, and Photothermal Spectroscopy Corp. The initiative focuses on a newly developed bio-nanoparticle platform for delivery of the therapeutic antibody Tocilizumab (TCZ), which is used in anti-inflammatory treatments

The researchers aim to investigate the structural and dynamic interactions between nanoparticles and antibodies in order to better understand how these systems behave and function. This work aims to contribute to the development of improved targeted drug delivery strategies and more effective treatments for inflammatory diseases.

In parallel, Heloisa also has received a grant from the Carlsberg Foundation to upgrade infrared spectroscopy capabilities through a new FTIR system. The project focuses on analyzing gases released during thermal decomposition of soil organic matter (plant and animal residues) to assess environmental pollution. By examining infrared spectra, the research quantifies relative concentrations of low molecular weight gases,



including water, carbon dioxide, carbon monoxide, and ammonia, which serve as proxies for ecosystem contamination levels. The upgraded FTIR system is expected to provide higher-resolution and more sensitive measurements, enabling improved characterization of soil health and more precise identification of pollution signatures across terrestrial ecosystems.

Claus Løland receives Lundbeck Foundation Fellowship and NNF Distinguished Investigator for dopamine transport research

Professor Claus Juul Løland (IN) continues to advance understanding of the molecular mechanisms underlying neurotransmitter signaling in the brain through a combination of structural biology, biophysical pharmacology, and protein engineering. His work focuses on membrane transporters that regulate dopamine and serotonin signaling and serve as central targets for psychiatric drugs and addictive substances.

Claus Løland has received two major grants this year. With an LF Professorship award of 20 M DKK, he is leading a project which aims to reveal that the human dopamine transporter (hDAT) not only transports dopamine but also mediates central signaling and regulatory roles within the neuron.

Structures of the signaling complexes will be solved by cryo-electron microscopy. With the NNF Distinguished Investigator grant of 11.4 M DKK, the Løland-group will investigate the structure and dynamic function of the hDAT, as a key regulator of dopamine homeostasis and the primary target of stimulants such as cocaine and amphetamine. The project combines cryo-electron microscopy with protein engineering to characterize how hDAT binds different compounds and shifts between functional states during transport. A central component in both projects involves engineering of a fluorescent hDAT using genetic code expansion to insert non-canonical amino acids, capable of reporting real-time conformational changes, allowing the group to integrate structural and dynamic



information to better understand dopamine signalling, addiction mechanisms, and therapeutic targeting. In parallel, headed by post doc Iris Kalenderoglou, the Løland-group published a structural study in Nature Communications of the serotonin transporter (SERT) and the antidepressant Vilazodone. Using cryo-electron microscopy and advanced pharmacology, they demonstrated that vilazodone binds simultaneously to SERT's primary serotonin-binding site as well as an allosteric site, revealing an unusual dual binding mode which could explain vilazodone's clinically distinct properties.

Céline Galvagnion-Büll Receives Major Grants for Neurodegeneration Research

Céline Galvagnion-Büll has been awarded both a Novo Nordisk Foundation Hallas-Møller Emerging Investigator Grant and funding for a Marie Skłodowska-Curie Actions (MSCA) Doctoral Network.

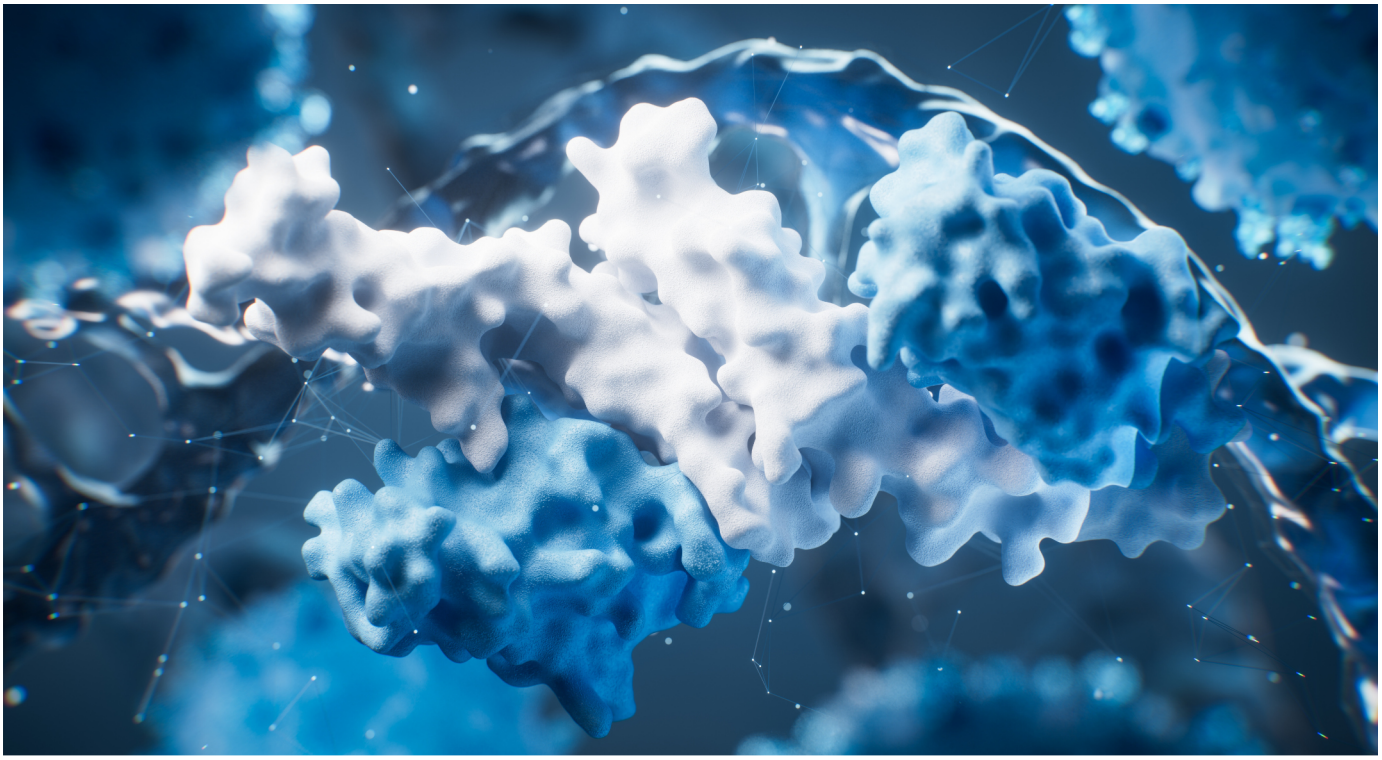
The Hallas-Møller grant supports the project “Reverting Brain Lipid Changes Associated with Parkinson’s Disease Pathology in Patients’ Neuronal Cells” with funding of DKK 11.4 million. The research aims toidentify strategies that reverse disease-associated lipid alterations in neuronal cells and reduce pathological protein aggregation linked to Parkinson's Disease. The project will investigate modulation of lipid synthesis and processing pathways as a potential therapeutic approach.

In parallel, Céline and international collaborators received MSCA Doctoral Network funding for theproject "LIPAGG – From Biophysical Chemistry to Cell Biology: Deciphering the Role of Lipids in theToxicity and Spreading of Protein Aggregation". The program will train 15 doctoral researchers, including three at the Galvagnion lab. The consortium combines expertise in biophysics, structural biology, peptide chemistry, and cell biology to study how lipid-protein interactions influence aggregation processes in Alzheimer's disease, Parkinson's Disease, and Type 2 Diabetes. The work is expected to improve understanding of amyloid-related diseases and support future diagnostic and therapeutic development.”

Kaare Teilum receives Carlsberg Foundation Grant for protein dynamics symposium

The symposium will bring together five internationally recognized researchers and seven local experts to discuss recent advances in understanding how protein structures move and change shape at the atomic level. Such conformational dynamics are essential for protein function and play key roles in processes ranging from enzymatic activity to molecular recognition and signaling. By highlighting new experimental and computational approaches for studying protein motion, the event aims to stimulate interdisciplinary discussion, strengthen scientific networks, and generate new research ideas within the rapidly evolving field of protein dynamics.





ISBUC funding news

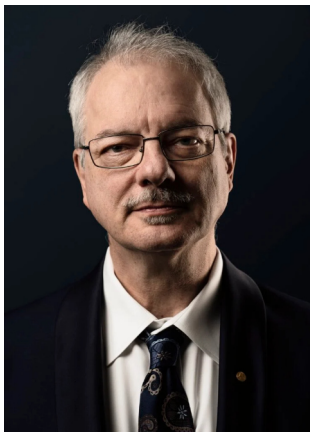
Wouter Boomsma receives DFF Grant for neuro-symbolic AI in biology



Professor Wouter Boomsma (DIKU) has received a DKK 6.57 million grant from Independent Research Fund Denmark for the project "TRANSFORMBIO: Tractable Neuro-Symbolic Foundations for Reliable Models in Biology", in collaboration with Antonio Vergari from the University of Edinburgh. The project addresses a major challenge in biological AI with large machine learning models transforming areas such as protein analysis and molecular design, but often struggling to incorporate biological constraints and mechanistic knowledge in a reliable way. TRANSFORMBIO will develop neuro-symbolic (NeSy) machine learning frameworks, combining neural networks with symbolic reasoning to create models that are both expressive and biologically interpretable. The research will focus on tractable inference methods capable of integrating structured biological constraints, such as codon organization and molecular interaction networks, into large biomolecular foundation models.

ISBUC staff news

Morten Meldal receives 2025 Hans Christian Ørsted ward



Professor Morten Meldal has been awarded the 2025 Hans Christian Ørsted Award in recognition of his pioneering contributions to chemistry and science communication. The award was presented in Rudkøbing, the birthplace of Hans Christian Ørsted, and honors individuals who advance both scientific development and public engagement with science. Meldal was recognized particularly for his role in developing Click Chemistry, a chemical strategy that enables simple and efficient joining of molecular components. The award also acknowledges Meldal's role as a prominent communicator and ambassador for chemistry, helping bring scientific research into broader public awareness.

Alexander Hauser elected to the Young Danish Academy

Associate Professor Alexander Hauser has been elected to The Young Danish Academy, a national academy for outstanding early-career researchers in Denmark. The Young Danish Academy works to strengthen basic research, promote interdisciplinary scientific exchange, and provide a public voice for young researchers within academia and society. Hauser's election recognizes his scientific contributions and positions him within a network of leading young scholars engaged in advancing research collaboration and science communication across many disciplines.



Amelie Stein elected awards chair to Rosetta Commons executive board

Associate Professor Amelie Stein has been elected to the Executive Board of Rosetta Commons, where she will serve as Awards Chair. Rosetta Commons is an international scientific community focused on biomolecular structure prediction, analysis, and design. It brings together more than 100 laboratories worldwide with the shared goal of advancing computational and experimental approaches to understand the relationships between biomolecular sequence, structure, and function. The consortium aims to develop leading-edge methods in protein science, with a long-term vision of establishing biomolecular design as a mature and reliable technology capable of addressing fundamental biological questions and enabling new applications in medicine and biotechnology.

CSSB Symposium brings international leaders in chemical and structural biology to Copenhagen

In 2025, ISBUC was honoured to collaborate with Professor and Nobel Laureate Morten Meldal (CHEM) to host the two-day symposium Chemical Solutions to Structural Biology. The program featured 20 presentations from world-leading experts including Nobel Laureate Brian Kobilka and was organized into five thematic sessions spanning a broad range of topics from drug discovery, cellular biology, enzyme and peptide design, synthetic approaches in structural biology and imaging technologies. The symposium brought together over 275 participants from 30 different universitites, 10 companies and infrastructure scientists. It included several prestigious networking events including a closing dinner in UCPH's beautiful Festsal. In parrallel, ISBUC hosted the PhD course “GPCR Structure and Function: Suitable Methods and Tools” from 9-17 June 2025. Several invited symposium speakers participated in teaching activities alongside local experts. The course covered topics ranging from the fundamentals of GPCR biology, including signaling, cellular function, and structural determination, to the development of novel ligands, molecular tools, and engineered GPCR systems. The symposium was generously supported by Lundbeck Foundation, Novo Nordisk Foundation, and Carlsberg Foundation. Given the tremendous success of CSSB, the ISBUC Steering Committee is now hoping to organise a follow-up event that will explore physical solutions to structural biology.

CHEMICAL SOLUTIONS TO STRUCTURAL BIOLOGY

Keynote and Invited Talks

1. Annette G. Beck-Sickinger, Leipzig Uni.
2. Ben Schuler, University of Zurich
3. Brian Kobilka, Stanford University
4. Christian A. Olsen, UCPH
5. Don Hilvert, ETH Zurich
6. Helma Wennemers, ETH Zurich
7. Ikuhiko Nakase, Osaka Metropolitan Uni.
8. Jin Zhang, Queen Mary Uni.
9. Jörg Rademann, Free Uni. of Berlin
10. Knud Jensen, UCPH
11. Kristian Strømgaard, UCPH
12. Markus Sauer, University of Würzburg
13. Morten Meldal, UCPH
14. Nieng Yan, Tsinghua University
15. Nikos Hatzakis, UCPH
16. Patricia Bassereau, Institut Curie
17. Sonja Schmid, University of Basel
18. Thomas B. Poulsen, Aarhus University
19. Yamuna Krishnan, Uni. of Chicago



Best Poster Awards

The symposium also placed an emphasis on supporting junior researchers and creating opportunities for scientific exchange across career stages. Five selected junior researchers presented flash talks, while an impressive 68 posters were presented, showcasing ongoing projects from early-career scientists. The poster sessions and networking activities culminated in the presentation of a best poster award. The award recipients were Anna Ida Trolle, Fabian Hink, Nadja Joachim, and Thea Schinkel. To our excitement, the awards also highlighted the breadth of topics represented at the meeting, spanning computational modeling, peptide design, sustainable biotechnology, and structural approaches for molecular engineering.

ISBUC welcomes the new Center for Protein Design

Artificial protein design is increasingly becoming one of the most promising frontiers in life sciences, with potential applications spanning medicine, biotechnology, materials science, and sustainability. To accelerate developments in this rapidly expanding field, the University of Copenhagen has launched the Novo Nordisk Foundation Center for Protein Design (CPD) in August 2025, supported by a DKK 700 million grant from the Novo Nordisk Foundation.



The center is led by Dek Woolfson, an internationally recognized pioneer in protein design who joined CPD from the University of Bristol. The CPD will unite researchers across biology, chemistry, drug design, and computer science from the Faculties of Health and Medical Sciences and Science, with the goal of establishing a world-leading environment for protein design research and applications. The ambition of the center is not only to advance fundamental understanding of how proteins can be designed, but also to translate these advances into real-world solutions. Recent progress in computational biology and artificial intelligence has dramatically increased the ability to design proteins with specific properties and functions, opening possibilities that only a few years ago seemed out of reach.

An important contribution to the development and strategic direction of CPD comes from several members of ISBUC, who play central roles within the CPD Integration Group, helping ensure that the center benefits from broad expertise across computational biology, structural biology, chemistry, education, and translational science.

ISBUC Members Take Key Roles at CPD



Professor Wouter Boomsma (DIKU) contributes expertise in machine learning and computational biology, with a particular focus on protein sequence-structure-function relationships and machine-learning guided optimization strategies for molecular design.



Professor Birthe B. Kragelund (BIO) advises on educational and training initiatives, helping integrate CPD activities into teaching programs across multiple levels. Birthe also contributes with expertise in structural biology and intrinsically disordered proteins.



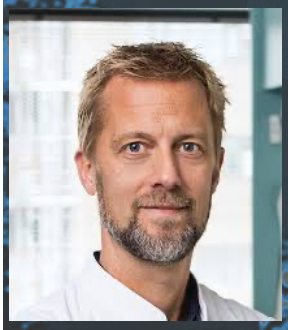
Associate professor Joseph Rogers (ILF) contributes expertise in high-throughput approaches for peptide discovery, computational design of protein binders, and experimental characterization of designed systems.



Professor Kresten Lindorff-Larsen (BIO) supports the integration of experimental protein science approaches and contributes expertise in combining machine learning, biophysics, and structural biology.

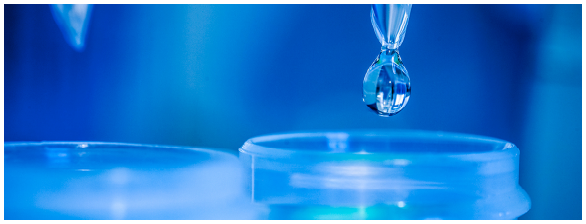


Professor Knud J. Jensen (CHEM) contributes expertise in peptide chemistry and medicinal chemistry, including synthesis approaches and development of novel functionalities in proteins and peptides.



Professor Kristian Strømgaard (ILF) advises on innovative protein design strategies and translation of designed proteins toward therapeutic applications.

For ISBUC, participation in the center represents a significant opportunity to help shape the future direction of protein design research. As CPD begins its activities, it marks the start of a major long-term effort to establish Copenhagen as an international hub for protein design research and innovation.



The first ever Junior ISBUC Summer Camp proves to be a valuable experience for junior researchers

In August 2025, ISBUC hosted its first-ever Junior ISBUC Summer Camp which was an overnight retreat dedicated exclusively to junior researchers. Held in the scenic surroundings of Hven Island, the retreat provided a unique opportunity for early-career scientists to connect, share research ideas, and support each other's professional development. Participants presented flash talks to their peers, to both practice in science communication, as well as increase the visibility of their projects within the ISBUC community. The camp also offered opportunities to exchange feedback on research, receive career advice from Junior ISBUC alumni, and discuss funding strategies with peers who had experience securing grants. Alongside the academic program, participants enjoyed a range of social activities, including beach barbecues and mini-golf. As the summer camp received overwhelmingly positive feedback from participants, plans are already underway for an expanded edition in August 2026, featuring even more professional development activities, and hopefully the amazing summer weather.



IDP Course

In May 2025, ISBUC hosted the five-day PhD course Keeping up with the interactome – how IDPs work. With talks by 13 internationally recognized leaders within the field of intrinsically disordered proteins, this intensive PhD course offered students a chance to study their interactions, their role in health and disease, as well as their potential drugability. Students on the course benefited from significant collaboration with industry including talks by senior scientists at Servier and a trip to Novo Nordisk. In addition, the course closed with a fantastic talk on science communication by the esteemed science writer Philip Ball.



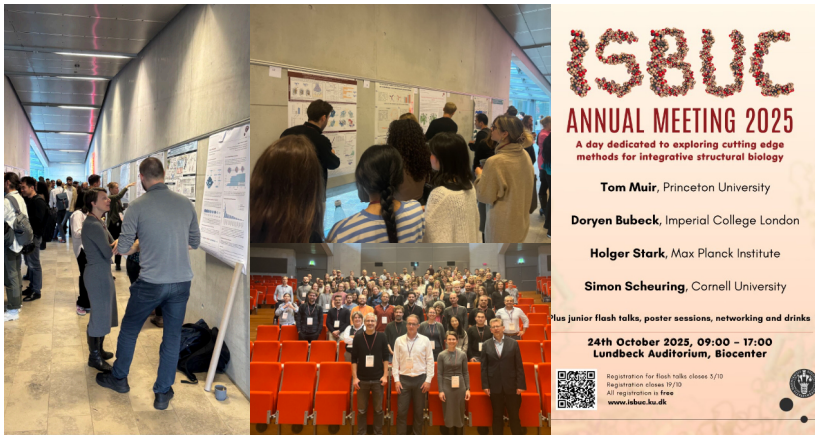
ISBUC Best Paper Award

In 2025, ISBUC started a new tradition with the introduction of the ISBUC Best Paper Award, presented at the ISBUC Annual Meeting. The first-ever award was presented to Haidai Hu for the paper Structure and mechanism of the Zorya anti-phage defence system.
Zorya is a recently identified and widely distributed bacterial immune system that protects bacteria against viral, or phage, infections. To uncover key aspects of the Zorya defence mechanism, the authors used a truly integrative approach, combining single-particle cryo-electron microscopy, mutagenesis, functional assays, proteomics, and total internal reflection fluorescence microscopy. Haidai Hu was the main driver of the study, particularly the structural biology results, and also led the writing, submission, and dissemination of the work.



The 2025 ISBUC Annual Meeting

The 2025 ISBUC Annual Meeting brought together the structural biology community for a day of inspiring science. The meeting featured four outstanding keynote lectures by Tom Muir (Princeton University), Doryen Bubeck (Imperial College London), Holger Stark (Max Planck Institute), and Simon Scheuring (Cornell University), showcasing cutting-edge developments across the field of structural biology. As always, the meeting also highlighted the excellent research taking place at UCPH through poster presentations and flash talks from junior researchers. We are pleased to congratulate Assistant Professor Haidai Hu (Taylor Group) on receiving the first ever ISBUC Best Paper Award. Congratulations also go to Postdoctoral Researcher Julien Streit, who won the Junior ISBUC Prize for Best Flash Talk, and to PhD Student Louise Helbig Nexø (Shahsavar Group) and Postdoc Christian Kofoed, who received the Junior ISBUC Best Poster Awards.





Junior ISBUC Lunch Talks connect early-career researchers with research leaders

The Junior ISBUC Lunch Talks continued in 2025 as an informal forum designed to connect junior researchers with the next generation of independent scientists working in structural biology and related fields. Held every other month, the series invited recently established group leaders from both academia and industry to present their research and discuss their career paths. Beyond the scientific presentations, speakers shared personal experiences and perspectives on securing independent positions, building research programs, and navigating career transitions.



The ISBUC PI Day brings together ISBUC group leaders

As an annual tradition ISBUC brings together its community of PIs for an inspiring half-day workshop focused on strengthening collaboration in structural biology. This time event featured a series of excellent research showcases from ISBUC PIs across SUND and SCIENCE, offering insights into exciting current projects, emerging research directions, and the diverse methodological approaches used across the community. The presentations sparked engaging discussions and have already led to several new collaborations in the works.

