PSB et al
Partnership for Structural Biology Newsletter

Scientific highlights

A Sliding Doors Mystery in Bacterial Division

How do bacteria divide? At first glance, it might seem simple: one cell splits into two. But behind this universal process lies a fascinating diversity of strategies, shaped by evolution, bacterial morphology and environment. Our recent study [1] sheds light on a particularly unusual case—the cell division of *Deinococcus radiodurans*, a bacterium renowned for surviving extreme doses of radiation.

Unlike most bacteria, *D. radiodurans* divides using a "sliding doors" mechanism. Instead of the cell wall closing like an iris or a diaphragm from all around the cell periphery, two new cell walls with flat leading edges grow inward from opposite sides of the cell, meeting and fusing at mid-cell. This curious strategy has long puzzled scientists, who wondered how such a complex division process is coordinated and achieved.

To tackle this question, researchers from the I2SR, MICA and PG groups at IBS combined cutting-edge imaging approaches (Figure 1A-B). Live fluorescence microscopy (conventional confocal microscopy and single-molecule localization microscopy) performed on the M4D imaging platform of the IBS/ISBG allowed them to watch dividing cells in real time, while cryo-electron tomography performed at the Umeå Centre for Electron Microscopy in Sweden, on thin, frozen lamellae of the bacteria, revealed various cell division intermediates and the cell wall's fine architecture at each step of the process. This powerful combination uncovered the complex layered structure of the bacterium's envelope and showed how the "sliding doors" septa grow, straighten, and fuse (Figure 2).

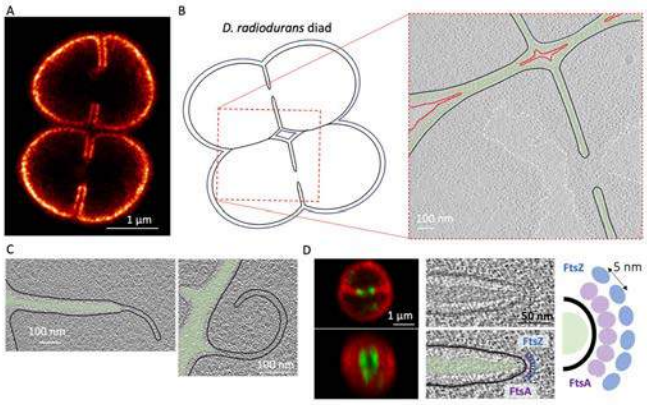

Figure 1: **(A)** High-resolution PAINT image of Nile Red-stained *D. radiodurans* membranes. **(B)** Left: Schematic diagram of a dividing *D. radiodurans* diad (two-cell unit) in the process of becoming a tetrad (four-cell unit). Right: Central slice of a typical cryo-electron tomogram of an actively dividing *D. radiodurans* diad. The field of view corresponds to the dashed red box presented on the left. The multilayered cell envelope is composed notably of the inner (black line) and outer (red line) membranes and a thick peptidoglycan layer (green line). The light gray density in the center of the cell delimited with a dashed white line corresponds to the nucleoid and the small dark densities distributed throughout the cytoplasm (and excluded from the nucleoid) are ribosomes. **(C)** Examples of tubular and curved membrane protrusions observed at the tips of growing septa, devoid of peptidoglycan. **(D)** Left: Top and side views of confocal images of dual-labelled *D. radiodurans*: Nile Red staining of the cell membrane and green labelling of FtsZ. Middle: Close-up view of a septal tip bearing a doubl-arched structure composed of FtsZ (blue) and FtsA (purple) filaments oriented perpendicular to the image plane. Right: Model of FtsA/FtsZ arrangement at the tip of growing septa in close proximity to the site of peptidoglycan synthesis.

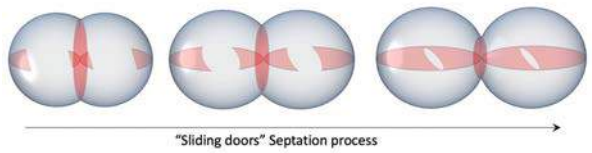

Figure 2: Schematic model of the 'sliding doors' septation process in *D. radiodurans*.

One striking discovery was the presence of thin membrane protrusions at the tips of the growing septa (Figure 1C). These flexible extensions may help align the two sides before they fuse. Another key player is FtsZ, a highly conserved protein that assembles into filaments at the division site [2]. In this study, FtsZ and its membrane anchor, FtsA, were found to form a double-arched structure at the tip of growing septa bearing a thick, rigid peptidoglycan layer (Figure 1D). These findings suggest that FtsZ plays a role in the rigidification of the septa by regulating the location of the peptidoglycan synthesis machinery with which it interacts.

Beyond revealing the mechanics of cell division, this work raises intriguing questions: why does *D. radiodurans* use such an unusual and elaborate strategy to divide? Although we do not have the answer to this question, we postulate that its unusual cell envelope composition, its cell morphology (diads and tetrads), and its remarkable resilience to DNA damage may have shaped this distinctive mode of division, potentially offering advantages in surviving extreme stress.

This work was the result of a true collaborative effort between three IBS teams with complementary expertise who joined forces to unlock mysteries of microbial life. This study is important not only because it reveals how one of the toughest bacteria on Earth orchestrates its division process, but also because it could inspire new strategies to combat microbes and the growing threat of antibiotic resistance.

J. Timmins, I. Gutsche and JP. Kleman (IBS)

[1] Gaifas L, Kleman JP, Lacroix F, Schexnaydre E *et al.* (2025) PNAS, **122**, e2425047122.
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CONTENTS

Understanding How Genes Are Turned On and Off in the Human Body

The way our genes are regulated—switched on or off in different cells—is far more complex than the basic genetic code itself. One reason is that there are over 1,600 proteins called transcription factors (TFs) that often work together to control gene activity. These partnerships between TFs are essential for determining what type of cell something becomes and how that cell performs its specific tasks. A key part of this process involves "enhancers"— the short regions of DNA that act like switches to turn genes on or off. The enhancers respond to signals from multiple TFs.

In this study, we used high-throughput technology CAP-SELEX (consecutive-affinity-purification systematic evolution of ligands by exponential enrichment) [1] to systematically map DNA-guided TF-TF interactions across more than 58,000 human TF pairs, identifying 2,198 interacting pairs [2]. The affinity of individual TFs for composite motif (the motif, found in the complex of at least two TFs bound to the same short DNA) was lower than their individual motifs, indicating a crucial rule of TF cooperativity *in vivo*. We also observed that these interactions often happen between TFs from different families, creating a complex and cooperative network.

To confirm our findings, we developed a new technique called **mixture-SELEX**, which successfully validated more than half of the composite DNA sequences we identified. These composite motifs were especially common in DNA regions that are active in specific cell types, are conserved through evolution, and often involve TFs that are active at the same time in development.

We further tested these DNA switches in developing mouse embryos and found that the composite motifs could drive strong and specific gene activity, confirming their importance in real biological settings [2].

To understand how these TFs physically interact with each other and DNA, we used classical 3D structural analysis. We solved 7 structures of TF:TF-DNA complexes using data collected at ESRF, at beamline ID23-1. These structures revealed that the contacts between TFs are often rather weak and most likely formed after TFs bound to their specific DNA sequence. Those contacts are hard to predict, even with modern AI tools like RoseTTAFold and AlphaFold. While these tools can predict the general shapes of TF-DNA complexes, they still struggle to accurately model the conformations of the amino acid side chains forming the contacts [2].

Our study helps explain a long-standing mystery: how similar TFs can lead to very different biological outcomes. It turns out that the way TFs pair up on DNA plays a critical role in determining their function. In summary, we show that TF pairing, guided by specific DNA sequences, is a key mechanism for precise control of gene activity during development.

A. Popov (ESRF), I. Sokolov (Cambridge University), E. Morgunova (Karolinska Institutet)

[1] Jolma A, Yin Y, Nitta KR, Dave K *et al.* (2015) Nature, **527**, 384-388
[2] Xie Z, Sokolov I, Osmala M, Yue X *et al.* (2025) Nature, **641**, 1329-1338

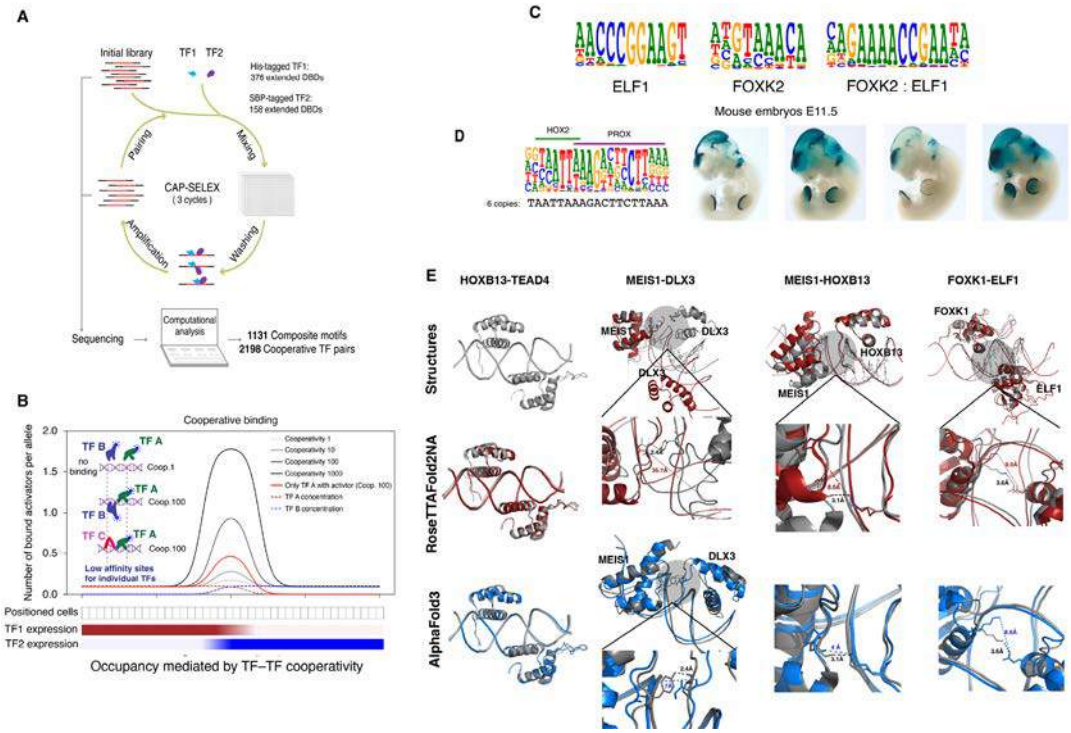

Figure 1: **A**. Schematic description of the high-throughput CAP-SELEX process. **B**. Composite motifs enable efficient integration of signals and high cooperativity. **C**. The indicated FOXK2–ELF1 composite motif detected by CAP-SELEX. **D**. Composite motifs of PROX–HOX2 drive highly specific expression of lacZ reporter gene in transgenic E11.5 mouse embryos. **E**. Both RoseTTAFold2NA (red) and AlphaFold3 (blue) fail to correctly position the side chains of the amino acids that form the contacts between the shown cooperative TF pairs.

Structural analysis of the snRNA nuclear export complex

In metazoans, RNA polymerase II transcribed immature U-rich small nuclear RNAs (snRNAs), ultimately destined to be incorporated into spliceosomal particles, are exported within a specific export complex from the nucleus to the cytoplasm, where further processing of the snRNA occurs. In the nucleus, nascent snRNAs are bound via their 5' m7G caps to the nuclear cap-binding complex (CBC, a heterodimer of CBP80 and CBP20). A protein called PHAX ('phosphorylated adapter for export') then links the cargo, CBC-bound snRNA, to the CRM1 nuclear export receptor, which is bound to its essential cofactor RanGTP. Although the snRNA-CBC-PHAX-CRM1-RanGTP export complex was first characterized 25 years ago (Figure 1a and b) [1], there are several long-standing questions that we sought to address by determining its structure and then using the structure to perform mutagenesis studies with a functional readout. Firstly, how exactly does PHAX, a 394 residue, largely unstructured protein (apart from a small RNA-binding domain) interact with both CBC and CRM1 and potentially the snRNA as well? Secondly, how can one explain the synergistic assembly of the complex, which requires mutual interaction of all components to be stable? Thirdly, why does PHAX have to be specifically phosphorylated (hence its name) by casein kinase II on an N-terminus proximal serine-rich region (known as ST2) for complex stability and export functionality?

We *in vitro* assembled the human snRNA export complex from its recombinant components (notably *in vitro* phosphorylated PHAX) and determined the structure at around 2.5 Å resolution using cryo-EM data collected on the Krios CM01 at the ESRF operated by the PSB partners (Figure 1c) [2]. Reconstructions using full-length U1 snRNA or with a short capped RNA gave similar results, showing that under these conditions only the cap structure makes interactions within the complex. The structure reveals that a central region of PHAX (residues 112-162) becomes fully ordered. This includes a long helix (residues 112-136), whose N-terminal end binds CBC and C-terminal end, containing the nuclear export sequence (NES), binds CRM1, thus directly bridging the cargo and export receptor moieties of the complex. Interestingly, Trp116 of PHAX binds into the so-called Trp-binding pocket of CBC that is competitively used by other CBC binding effector molecules [3]. In addition, other conserved residues of PHAX directly reinforce the already strong binding by CBC of the 5' cap, with notably R147 and Y154 sandwiching the second base in the dinucleotide cap structure. Finally, what about PHAX phosphorylation? Supported by confident AlphaFold predictions, we identified from the cryo-EM density, a short peptide of PHAX, containing the conserved 57-YR sequence, bound to a distant region of CRM1. This is immediately upstream of the ST2 phosphorylated region (residues 64-76, with up to four serines phosphorylated) of PHAX, which we predict to make a 'fuzzy' electrostatic interaction with the well-characterized, neighboring positively charged surface of CRM1/RanGTP (Figure 2). This surface is implicated in direct binding of other, potentially competing, RNA cargoes in tRNA, microRNA or HIV Rev-RRE RNP export complexes [4].

To test the importance of these interactions on complex stability, collaborators at the University of Aarhus developed a cellular assay involving degron-mediated knockdown of the endogenous PHAX and its replacement by structure-based point mutants. A proximity labeling pulldown was then used to identify the recruitment of proteins to mutated PHAX, compared to wild-type. Whereas the mutation W116A in PHAX abolished assembly of the entire complex *in vivo*, individual PHAX mutations R147A and Y154E maintained PHAX-CBC binding but prevented recruitment of CRM1-RanGTP. Mutagenesis of PHAX R58E or the ST2 phosphorylation region abolished complex assembly. These structural and mutagenesis results reveal the sensitivity of the snRNA export complex stability to each individual interaction mediated by PHAX, highlighting its role as a molecular glue and explaining the synergistic nature of functional complex assembly.

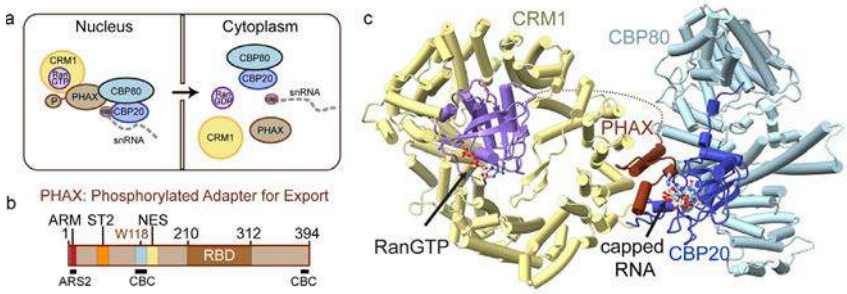

Figure 1: (a) Schematic of snRNA nuclear export [1]. (b) Functional regions of PHAX, (c) Cryo-EM derived structure of the snRNA nuclear export complex.

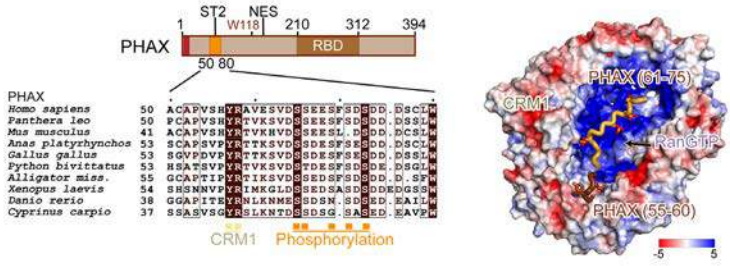

Figure 2: Interaction of the PHAX ST2 phosphorylated region with the prominent basic surface of CRM1-RanGTP, is anchored by 57-YR of PHAX binding to CRM1.

S. Cusack (EMBL), J. Kadlec (IBS), E. Dubiez (EMBL and IBS)

[1] Ohno M, Segref A, Bachi A, Wilm M *et al.* (2000) Cell, **101**, 187-198
[2] Dubiez E, Garland W, Finderup Brask M, Boeri Erba E et *al.* (2025) Nat Struct Mol Biol, **32**, 1555-1566
[3] Dubiez E, Pellegrini E, Finderup Brask M, Garland W *et al.* (2024) Cell Reports, **43**, 11639
[4] Smith A, Li Y, Velarde A, Cheng Y *et al.* (2025) Molecular Cell, **85**, 3108-3122

Illuminating Protein Crystallization: A Decade of Technique Development and Discovery

Understanding how proteins crystallize remains a long-standing challenge in structural biology. While the final crystals are essential for techniques like X-ray diffraction, the early stages of crystallization—where molecules begin to organize—remain largely invisible. Over the past decade, our team has tackled this challenge through a sustained, collaborative effort across the PSB network, advancing both our scientific understanding and the experimental tools needed to probe these hidden processes.

As model systems, we investigated various globular proteins in the presence of multivalent salts. The overall phase behavior in these systems can be described by a reentrant phase diagram and may additionally feature liquid–liquid phase separation (LLPS), cluster formation, or crystallization. Using kinetic small-angle scattering studies, we have previously revealed several nonclassical pathways for salt-induced protein crystallization [1]. However, the underlying reasons for these different pathways remained unclear. To gain complementary insights, we investigated the diffusive properties during the kinetic process using different spectroscopic techniques (NSE and NBS). In an initial study [2], we demonstrated the feasibility of this approach by examining the crystallization process of β-lactoglobulin in the presence of zinc chloride, which follows a classical crystallization pathway.

The development of new acquisition modes and analysis frameworks significantly reduced the acquisition time for neutron backscattering measurements to just a few minutes. In our most recent study [3], this allowed us to compare different crystallization processes using complementary techniques (NSE, NBS, DLS, SANS, microscopy) and to characterize multiple distinct pathways. These pathways included initial gel phases with metastable intermediates, the continuous presence of protein assemblies, and crystal growth directly from monomeric solutions.

Scattering experiments were essential for investigating these different pathways. The larger neutron beam size ensures spatial averaging, enabling the detection of rare crystallization events. The use of neutrons further allows continuous observation without the risk of radiation damage and makes it possible to study turbid samples. For samples that remain clear during the process, light scattering provides additional insights. Combining these techniques revealed information about the lifetime of different particles in solution, their individual and collective diffusive behavior, and the nature of particle interactions.

In summary, we have advanced the understanding of protein crystallization by employing a combination of neutron and light scattering techniques to uncover distinct crystallization pathways, including gel-like intermediates and direct crystal growth from monomeric solutions. Our work highlights the importance of complementary methods for probing early-stage dynamics and particle interactions in these complex processes.

C. Beck (ILL, University of Tübingen)

[1] Sauter A, Roosen-Runge F, Zhang F, Lotze G *et al.* (2015) Faraday Discuss., **179**, 41-58

[2] Beck C, Grimaldo M, Roosen-Runge F, Maier R *et al.* (2019) Cryst. Growth Des., **19**, 7036-7045

[3] Beck C, Mosca I, Miñarro LM, Sohmen B *et al.* (2025) J. Appl. Cryst., **58**, 845-858

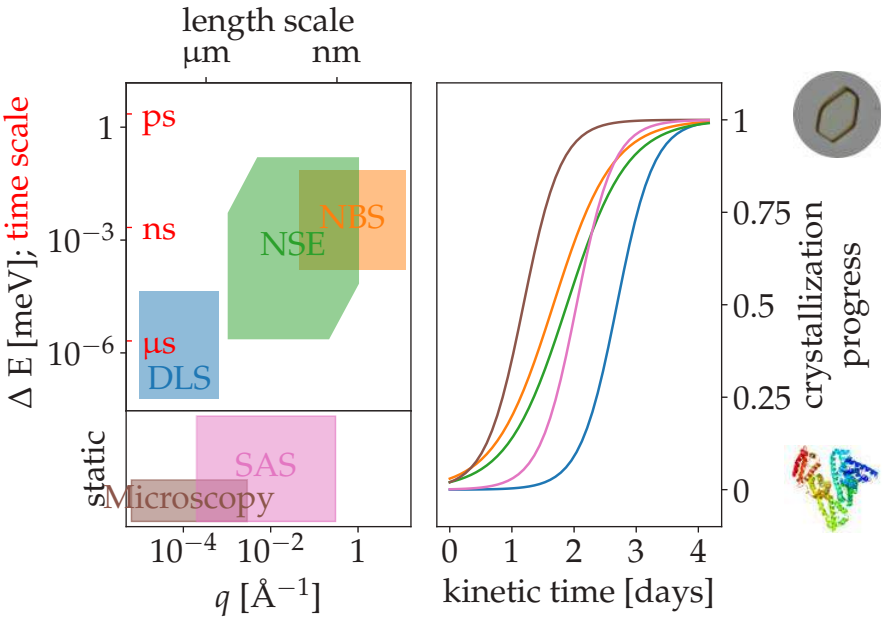

Figure 1: Time- and length-scales investigated with the different techniques. The kinetically observed time-dependencies of the crystallization process fraction shows the nice reproducibility of the system.

Unraveling the complete Baculovirus nucleocapsid structure

Baculoviruses are large viruses with circular double-stranded DNA (dsDNA) genomes. They specifically propagate amongst insect cells, playing a natural role in regulating insect populations and therefore are used as biological control agents in agriculture, a rising alternate to chemical pesticides. Beyond their ecological role, baculoviruses are also valuable biotechnological tools: they are used extensively worldwide, including by EPN campus researchers, as expression systems for producing recombinant proteins in insect cell cultures and as delivery vehicle for gene therapy and vaccine development.

Despite their widespread use, detailed structural studies of baculovirus nucleocapsids, the protein shells that protect and package the viral DNA, were still limited when this project began. To address this, a collaboration was established between Martin Pelosse (EMBL), Eaazhisai Kandiah (ESRF), and Gregory Effantin (IBS) to investigate the most studied baculovirus, *Autographa californica* Multiple NucleoPolyhedroVirus (AcMNPV).

AcMNPV particles consist of a nucleocapsid surrounded by a lipid envelope decorated with viral glycoproteins. The nucleocapsid itself is composed of hundreds of proteins and exhibits an elongated structure, approximately 50 nm in diameter and 300 nm in length, with two distinct termini: the “apical cap,” through which viral DNA enters and exits, and the “basal” structure. These termini are linked by the capsid body that encloses the viral genome. Despite the wealth of biochemical knowledge on the virus, the project began with the challenge of an unknown nucleocapsid proteome (its protein composition).

Using cryo-electron microscopy (cryo-EM) data collected at the CM01 facility of the ESRF on the baculovirions routinely used at the EMBL Eukaryotic Expression Facility (EEF), the team focused on both the apical and basal regions of the nucleocapsid. Multiple 3D maps, spanning resolutions from medium to high, were determined to assign and position proteins within these structures. The remarkable feature of AcMNPV nucleocapsid is its composition of several distinct protein sub-assemblies, each with a different symmetry. By elucidating the various symmetries within these sub-assemblies, a composite pseudo-atomic model representing the complete AcMNPV nucleocapsid was obtained for the first time [1]. To delineate the proteome of these individual sub-assemblies, cutting-edge modelling tools were employed. At resolutions better than 4 Å, protein identities were determined using Modelangelo, a machine learning program designed to build atomic models of proteins into cryo-EM density without prior knowledge of the amino acid sequence [2]. For lower resolution maps, AlphaFold2 predictions were essential for determining the identity and placement of several proteins [3]. Beyond predicting the structures of the 155 proteins encoded by the AcMNPV genome, Alphafold was also used to identify possible interaction partners, thus facilitating the interpretation of complex assemblies.

This integrative approach led to the elucidation of the peculiar structure of the apical cap and the discovery of eight previously uncharacterized proteins as well as a fragment of the viral genome at the apex. These findings provide direct experimental support for the proposed role of the apical cap as the entry and exit point of viral DNA. The unambiguous presence of two dsDNA strands at the apical cap not only suggests that the baculoviral genome is packaged as covalently closed circular dsDNA (cccdsDNA) but also provides, for the first time, insights into the dsDNA packaging mechanism of baculoviruses and other cccdsDNA viruses.

This study delivers a near-atomic resolution model of the entire nucleocapsid of AcMNPV. Beyond offering fundamental insight into baculovirus architecture and function, it significantly enriches the structural database of this virus and opens the way for more rational design of baculovirus-based biotechnological applications.

G. Effantin (IBS), E. Kandiah (ESRF), M. Pelosse (EMBL)

[1] Effantin G, Kandiah E, Pelosse M (2025) Nat Commun., **16**, 4844.
[2] Jamali K, Käll L, Zhang R, Brown A *et al.* (2024) Nature, **628**, 450–457.
[3] Jumper J, Evans R, Pritzel A, Green T *et al.* (2025) Nature, **596**, 583–589.

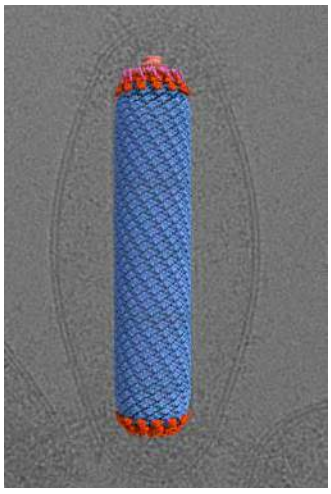

Figure 1: Superimposition of a composite 3D map of the complete nucleocapsid of AcMNPV over a cryo-EM image of an intact AcMNPV viral particle.

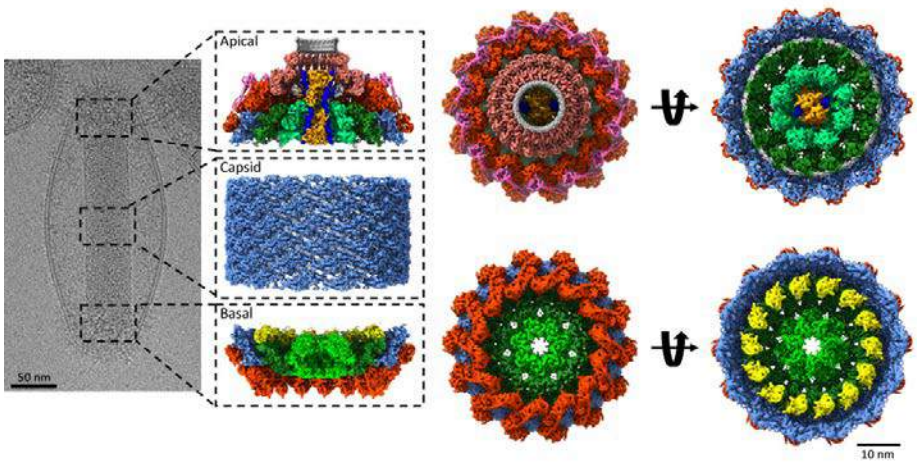

Figure 2: Structures of the AcMNPV nucleocapsid obtained by cryo-EM. Left panel: electron micrograph of an AcMNPV virion with enlarged 3D reconstructions of the apical cap, the capsid sheath and the basal structure. Right panels, upper row: isosurface representations of the 3D composite map of the apical cap: – side view (left), top view (center) and bottom view (right). Lower row: isosurface representations of the 3D composite map of the basal structure: side view (left), top view (center) and bottom view (right).

News from the platforms

Counter diffusion crystallization of human transthyretin: a pipeline to produce high-quality crystals for neutron studies

Human transthyretin (TTR), a thyroxine and retinol-binding protein transporter in the blood and cerebrospinal fluid, can become amyloidogenic with age or by single point mutations causing hereditary and early-onset forms of the disease. *In vitro* studies have identified tetramer dissociation followed by monomer misfolding as the rate-limiting step in TTR amyloidogenesis. X-ray and neutron diffraction studies have been fundamental in understanding the architecture of TTR and its propensity to become amyloidogenic. In particular, neutron studies have provided unique details on how point mutations can alter hydrogen bonding underlying loss of tetramer stability in pathogenic mutants [1].

Due to the weaker flux of neutron beams, as compared to X-rays, much larger crystals are required for neutron studies, limiting its application for protein targets that are difficult to crystallize. Thus, the growth of large crystals remains a constant technical challenge for 'new' targets. Counter diffusion (CD) crystallization is an alternative method to obtain protein crystals. In this approach, the protein is filled in a capillary and immersed by its open end in a highly saturated precipitant solution. Diffusion of the precipitant in the capillary creates a 'supersaturation wave' that screens a wide range of crystallization conditions within a single capillary. This culminates in the formation of a metastable region (typically at the furthest end of the capillary from the precipitant) where large and high quality crystals grow [2].

As part of a collaborative study involving ILL, EMBL, ESRF and the Instituto Andaluz de Ciencias de la Tierra (IACT) in Granada, De'Ath, Oliva and colleagues [3] used CD crystallization to study TTR, defining a pipeline to optimize crystal growth and obtain large crystals suitable for neutron studies. Feasibility experiments were first carried out in small diameter capillaries (0.2 mm) whereby the typical CD growth pattern was observed alongside with an unexpected growth behavior. This produced rod-like crystals that extended alongside the capillary wall. Samples were characterized by X-ray diffraction on the MASSIF-1 beamline (ESRF), using a combination of mesh scans and full dataset collection. The data obtained confirmed previous observations that crystal size and quality increased at the top end of the capillary when the typical CD crystal growth was obtained (Figure 1). Thanks to the small size of the beam, the rod-like crystals were analyzed by acquiring several datasets at regular intervals along their entire length, showing their high overall homogeneity. When larger diameter capillaries (1 mm) were used, crystals grew to a sufficient volume for preliminary neutron diffraction tests. Data were acquired on the LADI-III beamline (ILL). The same crystal was recorded first in hydrogenated buffer and again after exchange into fully deuterated buffer, revealing a clear increase in the diffraction quality and thus proving that such crystals are suitable for neutron crystallography studies (Figure 2).

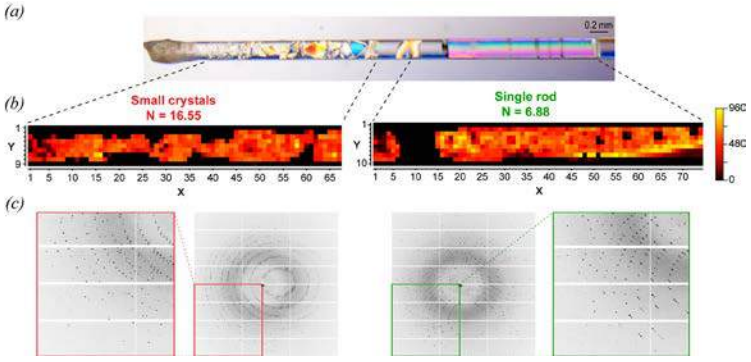

Figure 1: Variation of crystal quality over the supersaturation gradient within a capillary. **(a)** Photograph showing the 0.2 mm capillary (TTR at 60 mg/mL) under cross polarized light. The dashed lines indicate the regions used to acquire the mesh scan (bottom end of the capillary shown on the left at the site of precipitant entry). **(b)** The mesh scans are plotted as total integrated signal over the defined area (X, Y) with the relative intensity signal scale bar on the right and the N scores calculated for each area indicated above. **(c)** Diffraction pattern corresponding to the mesh scans above. The red and green box regions show enlarged portions to emphasize differences in the quality of diffraction spots (d spacing at the corner of the diffraction images is 1.25 Å).

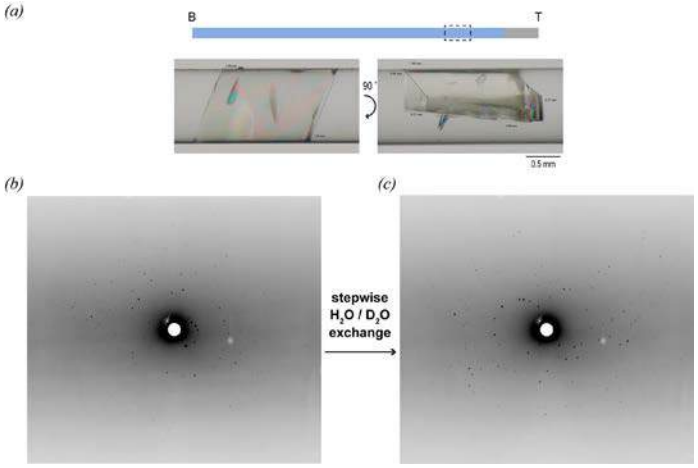

Figure 2: Neutron diffraction patterns recorded at the LADI-III diffractometer (ILL), using a crystal of ~ 0.7 mm³ obtained in the 1 mm capillary set-up using 30 mg/mL protein with 0.15% (w/v) agarose gel. **(a)** The position of the crystal in the capillary is marked as a boxed area in the schematic (B = bottom; T = top). **(b)** Test neutron diffraction pattern recorded from TTR crystal hydrated with natural-abundance H_2O. **(c)** Neutron diffraction pattern recorded from the same sample following stepwise exchange of H_2O by D_2O.

This work was possible thanks to the collaboration with Dr. José Gavira (IACT) and the use of different PSB facilities: the D-LAB (ILL) for protein production and labelling, the ESRF and EMBL for the data acquisition on MASSIF-1, the ILL for the data collection on LADI-III.

C. De'Ath (ESRF / ILL), M. F. Oliva (ILL), M. P. Blakeley (ILL), M. Moulin (ILL), E. P. Mitchell (ESRF), M. W. Bowler (EMBL), T. Forsyth (ILL)

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[3] De'Ath C, Oliva MF, Moulin M, Blakeley MP *et al.* (2025) J Appl Crystallogr., **58**, 107–118

The new IBS Aquilos2+ FIB/SEM

The new cryo-FIB/SEM Aquilos2+ (ThermoFisher Scientific) acquired by the IBS/ISBG will serve several key purposes:

• Sample preparation for cryo-electron tomography (cryo-ET): The cryo-FIB/SEM (Focused Ion Beam) enables the milling of ultrathin lamellae directly from vitrified samples. These lamellae, with an optimal thickness for cryo-EM observation, allow the exploration of the 3D architecture of cells and bacteria. The prepared samples will be analyzed using Titan Krios CM01 or CM02.

• Localization of proteins of interest via fluorescence: An integrated fluorescence microscope within the FIB enables the detection of fluorophores tagged to proteins of interest, facilitating the identification of rare events under investigation. This allows for correlative studies, bridging global cellular imaging with detailed structural analysis.

• Study of complex biological systems: This tool facilitates access to otherwise difficult-to-analyze structures, such as macromolecular interactions in their native cellular context, viruses, or specific organelles.

The Aquilos2+ was delivered on December 19th 2024 and installed in February 2025. The FIB is now fully operational (for research use in 2025, followed by platform access in 2026).

Importantly, the room housing the Aquilos2+ is fully equipped for cell culture workflows between sample transfer and cryopreservation. The lab includes a Leica GP2 cryo-plunger, two CO_2 incubators, a biosafety cabinet (PSM), a Leica MATEO brightfield fluorescent microscope, a MiniQ glow-discharge device and other essential equipment. The laboratory is certified as a BSL-2 (Biosafety Level 2) facility, ensuring safe handling of relevant biological samples.

If you have a project that may require the use of this equipment, please don't hesitate to contact us (ibs-pf-cellularem.contact@ibs.fr). We kindly ask that you reach out well in advance, so that any potential biosafety issues can be properly assessed and addressed, and the necessary administrative procedures — which may take several months — can be completed in time.

This new installation significantly enhances the IBS/ISBG and more widely EPN's capabilities in cellular structural biology.

Acknowledgements: The acquisition of the Aquilos2+ and most of the equipment in room 159/159A was made possible thanks to funding from CPER GrInBio, France 2030, and additional financial support from the Bettencourt-Schueller Foundation (as part of Rebekka Wild's research project). The Leica GP2 cryo-plunger, MiniQ glow discharge unit, and other small equipment were purchased with ANR funding secured by the MEM group. We are grateful to the management and administrative teams of the IBS, ISBG, and CEA for their support throughout the acquisition and installation process.

B. Gallet and G. Schoehn (IBS)

Enhanced capabilities for multi-crystal data collection based on double mesh scans.

Two-dimensional X-ray mesh (raster) scans are broadly used in macromolecular crystallography to identify positions on the sample holder at which diffraction images can be collected. Based on a single mesh scan, the commonly known method *Mesh&Collect* allows collecting small angular wedges of diffraction data from multiple crystals identified in the mesh scan area. Recently, we have extended the method capabilities by using two 2D mesh scans (double mesh scan) done at different orientations and subsequent automatic analysis by a software.

The new programs (*Dozor, Dozor-m²* and *Resheteau*) execute the already established procedure of finding 2D positions of individual crystals in each of the two mesh scans, however the core of the newer version is to identify the correspondence between crystal areas in different scans, which can, finally, bring the optimal 3D centring and optimal beam size selection (if selectable) for multi-crystal data collection. As a result, the new *DoubleMesh&Collect* method allows to measure wider wedges (up to 360°) for each crystal. Sample rotation between the two mesh scans can be substantially less than 90°, which is especially important in MX experiments with restrictions on rotation range, for example, in measurements using crystallisation plates or chips, Figure 1. *DoubleMesh&Collect* approach should provide the information about 3D positions for all crystals inside the sample holder and thus allow to rationally organise completely automatic multi-crystal data collection. .

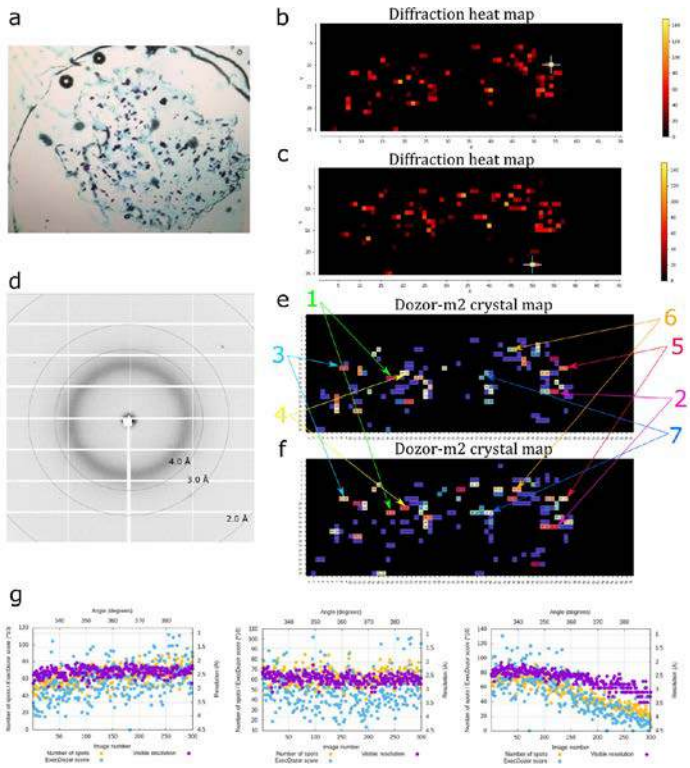

Figure 1: Multi-crystal data collection from crystals of the membrane protein bacteriorodopsin (a) A snapshot illustrating crystalline sample sandwiched between two Mylar foils. (b, c) Two diffraction heat maps of the mesh scans separated by 60° of sample rotation. (d) A sample diffraction image from the mesh scans. (e, f) Two crystal maps for the mesh scans produced by *Dozor-m²*. Crystals at which the data have been collected are indicated by arrows. (g) Data collection plots for three selected c rystals.

I. Melnikov (ESRF), O. Svensson (ESRF), G. Bourenkov (EMBL), A. Popov (ESRF)

[1] Melnikov I, Svensson O, Bourenkov G, Popov A (2025), Acta Crystallogr D Struct Biol., **81**, 344–356

Structural biology at EPN Grenoble in a new era

The European Photon and Neutron (EPN) campus in Grenoble, home to ESRF, ILL, EMBL, and IBS, continues to stand as a global leader in structural biology. In a recent publication [1], scientists from the different facilities outlined a shared vision for the future, in an age of 4th generation synchrotrons, free electron lasers, spallation sources, and artificial intelligence (AI) for structural prediction.

The next frontier in structural biology extends beyond static structural determination, and explores dynamic behaviour of biological macromolecules, key to understanding their function. This future emphasizes the use of complementary techniques, leveraging X-ray, electron microscopy, and neutron techniques, NMR spectroscopy, and other biophysical approaches, increasingly performed under near-physiological conditions.

Automation and high-throughput capabilities across all facilities are central to both current and future ambitions. Web-based tools such as MXCuBE-Web provide a user-friendly environment that enables efficient remote data collection, while migration to the new ISPyB-DRAC should streamline data processing workflows. Incorporation of automated workflows at MASSIF-1 enable efficient use of beamtime, such as multi-orientation data collection, and in the future fragment-based drug discovery screening. The increased availability of AI and machine learning (ML) tools could provide new solutions to existing and new tasks such as sample centring and workflow decision making.

Automation has significantly improved operational efficiency across ESRF's MX facilities. Jointly with the EMBL, continued development will support fragment-based drug discovery and enable high-throughput room-temperature data collection using 96-well plates at MASSIF-1 and ID23-2. At ID30B, higher X -ray energies, a new detector, and automated X-ray fluorescent scanning will provide richer datasets. To lower the barrier for serial crystallography, method development at ID23-2 and MASSIF-3 will allow users to assess sample suitability. At ID29, automation of fixed target experiments and other developments developments continue to improve beamtime efficiency. Enhancing sample efficiency and deeper integration of complementary spectroscopic analyses, such as those provided by the *in crystallo* optical spectroscopy (*ic*OS) lab, remain priorities. Expanding the range of spectroscopic techniques at *ic*OS will allow more enzyme systems to be studied. The high pressure MX lab will broaden the range of biologically relevant gases and support room-temperature studies. Upgrades to the LADI-DALI instruments at ILL complement X-ray based MX, enabling dynamic studies under near physiological conditions and revealing hydrogen positions critical for understanding protein-drug interactions.

Solution-based scattering studies at BM29, D11, and D22 are undergoing enhancements in sample environment, automation, and instrumentation, enabling high-resolution and millisecond timescale measurements. These SAXS/SANS/WAXS approaches are well complemented by techniques such as atomic force microscopy and NMR spectroscopy at IBS, and cryo-EM at ESRF. The CM01 and CM02 cryo-EM facilities stand to benefit from wider adoption of ML and AI tools, which reduces manual input and improved throughput.

These collaborative efforts, driven by the Partnership for Structural Biology (PSB) across ESRF, EMBL, ILL, and IBS, establish the EPN campus as a global hub for interdisciplinary research by combining complementary techniques to address complex biological questions.

M. Soler-Lopez and J. J. A. G. Kamps (ESRF)

[1] McCarthy AA, Basu S, Bernaudat F, Blakeley MP *et al.* (2025) J Synchrotron Radiat., **32**, 577-594

The ILL Science Strategy: A Vision for the Decade Ahead

The newly released ILL Science Strategy sets out the vision for the Institute's scientific direction over the coming decade. Developed in close collaboration with external experts, it builds on the Endurance upgrade programme and outlines how the ILL will maximise the impact of its world-class instruments and facilities.
With renewed commitments from France, the UK, and Germany ensuring operations through 2033, the ILL is well positioned to remain a cornerstone of the European neutron landscape.
The Strategy provides a framework for strengthening the user programme, expanding the scientific community, and focusing on research that addresses major societal challenges.
Among the key initiatives are new Science Hubs — centres of expertise designed to foster collaboration, support emerging research areas, and enhance industrial engagement. Each Hub will unite internal and external scientists under the leadership of a prominent researcher to deliver ambitious five-year projects. The four initial themes are Li-ion batteries, advanced manufacturing, quantum materials, and liquid–liquid phase separation.
The Strategy also introduces Showcase Experiments, high-impact projects that will open new fields of research and attract new users. The first topics include superconducting wires, bio-imaging of cell structures, and water membranes for a sustainable future.
In addition, the nuclear medicine programme will be expanded to increase isotope production for cancer therapies and to develop new isotopes for diagnostics.

L. Gajdoš (ILL)

EVENTS

PSB Spotlight on Liquid-Liquid Phase Separation

Scientists from the EPN campus and beyond gathered on 18 September to discuss research on liquid–liquid phase separation (LLPS) in biology. LLPS is a process in which two or more liquid phases form from a homogeneous solution, typically in response to changes in temperature, pH, concentration, or other factors. In living organisms, LLPS underlies the formation of membrane-less condensates, or cellular "compartments."

Researchers from the ILL, IBS, CEA, Imperial College London, and the University of Tübingen shared their latest work, revealing LLPS phenomena associated with neurodegenerative diseases, measles and rabies viruses, or temperature-sensitive growth in plants.

The new ILL Science Strategy will promote research in this field through the creation of a Science Hub on LLPS, focused on questions relevant to human health and disease. The Hub will consolidate internal expertise and strengthen collaborations across the EPN campus and with the wider international scientific community.

L. Gajdoš (ILL)


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International Conference on Neutron Scattering 2025

The International Conference on Neutron Scattering (ICNS 2025) took place from 7–10 July in Copenhagen and Lund, bringing together more than 750 participants – including a strong ILL delegation of 66 scientists. The meeting was marked by major ILL recognitions: Juan Rodriguez-Carvajal received the ENSA Walter Haelg Prize for his pioneering work on the FullProf software, and Iurii Kibalin was honoured with the Neutron Instrumentation and Innovation Award for advancing polarized neutron diffraction. Keynotes included Frank Gabel on the essential role of support labs, while ILL's Ken Andersen and Jacques Jestin shared exciting updates on the institute's future. Fourteen ILL talks and lively poster sessions, with several prizes awarded to ILL scientists and students, highlighted the breadth of contributions. The conference concluded with a visit to the European Spallation Source and the announcement that ECNS 2027 will be hosted in Grenoble, coinciding with 70 years of neutrons in the city and the 60th anniversary of ILL.

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L. Gajdoš (ILL)

EMBL Grenoble celebrates 50 years of research in structural biology

EMBL Grenoble celebrated its 50th anniversary on Friday, 4 July 2025, at the historic Château de Sassenage. The event brought together institutional partners, alumni, and collaborators to reflect on the site's key scientific milestones in structural biology and the development of new technologies.

The first session featured speakers from French institutions and international scientific organisations who emphasised the importance of collaboration. EMBL's Interim Director General, Peer Bork, and Interim Executive Director, Ewan Birney, highlighted the strong relationship with France and shared their vision for EMBL's future.

The second session included discussions on scientific advancements, personal stories, and future perspectives. The celebration also included a cake cutting by Kristina Djinović-Carugo and a rock and roll performance by the band Monsieur Manchango, featuring EMBL Grenoble Team Leader Gergely Papp on drums. Guests also had the opportunity to explore the château and its botanical gardens.

More info about EMBl Grenoble history:
https://www.embl.org/sites/grenoble/history/

K. Nalin, J. Marquez and E. Kowalinski (EMBL)

PSB x GRAL Student Day

The annual [PSB x GRAL] Student Day, held on the EPN campus at the Institut de Biologie Structurale (IBS) that took place the 3rd of June, was once again a great success, bringing together around 100 participants! This event provided an excellent opportunity for students from the EPN campus and from the GRAL Labex (BioSanté, BGE, IBS, ISBG, LCBM, and LPCV) to meet, exchange ideas, and discuss diverse topics in cell and structural biology.

The invited speakers, Homaira Nawabi (GIN) and Robert Schneider (IBS/CEA), opened the morning and afternoon sessions respectively by sharing not only their research but also their personal experiences, offering students valuable insights and inspiration for their future careers.

In addition, several students presented their work: Serena Sleiman (IBS), Nikita Sharaev (EMBL), Poushalee Dutta (IBS), Mrinalini Lianne Rao (IBS), Théodore Arnaud (ILL), and Ananya Kedige Rao (LPCV), engaging the audience with their presentations and discussions. Serena Sleiman (IBS) was recognized with the award for Best Oral Presentation.

The poster session was another highlight, with 26 posters displayed

in the IBS hall. The audience prize for Best Poster was awarded to Maxime Bierre (IBS) for his outstanding presentation.

The day concluded with a lively team quiz and an informal gathering at Le Chalet on the EPN campus, which provided a convivial way to wrap up the event.

The organizing committee—A.-M. Anastasova (EMBL), T. Arnaud (ILL), F. Bernaudat (PSB), J. Eum (EMBL), F. Foudalkar (IBS), I. Boukherrouba (ESRF), R. Perez-Bucio (IBS), and S. Vittu (GRAL)—warmly thank all participants for contributing to the success of this event, and look forward to seeing everyone again at next year's [PSB x GRAL] Student Day!

[PSB x GRAL] Organizing Committee

User Dedicated Microsymposium-1 on "Tomography in and for Structural Biology"

Tomography has developed as a key method in structural biology. X-ray and electron tomography let researchers view 3D biological structures at different scales to better understand complex systems that once were too hard to study. To publicize and promote these techniques at the ESRF, a microsymposium on "Tomography in and for Structural Biology" was held on February 12, 2025, focusing on how tomography techniques do and can support structural biology research. The symposium highlighted tools already available at ESRF including X-ray nanotomography (performed on ID16A) and cryo-electron tomography (on CM01) as well as X-ray microtomography (on ID30B), which is still being commissioned but will be open to users soon.

The event drew nearly 90 participants, filling the IBS seminar room, with about a third coming from outside institutes. Michael Krisch, Director of Life Sciences and Chemistry, opened the symposium with a warm welcome.

The program featured four keynote speakers: Carles Bosch Piñol (Francis Crick Institute, UK) presented insightful imaging work on brain samples using X-ray nanotomography and AI-based method analysis, while Thomas van de Kamp (KIT, Germany) spoke about captivating high-throughput X-ray microtomography for insect fossils. Alessia Cedola (Nanotechnology Institute, Italy) shared compelling research on Alzheimer's disease using an integrated structural biology technique. To finish, Benjamin Engel (Bio-Zentrum, Switzerland) presented his work on fascinating molecular machines involved in photosynthesis process using cryo-electron tomography. Several abstract talks emphasized the important role ESRF tomography beamlines played in advancing their research.

A closing round-table discussion focused on future access and development of tomography at the ESRF. There was strong support for expanding BAG access and recognition of use of these techniques across many research areas.

We would like to thank all the speakers for bringing valuable insights and fostering fruitful discussions, and we also sincerely appreciate the ESRF management and the User Office for their essential support.

A. Pacureanu, C. Mueller-Dieckmann and E. Kandiah (ESRF)

PSB Symposium on Machine Learning in Cellular Structural Biology

On 26 - 27 June 2025, the Partnership for Structural Biology (PSB) hosted its 5th biennial PSB Symposium at the EPN Science Campus in Grenoble, drawing nearly 150 participants from 12 countries. This year's exciting theme, "Machine Learning in Cellular Structural Biology" highlighted recent advances at the intersection of computational and experimental approaches in structural biology and sub-cellular imaging. It aimed to showcase how artificial intelligence (AI) and machine learning (ML) are being applied not only in fundamental molecular and cellular research but also in translational and therapeutic contexts.

The two-day event featured 13 invited talks by leading experts from Europe and the United States, who presented their latest research across four thematic sessions: "Computational Tools and Databases", "Proteome Wide Approaches", "Applied Protein Design", and "Integrated Approaches in Life Science". In addition, eight participants selected from abstract submissions delivered engaging short talks, and a lively poster session, provided a platform to early-career scientists to present their recent findings, and discuss challenges and future directions in applying ML to structural biology. Two "Best Poster" prizes were awarded to Maxime Bierre (IBS) and Melanie Schneider (EMBL). The event also offered a unique opportunity to discover the EPN campus and the collaborative environment of the PSB, as external participants could enjoy a guided tour of a selection of platforms and facilities including the MASSIF-1 and CM01 ESRF beamlines, the HTX crystallisation platform at EMBL, and the NMR platform and new FIB-SEM instrument at IBS.

The organisers gratefully acknowledge the symposium's sponsors - Arinax, Bioligomer, BIOSAXS GmbH, the Grenoble Alliance for Integrated Structural & Cell Biology (GRAL), the Grenoble-Alpes Métropole, the Région Auvergne-Rhône-Alpes, and the Université Grenoble Alpes (UGA) – for their generous support, and sincerely thank all the participants for their contributions to the success of the event. See you in 2027 for the 6th edition of the PSB Symposium!

F. Bernaudat (PSB)

French neutron scattering community meets in Annecy

From 2–5 June, *the Journées de la Diffusion Neutronique* (JDN 2025) gathered the French neutron scattering community in the inspiring setting of Lake Annecy. Over four days, participants enjoyed a rich mix of scientific talks spanning physics, biology, and materials science, as well as engaging sessions on research infrastructures and inclusion in science. Among the highlights of the meeting was the Best PhD Thesis Award, presented to Valentin Czamler for his impactful work on very cold neutrons within the ILL's Nuclear and Particle Physics group (NPP). Beyond the science, JDN confirmed its role as a key meeting point fostering exchange, collaboration, and support for early-career researchers.

L. Gajdoš (ILL)

7th International Symposium on Diffraction Structural Biology (ISDSB2025)

The 7th International Symposium on Diffraction Structural Biology (ISDSB2025) was held from 5 – 7 May 2025 on the European Photon and Neutron Science (EPN) Campus in Grenoble, and was hosted by the Partnership for Structural Biology (PSB). Launched in 2003 in Tsukuba, the ISDSB series has since been hosted in cities such Tokyo, Paris, Nagoya, Knoxville and Osaka, and aims to foster collaboration between structural biologists using diffraction, and those applying complementary technologies, as well as to bridge basic research and industry.

This edition welcomed close to 130 participants and featured a rich scientific programme, including four keynote lectures by Thomas Barends (Max Planck Institute Heidelberg), Ashwin Chari (Max Planck Institute Göttingen), Brent Nannenga (Arizona State University), and So Iwata (Kyoto University), together with twenty-five invited talks by leading scientists from around the world, and seven presentations by young scientist selected from abstract submissions. These talks were organized across eight scientific sessions, providing valuable insights into the latest developments and future directions in structural biology. In recognition of the scientific impact of the event, IUCr Journals have endorsed the publication of a Collection of articles from ISDSB2025 in *Acta Crystallographica D* or *Acta Crystallographica F*. The programme also included a poster session, giving an opportunity, particularly for junior scientists, to discuss their latest findings. Attendees were also offered guided tours of some of the EPN facilities including electron diffraction at IBS, ESRF-EMBL jointly operated beamlines ID29, MASSIF-1, and CM01, as well as the HTX platform at EMBL, thereby showcasing the unique and collaborative environment on the EPN campus.

The organisers wish to thank all the participants and the event's valued sponsors - ALPX, ARINAX, Bioligomer, DECTRIS, the "Fédération Française de Diffusion Neutronique", and the Labex GRAL - for their support, which contributed to the success of ISDSB2025.

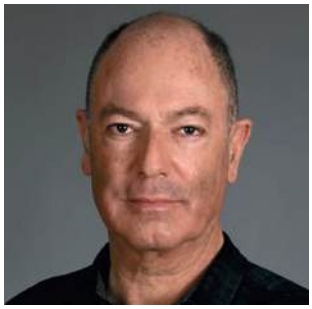
F. Bernaudat (PSB)

ANNOUNCEMENTS

Eva Kowalinski, (EMBL Grenoble) together with **Stefanie Kaiser** (Goethe University, Frankfurt) received the Franco-German science prize "Prix Forcheurs Jean-Marie Lehn". The award recognizes a collaborative research partnership in chemistry, biochemistry, pharmacology, or fields at the intersection of chemistry and health sciences, aimed at strengthening scientific cooperation between France and Germany. It was first presented in 2017 by the Franco-German University (FGU) and the French Embassy in Germany. The 2025 prize honors the two scientists' joint research project focused on identifying new cancer therapeutics targeting RNA modifications.

A new EMBL spin-off **Cerelixis** has won the Venturelab competition from the Bio Innovation Institute, and secured funding to develop precision solutions for resilient agriculture. Research from EMBL Grenoble's Marquez Team on the mechanistic understanding of plant signaling pathways, combined with CrystalDirect technology, enabled the development of precision phytostimulants to help crops better withstand adverse conditions. Cerelixis aims to translate these discoveries into sustainable agricultural solutions. Press release https://www.embl.org/news/science-technology/new-embl-spin-off-cerelixis/

Photo: BioInnovation Institute/Esben Zøllner



EMBL Grenoble alumnus, **Florent Cipriani** (EMBL Grenoble, 1991-2020), was awarded the 2025 Lennart Philipson Award in recognition of his exceptional contributions to structural biology instrumentation. As Head of the EMBL Instrumentation Team, Florent led the collaborative development of a number of pioneering technologies with EMBL, ESRF and ILL colleagues. These include micro-diffractometers, robotic sample changers, and, jointly with J.A. Márquez (Grenoble HTX team), the CrystalDirect Harvester. Many of these innovations have advanced automation, throughput, and precision in macromolecular crystallography to transform how structural biology experiments are now conducted on the ESRF-EMBL jointly beamlines. Many of these innovations have now been licensed to commercial partners and are implemented at synchrotron radiation facilities globally.

Photo: Atelier Photo 38

Alicia Vallet and Lionel Imbert, crystal medals of the CNRS

Photo: CNRS – P. Carrel

Alicia Vallet, research engineer in the NMR Group at IBS, has been awarded the crystal medal for her role in the Infranalytics national research infrastructure, for which she is responsible of relationships with industrial partners, including the preparation of contracts. Besides, she is in charge of the solid NMR aspects of the NMR platform of the IBS.

Photo: CNRS – P. Carrel

Lionel Imbert, research engineer in the NMRLA Group at IBS, has received the crystal medal for his role in the development and promotion of isotopic labelling using a cell-free system. Lionel is responsible for the Cell-free expression platform for the large-scale production of proteins and RNA.

NEWCOMERS

Sophie Ayscough started at the ILL in June 2025 as a reflectometry instrument scientist, co-responsible on D17. She undertook a PhD at the University of Edinburgh and ISIS neutron and Muon Source in membrane biophysics, developing novel membrane mimetics and investigating membrane protein conformational changes. She continued her biophysics research with Post doctoral positions at the European Spallation Source and Lund University investigating light-responsive cyanobacterial membranes and then protein-protein interactions in apoptosis. She has a strong interest in working with complex lipid models and using reflectometry to characterize protein-membrane kinetics.

PROFILE

Photo: Margaux Molinas

Rebekka Wild joined the IBS in 2019 to start her team in the Structure and Activity of Glycosaminoglycan Group, and in recent years, she has been awarded two prestigious prizes, the Impulscience® fellowship from the Bettencourt-Schueller Foundation in 2023, and the CNRS Bronze medal in 2024. The PSB Newsletter interviewed Rebekka, to know more about her and her work, and to discuss her views on how to become a successful scientist.

Could you tell us a bit about yourself and your scientific background?

Pursuing my genuine interest in natural science, I decided to do a Master's in Biochemistry at the University of Tübingen in Germany. During this time, I developed a strong interest and admiration for protein structures. I thus started a PhD focusing on protein structure characterization using X-ray crystallography. My PhD work was carried out partially in Tübingen and partially in Geneva, Switzerland, and it led to the discovery of a small protein domain that acts as a phosphate sensor. During my search for postdoc positions, the "resolution revolution of cryo-EM" was about to emerge, and I thus chose to do a postdoc at ETH Zürich, Switzerland, aiming to learn cryo-EM to study high-resolution structures of membrane protein complexes. More precisely, I studied a eukaryotic enzyme complex carrying out a central step in N-linked glycosylation and was fascinated by the complexity and challenges of glycobiology. From this point, my future goal was clear: establishing a research team characterizing complex glycans. In 2019, I was recruited by the CNRS and joined the Structure and Activity of Glycosaminoglycan Group at IBS in Grenoble.

What brought you to Grenoble and the IBS?

When I started looking for permanent researcher positions, I had two core interests: structure determination by cryo-EM and addressing fundamental questions in glycobiology. Grenoble is one of the few places in Europe that brings together these two fields. The IBS and the EPN campus offer strong expertise and state-of-the-art equipment in cryo-EM, while the Glyco@Alps program unites more than 200 researchers interested in various aspects of GlycoSciences. It was the perfect environment to get started. And, okay, I would be lying if I said the beautiful mountain setting didn't influence my decision.

What is the focus of the research topics of your team?

With my team, we are interested in studying the biosynthesis machinery that generates long, complex polysaccharide chains in the human body. These polysaccharides, called glycosaminoglycans, regulate many different cellular processes, such as cell growth and differentiation. At the same time, they also play roles in diverse pathologies, including Alzheimer's disease and cancer. We aim to understand this biosynthesis machinery at the atomic level, which lays the cornerstone for future structure-based drug design.

In 2023 you have been awarded the Impulscience® fellowship from the Bettencourt-Schueller Foundation, and the CNRS Bronze medal in 2024. Could you first tell us how these awards have impacted your daily work and the way you envisage the future developments of your research and your team? Did receiving these awards open up new opportunities for you and/or initiate new collaborations?

I was sincerely honored to receive these prestigious prizes. Being recognized for the work we are doing, even though it is fundamental research on a niche topic, was very reassuring and motivating for me. For junior team leaders, receiving such awards increases visibility at the national level, which has helped me establish new collaborations and recruit additional team members. The Impulscience® fellowship has transformed the research in our team, as the extensive financial resources allowed me to substantially grow the team, expand the range of biophysical methods we use, and tackle more competitive and ambitious research questions.

Had you heard about the PSB before coming here and how would you say this environment contributes or helps you in your research projects?

Yes, I learned about the PSB while searching for a host institute during my CNRS application. I was particularly drawn by the accessibility of state-of-the-art equipment for the biophysical characterization of protein samples. We now routinely use a wide range of these techniques to study our protein complexes.

What advice would you give a young researcher aspiring to lead their own lab or team one day?

I believe everyone excels at doing what they truly enjoy. And if you are good at something, you will likely succeed. So, if you are passionate about research, don't let setbacks discourage you, but stay persistent and follow your dreams.

What qualities do you think are important for this role, and what would you say your best one is?

I was surprised by the diversity of tasks I have to manage, many of which I had little prior experience with - managing a team and grants, purchasing new equipment, setting up IT infrastructure for data processing and storage, as well as committee and evaluation work. But as researchers, we have the necessary toolbox to tackle these tasks: we can adapt to new situations, are used to constantly learning new things, and know how to troubleshoot effectively. I also believe that good communication skills are crucial, not only for conveying research results but also for interacting with colleagues and mediating potential conflicts.

What am I good at? I think I have fairly strong organizational skills, which are absolutely essential if you want to juggle research activities and family life.

F. Bernaudat (PSB) and A. Royant (IBS)

DATES FOR YOUR DIARY

4th November 2025 – PSB Seminar "Tracking membrane transport and regulation in real time" by Magnus Andersson, Umeå university

The PSB Seminar will be held on Tuesday 4 November at 11:00 in the EMBL seminar room.
P-type ATPase transport is carried out in a complex lipid environment and is regulated by both external and internal factors. We have developed a methodology to track P-type ATPase domain rearrangements in real time triggered by laser-induced release of ATP and subsequent monitoring by synchrotron X-ray pulses. We used this time-resolved X-ray solution scattering (TR-XSS) technique to capture the dynamics of eukaryotic and prokaryotic calcium transport (SERCA and LMCA1). We then explored regulatory dynamics induced by the surrounding lipid/detergent environment. We developed structural refinement approached based on MD simulations and ensemble learning algorithms. The results show both subtle and drastic effects on the protein dynamics and kinetics induced by lipid/detergent regulatory processes.

17th and 18th November 2025 - 48H of GRAL 2025

The "48H of GRAL" is an excellent opportunity to strengthen interactions within the GRAL community, and includes plenary lectures, poster sessions, and discussions. Approximately 150 participants from the GRAL labs (BioSanté, BGE, IBS, LCBM, and LPCV) as well as close collaborators in Grenoble (DPM, EMBL, ESRF, GIN, IAB, ILL, LBFA, LIPHy, SyMMES, TIMC, ...) are expected. All researchers, Post-Docs, PhD students of the Gral perimeter and collaborators are welcome to attend!
For further information and registration: https://www.labex-gral.fr/events/48h-of-gral-seminar-2025/

2nd to 4th February 2026 - ESRF User Meeting 2026

The event will gather the international ESRF community, the beamline staff and the ESRF User Organisation for a rich program featuring tutorials, plenary sessions with a round-table discussion, and user-dedicated microsymposia.
A series of engaging tutorials will be offered to help both newcomers and experienced users in making the most of their data, while introducing recently developed tools and techniques. The plenary session will highlight outstanding research from leaders in synchrotron science research. They shall serve as a platform to share latest discoveries and explore how synchrotron science can impact various areas of research.
Finally, three User Dedicated Symposia (UDMs) will focus on the topics of neurobiology, quantum & magnetic materials as well as the use of coherence to explore new spatial and temporal domains. In addition, a dedicated satellite event for the European Battery Hub will offer insights into the organisation and scientific scope of this project. The UDMs are intending to serve as topical forums, enabling researchers to gather, share knowledge, and discuss scientific challenges within their respective communities.
For further information and registration: https://www.esrf.fr/UM2026

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The Partnership for Structural Biology (PSB) is a collaboration between a number of prestigious European and French scientific laboratories in Grenoble. The PSB is unique in combining world leading user facilities for synchrotron X-ray and neutron scattering with NMR, electron microscopy, molecular biology and high throughput techniques on a single site together with strong projects in a broad range of structural biology.