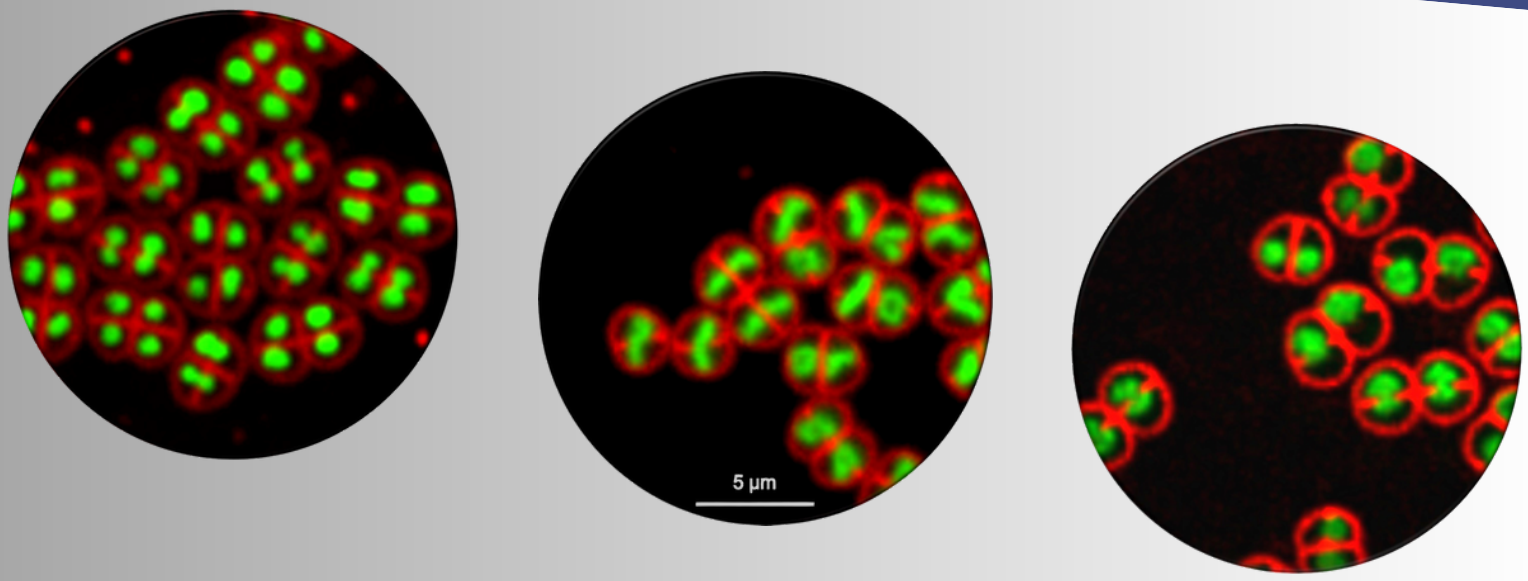
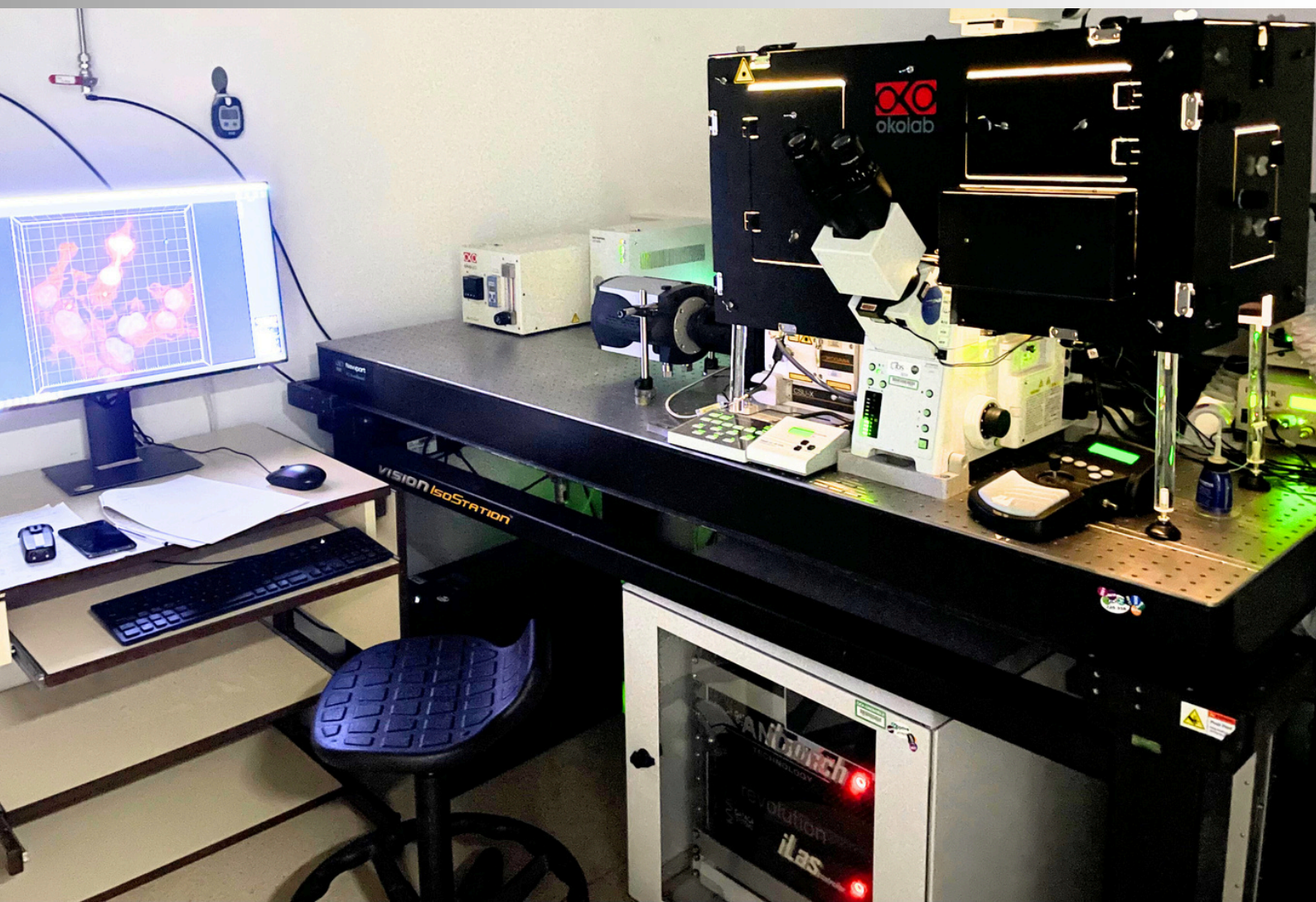
Scientific Newsletter

WINTER 2024

cea irig





EDITORIAL

Dear All,

Here we are, already at the dawn of a new year.

I wish you a very happy 2025! May it be full of exciting projects, successes and, above all, good times, both in your professional and personal lives. I wish you a fulfilling year, rich in new opportunities.

2024 was a very busy year for our IRIG institute. It marked five years of existence, and I think we can all be proud of what we've built. This has been made possible thanks to your commitment and your passion for advancing our research projects, supporting young people and helping them to grow and prepare for their future, as well as promoting our results to society, so that our research can find its place at the service of the world's major challenges.

Once again this year, IRIG has been very active, with a number of successes to mark the period. For example, many prestigious prizes were awarded to several of our researchers: some rewarding rich and fruitful careers, others celebrating encouraging milestones for the future.

Last year, I told you about our successes in the major France 2030 programmes, and in particular our exceptional involvement in the PEPR (Priority Research Programmes and Equipment) in the four thematic pillars of IRIG's research (Biology and Health, Energy and Environment, Physics and Numerics, Cryotechnologies). This dynamic has enabled us to strengthen our involvement, with a number of new successes, particularly in the PEPR calls for projects. These successes testify to our recognised excellence, our active role in national networks and our capacity to innovate.

The year 2024 also marked the start of high-risk research programmes led by research organisations. The DRF, which is in charge of the programme for the CEA, launched its Audace! programme, which supports very ambitious structuring projects as well as seed projects. We are proud to see three of our structuring projects rewarded: one on CO_2 capture, another on neural networks for AI computing based on magnetic memories, and the last on advanced instrumentation for DNP imaging. Many other topics and successes marked this year 2024, several of which were presented in our scientific newsletter.

At the same time, the year saw significant progress on the important QWL (Quality of Life and Working Conditions) project, thanks in particular to our ambitious programme to renovate our buildings. In September, we inaugurated the completion of major works on building 1005, with a magnificent new façade. Work is progressing on the renovation of C3, a new project is starting at D1, and we will be continuing with the necessary preparatory stages for the renovation of C5.

The year 2025 is already shaping up to be a very busy one. It will be particularly important for all the UMRs, with the preparation of the HCERES dossier. This evaluation will be a milestone for our laboratories, providing an opportunity to take stock of the last five or six years and look to the future.

I wish you all the best for 2025, and I look forward to sharing our successes with you at our Annual Meeting on 14 March.

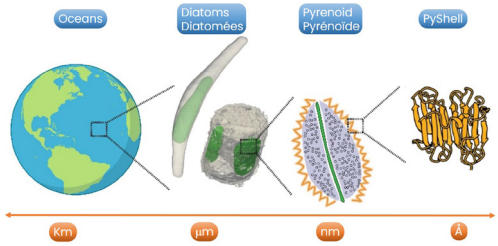
Pascale BAYLE-GUILLEMAUD
Head of the Interdisciplinary Research Institute of Grenoble

On cover : photo of the microscope and images of bacterium's nucleoid © CEA

How diatoms enhance their CO_2 assimilation efficiency

Giovanni Finazzi LPCV Cell & Plant Physiology Laboratory

Diatoms are very abundant oceanic organisms that contribute up to 20% of the daily planetary carbon assimilation. This function is mediated by their pyrenoid, a structure that concentrate the CO_2 fixing enzyme Rubisco inside the PyShell, a protein barrier that modulates gas exchanges with the cell. By concentrating Rubisco inside a specific compartment, the pyrenoid increases the efficiency of CO_2 assimilation in an oxygen-free environment.



Focus on the diatoms Pyshell © CEA

Despite the importance of this process, the molecular mechanism allowing diatoms to efficiently assimilate CO_2 via their pyrenoids remains poorly understood. In this study a French, Japanese and Swiss consortium combine state of the art imaging and photophysiology to characterise the pyrenoid shell (PyShell) layer in vivo. This proteinaceous ordered assembly is localized at the pyrenoid periphery of Diatoms.

Using in situ cryo-electron tomography (cryo-ET), single particle cryo-ET and Focused Ion Beam Scanning Electron Microscopy (FIB-SEM), researchers reveal that the PyShell encased in a lattice-like protein sheath -instead of a lipid membrane. Disruption of the PyShell protein sheath by targeted mutagenesis leads to a fragmented pyrenoid structure, high-CO_2 requiring-photosynthesis and reduced cell growth. Recombinant PyShell proteins self-assembled into helical tubes enabling the researchers to determine a 3.0 Å-resolution PyShell structure and fit it into the *in vivo* structure.

Overall the structure and function of the diatom PyShell provides new molecular insights for how CO_2 is assimilated in the ocean, a crucial biome to mitigate climate change. Diatoms are marine organisms that assimilate almost 20% of the world's carbon on a daily basis. Thus, the study of their pyrenoid open new insights into the mechanism of this greenhouse gas assimilation in the ocean.

REFERENCE

Shimakawa G, Demulder M, Flori S, Kawamoto A, Tsuji Y, Nawaly H, Tanaka A, Tohda R, Ota T, Matsui H, Morishima N, Okubo R, Wietrzynski W, Lamm L, Righetto RD, Uwizeye C, Gallet B, Jouneau PH, Gerle C, Kurisu G, Finazzi G, Engel BE and Matsuda Y.
Diatom pyrenoids are encased in a protein shell that enables efficient CO_2 fixation
Cell 2024

Predicting viral mutations using digital simulation

Luigi Genovese MEM Modeling and Exploration of Materials laboratory

The equations of quantum mechanics are used to describe and predict the structures and properties of molecules. However, until now, few methods are able to calculate more than a few hundred atoms. Researchers at our institute have developed a simulation method QM-CR, which enables thousands of atoms to be simulated using quantum mechanics (QM) combined with a reduction in the complexity of the degrees of freedom (CR). In this study, they succeeded in simulating the electronic structure of around 13,000 atoms to predict and characterize the binding of variants of the SARS-CoV-2 spike protein to the human haACE2 receptor.

The researchers [**Collaboration**] compared four variants of the spike protein: Wuhan, Omicron, and two variants based on Omicron. To assess their binding to the haACE2 receptor, the scientists took into account the energetic contribution of the amino acids, and simulated a projection of the effect of certain mutations for each amino acid. This study provided a more detailed understanding of how different mutations affect the interaction between the spike protein and the hACE2 receptor. In addition, the predictions of the simulations were validated by comparing the efficiency of the spike protein variants in binding to cells expressing hACE2 (see **figure**).

These results are remarkable because when they were published in 2021, the A484K mutation thought to be involved in binding to ACE2 had not yet been identified by epidemiology laboratories. Only 20 months later this mutation was actually observed in the BA.2.86 variant, confirming the value of quantum simulations for obtaining highly advanced predictions.

This QM-CR quantum simulation model has demonstrated its ability to identify mutations crucial to intermolecular interactions. This method not only helps to understand the underlying mechanisms of protein binding, but can also guide the design of new, highly specific treatments. This work highlights the importance of advanced modelling tools in the study of complex biological interactions and their potential for monitoring the evolution of viruses and designing more robust vaccines.

Collaboration

- Boston College Department of Biology (USA)
- Harvard Medical School (USA)
- RIKEN Center for Computational Science (Japan)

REFERENCE

Zaccaria M, Genovese L, Lawhorn B, Dawson W, Joyal As, Hu J, Autissier P, Nakajima T, Johnson W, Fofana I, Farzan M and Momeni B.
Predicting potential SARS-CoV-2 mutations of concern via full quantum mechanical modelling.
J. R. Soc. Interface 2024

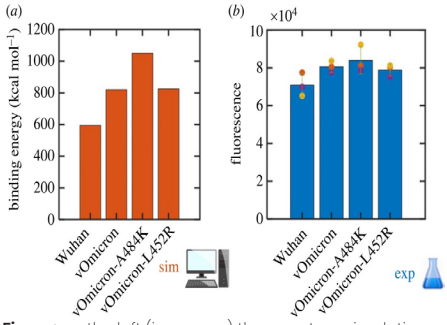


Figure: on the left (in orange) the quantum simulation of the virulence of the four SARS-CoV-2 variants is confirmed by experimental tests, on the right (in blue). © CEA

Behind the scenes at Iron-Sulphur Centre factories

Sandrine Ollagnier LCBM Chemistry and Biology of Metals Laboratory

Proteins containing iron-sulfur (Fe-S) clusters are involved in many cellular processes, such as DNA replication and repair, respiration and photosynthesis. Their importance lies in their functional versatility, including electron transfer, redox and non-redox catalysis, regulation of gene expression and the supply of sulfur atoms. These Fe-S clusters do not form spontaneously *in vivo*, but require complex multi-protein machineries, known as Fe-S factories, to assemble them.

Researchers at CEA-IRIG have long focused on understanding these factories that preform Fe-S clusters before transferring them to target proteins in the cell, such as respiratory complexes. The exact nature and ligands of the Fe-S clusters within these factories remain a mystery, despite recent advances in biophysics and genetics.

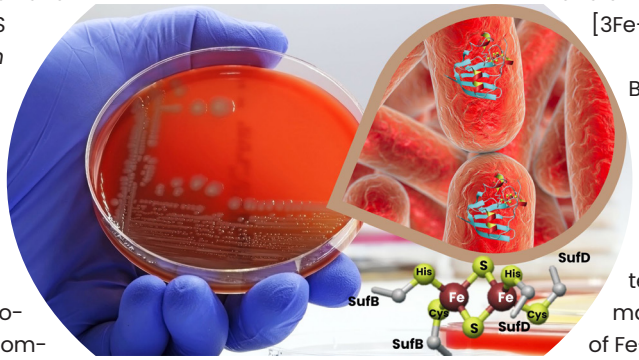


Figure: Study of the SufBC$_2$D factory in bacteria E. coli. © CEA

In this article, the researchers [**Collaboration**] studied the SufBC$_2$D Fe-S cluster factory in bacteria. Using a native purifiedsystem , they characterized this factory containing natural Fe-S clusters. Using biophysical characterization techniques such as X-ray absorption spectroscopy, Mössbauer spectroscopy, Electron paramagnetic resonance spectroscopy and UV-visible absorption spectroscopy, they found that SufBC$_2$D mainly contains a [2Fe-2S]-type cluster, and an unidentified species, possibly a [3Fe-5S]-type cluster.

By analyzing protein variants, the researchers identified several amino acids involved in the coordination of the [2Fe-2S] cluster, suggesting a coordination at the interface of the SufB and SufD proteins. This study provides new information on the molecular organization of Fe-S clusters in the SufBC$_2$D factory and raises questions about the nature of the second iron-sulfur species observed, a topic to be further explored in the context of Fe-S cluster biosynthesis and more broadly in bioinorganic chemistry.

This work will provide a better understanding of the mechanisms by which Fe-S clusters are formed *in vivo* with a view to opening up new avenues for biotechnological and medical applications.

REFERENCE
Veronesi G, Pérard J, Clémancey M, Gerez C, Duverger Y, Kieffer I, Barras F, Gambarelli S, Blondin G and Ollagnier de Choudens S.
Multimodal Spectroscopic Analysis of the Fe-S Clusters of the as-Isolated Escherichia coli SufBC$_2$D Complex.
Inorganic Chemistry 2024

Collaboration
- IRIG/SYMMES
- Institut Pasteur
- LCB, Marseille

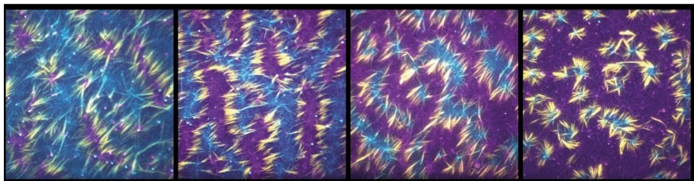
Fundings
- French ANR grant FeStreS (2012-2016)
- French ANR grant MASTIC (2023-2027)

New insights into the internal organization of cells

Manuel Thery LPCV Cell & Plant Physiology Laboratory

Morphogenesis encompasses all the mechanisms that induce the appearance of forms from initially homogeneous systems. Revealed by chemistry and physics, these mechanisms are responsible for the appearance of regular structures in biology. A new morphogenesis has just been discovered by studying the self-organization of microtubules.

By reconstituting an in vitro system with molecular motors directed at both ends of the microtubules, the researchers discovered that these motors not only moved the microtubules, but also aligned them, forming “barriers”. At the same time, these motors separated into distinct domains, creating an ordered yet dynamic structure where microtubules and motors influence each other. This organization is constantly evolving, changing shape or disappearing according to the forces implicated.A theoretical approach equated the necessary balance between transport and diffusion of molecular motors, determining the precise conditions for the appearance of regular patterns, and revealed that an imbalance in motor concentration, and therefore in the forces exerted on microtubules, prevented pattern formation, causing constant microtubule movement. It also identified the exact conditions under which a slight variation in motor concentration caused the experimental system to switch from constant microtubule movement to sudden immobilization, resulting in the appearance of alternating domains. Mirroring the self-organization observed in vitro, microtubules often align in cells with polarities oriented in the same direction, and motors of the same polarity tend to form more concentrated domains in line with their direction of travel.



Superposition of images obtained by TIRF microscopy (evanescent wave imaging) to visualize microtubules (yellow) and two molecular motors KIF5B (magenta) and NCD (cyan).From left to right, KIF5B concentrations increase while NCD concentrations decrease. Microtubule density is around 1 microtubule per µm². © CEA

This hypothesis could challenge current models of the mechanisms by which cells define their orientation axes. This work opens up new perspectives on the internal organization of cells.

Collaboration
- ESPCI
- CNRS
- Collège de France

REFERENCE
Utzschneider C, Suresh B, Sciortino A, Gaillard J, Schaeffer A, Pattanayak S, Joanny JF, Blanchoin L and Théry M.
Force balance of opposing diffusive motors generates polarity-sorted microtuble patterns
PNAS 2024

Fundings
- ANR Sharp AAPG2022-PRC-SHARPI
- ANR Sensation ANR-23-CHBS-0013 France 2030

The bacterium that survives everything

Joanna Timmins IBS Institut de Biologie Structurale

A team from CEA-IRIG, among the few researchers studying Deinococcus radiodurans, has used advanced fluorescence microscopy techniques to reveal, for the first time, the process of nucleoid remodeling in this bacterium. This remodeling is crucial for its exceptional resistance to extreme conditions such as ionizing and UV radiation and prolonged drought. This discovery adds to our understanding of the survival mechanisms of this unique bacterium.

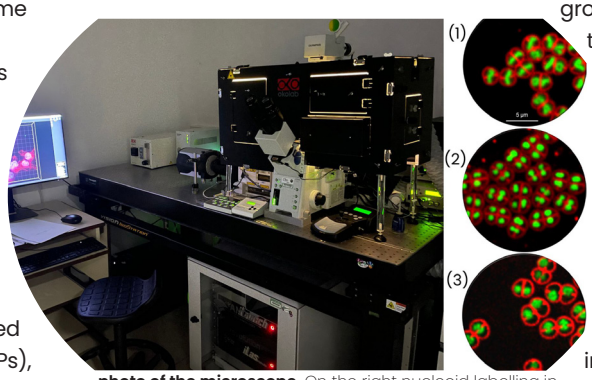


photo of the microscope. On the right nucleoid labelling in green and membrane labelling in red. © CEA
(1) Normal nucleoides.
(2) Compact nucleoides following nutrient deficiency.
(3) Compact nucleoides following UV-C irradiation.

Nucleoid remodeling is a common strategy used by bacteria to protect their DNA in response to external stress. This process is mainly controlled by nucleoid-associated proteins (NAPs), which interact with DNA to compact the genome. This compaction helps to maintain the integrity of the genetic material under adverse conditions.

In previous studies, researchers from this team have shown that the D. radiodurans nucleoid is compact, yet sufficiently dynamic to adapt to the morphology of the cell during the cell cycle.

This new study now examines the impact of two stresses on the morphology and state of compaction of the nucleoid: exposure to UV-C radiation, which damages the genome, and nutrient deprivation which leads to stationary phase and growth arrest. The study also assesses how these stresses affect the mobility of the HU protein, the main NAP in these nucleoids, in order to probe its interaction with the DNA.

The study shows that nutrient and UV-C stress cause rapid nucleoid compaction, but by distinct mechanisms. HU mobility decreases in response to nutrient deprivation, whereas it increases in response to UV-C light. After a phase of rapid condensation due to UV-C, the nucleoid slowly decompacts, allowing HU to regain its normal mobility and the nucleoid to return to its initial structure, before recovery of cell growth.

For the first time, this study has allowed the visualization in real time of the nucleoid remodeling process in D. radiodurans using advanced fluorescence microscopy techniques. This direct observation has contributed to a better understanding of the resistance mechanisms of this exceptional bacterium.

REFERENCE

Vauclare P, Wulffelé J, Lacroix F, Servant P, Confalonieri F, Kleman JP, Bourgeois D and Timmins J.
Stress-induced nucleoid remodeling in Deinococcus radiodurans is associated with major changes in Heat Unstable (HU) protein dynamics
Nucleic Acids Res 2024

An unexpected immune defect revealed by COVID-19 in Incontinentia Pigmenti patients

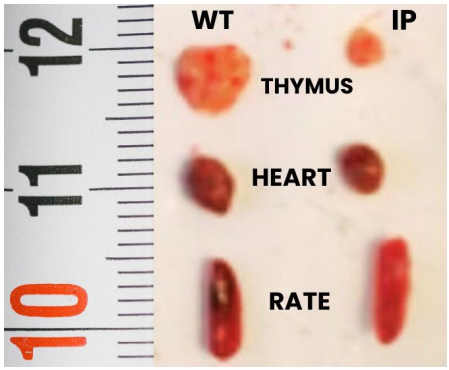
Marie Odile Fauvarque BGE Biosciences and bioengineering for health Laboratory

Incontinentia pigmenti (IP) is characterized by skin inflammation at birth, accompanied by complications that can differentially affect various organs throughout life, including the eyes, teeth, bones, and brain. This condition is caused by a mutation in the NEMO gene (Nuclear Factor Kappa B Essential Modulator), located on the X chromosome. NEMO plays a crucial role in regulating the immune response and cell survival. In female patients, the mutation is present in a heterozygous state, meaning that only one copy of the gene is altered. In contrast, the functional absence of NEMO in male fetuses is lethal.

In 2020, it was demonstrated that 15% of patients severely affected by COVID-19 express autoantibodies against interferons-α, cytokines essential for antiviral immunity. The production of these autoantibodies is often linked to genetic predispositions. An international clinical consortium studied a cohort of 131 female patients with incontinentia pigmenti and unexpectedly found that 36% of them express anti-interferon-α antibodies. Increased susceptibility to COVID-19 was also observed in this population during the pandemic.

Researchers at CEA-IRIG developed a genetically modified mouse model mimicking the disease characteristics. These mice exhibit abnormal thymus, an organ essential for regulating autoimmunity. This anomaly was also observed in some incontinentia pigmenti female patients, as well as in a deceased male fetus carrying the NEMO mutation.

This study revealed an unsuspected vulnerability of incontinentia pigmenti patients to viral infections, highlighting the need for special attention during epidemics. It also demonstrates a new role for the NF-κB pathway in thymus development and function.



Thymus of 7.5-day-old mice with incontinentia pigmenti (IP). IP mice are generally smaller than control mice, with the relative reduction in weight and size of the thymus being even more pronounced, surpassing that observed for other organs as shown here for the heart or spleen..

Fundings
La fondation Incontinentia pigmenti

REFERENCE

Rosain J. et al.
***Incontinentia pigmenti* underlies thymic dysplasia, autoantibodies to type I IFNs, and viral diseases**
Journal of Experimental Medicine 2024

SHARPER a french neutron spectrometer at ILL

Quentin Berrod SyMMES Molecular Systems and nanoMaterials for Energy and Health laboratory

The detection chamber © CEA, ILL, Ecliptique.

Scientists at CEA-Irig and CEA-Iramis have built and now operate SHARPER, a time-of-flight neutron spectrometer installed at the Institut Laue Langevin. This instrument is designed to probe dynamical processes by inelastic neutron scattering.
The modernization of the IN6 spectrometer to SHARP (Spectromètre Hybride Alpes Région Parisienne) and then to SHARPER (SHARP Extended in Resolution) initiated by the Laboratoire Léon Brillouin in 2021, is now complete. The new spectrometer brings performances for a better counting rate, with an extension of accessible resolutions, energy range, and scattering vectors.

The neutron spectrometer SHARPER was designed to meet the needs of diverse scientific communities, enabling it to address societal challenges in the fields of energy, health, quantum physics, and the environment.

The SHARPER allows measuring precisely the energy transferred from the neutrons to the sample with high precision and give insight in the excitations and relaxational phenomena in condensed matter. The so-called Quasi Elastic Neutron Scattering (QENS) signal, gives access to both correlation times, transport properties and the geometry of the movements at the molecular level.

SHARPER delivers unparalleled performance across a wide range of time and length scales. This advanced instrument combines high neutron flux and exceptional energy resolution, achieving 50 µeV, making it ideal for investigating intricate material dynamics. The huge 23 m^3 chamber under vacuum containing 240 positon sensitive detectors (two meters long) greatly improve the background noise and the definition of diffraction patterns.

Optimized for a diverse range of scientific applications, SHARPER sets a new standard in the study of complex material behavior. For example, in the field energy storage the inelastic neutron scattering uncovers mechanisms like ion mobility and lattice dynamics, for the optimization of batteries and hydrogen storage systems (**Fig. 1**).

In the field of quantum materials low-energy excitations arising from atomic vibrations and electronic interactions, offer valuable insights into temperature-dependent properties critical for quantum computing and advanced electronics (**Fig. 2**).

First friendly users are expected in June 2025. A new monochromator is under development to extend the energy resolution and bridge the temporal gap with backscattering spectrometers.

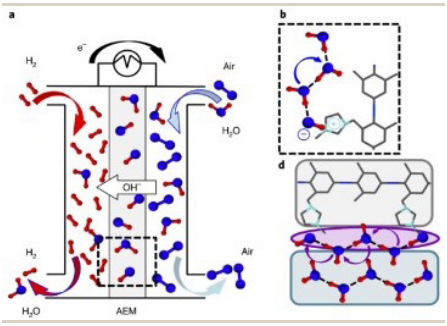


Figure 1: Schematic illustration of an AEM-Fuel Cell and its mode of operation. Sketches illustrating the polymeric membrane, ions and water dynamics (adapted from Foglia, Nat. Mat.).

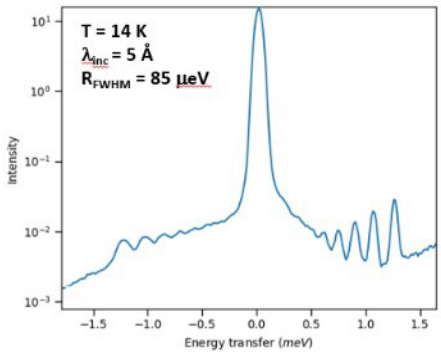
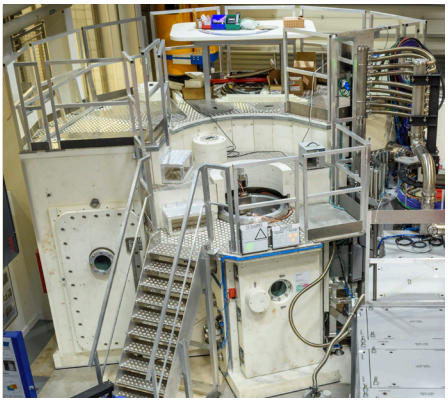


Figure 2: Low-energy magnetic excitations of Mn_{12} Acetate spin cluster.



Sky view from outside SHARPER © CEA, ILL, Ecliptique.

See also

SHARPER on the move
Video on CEA-IRAMIS website

REFERENCES

[1] F. Foglia, Q. Berrod et al.
Disentangling water, ion and polymer dynamics in an anion exchange membrane
Nature Materials 2022
[2] Kellouai et al.
Free volume theory of self-diffusion in zeolites: Molecular simulation and experiment
Microporous and Mesoporous Materials 2025

Fundings

• French-Swedish protocol and agreement (CEA - CNRS - Swedish Research Council) for the design and construction of neutron spectrometers, initiated as part of the European Spallation Source (ESS).
• Program 172 of the French Ministry of Research.
• French Fédération de la Diffusion Neutronique (2FDN) for the sample well lift.

Vibrating microwires raise the treble

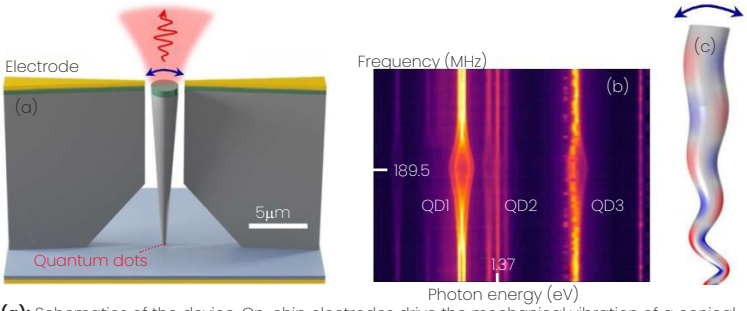
Julien Claudon Pheliqs Quantum Photonics, Electronics and Engineering laboratory

Nowadays, researchers can control the quantum state of various real or artificial atoms. Is it possible to extend this capability to a much larger object, such as a mechanical resonator? The generation of quantum states of motion in a "macroscopic" object will answer fundamental questions and open the way to new applications in quantum information technologies. To achieve this ambitious goal, one promising strategy is to couple the mechanical resonator to an atomic-like system.

Together with colleagues at Institut Néel (Grenoble) and Lumin (Orsay), the team pioneered a device based on a vibrating microwire made of gallium arsenide, which embeds a single quantum dot made of indium arsenide. A quantum dot is a semiconductor nanostructure that behaves as an atom. Indeed, it features discrete energy levels, as well as remarkable optical properties at liquid-helium temperature.

Moreover, the bandgap energy of a semiconductor material is extremely sensitive to deformation of the crystal lattice. This simple mechanism strongly couples the emission wavelength of the quantum dot to the displacement of the microwire. Early studies focused on the fundamental, sub-megahertz resonance of the microwire, which behaves as a classical oscillator. Entering the quantum regime calls for a massive increase in the mechanical frequency, in order to minimize thermal noise. In addition, this will enable the all-optical control and detection of mechanical motion.

The team developed a new device in order to explore the high-frequency mechanical resonances of the microwire (**Fig. a**). A set of on-chip electrodes applies an oscillating electrostatic force to the microwire. Mechanical motion is detected thanks to a few quantum dots, whose luminescence is excited by a laser. When the wire vibrates, the optical emission line of each quantum dot is spectrally broadened (**Fig. b**). Experiments already revealed a flexural resonance with a frequency as high as 190 MHz, one thousand times larger than the one of the fundamental mode. Moreover, the coupling strength to this high-order vibration mode reaches a record value.



(a): Schematics of the device. On-chip electrodes drive the mechanical vibration of a conical microwire that embeds a few QDs near its base.
(b) Detection of the flexural resonance: when the wire is at rest, each quantum dot features a narrow optical emission line (the color codes the light intensity). The excitation of a mechanical resonance (here close to 189.5 MHz) leads to a spectral broadening. Because of the inhomogeneity of mechanical strain in the wire cross-section, this spectral broadening is different for each quantum dot.
(c) Mode shape of the flexural resonance F7: the color codes the local mechanical strain (red: extension, blue: compression).

These findings pave the way towards the optical generation of quantum state of motion and the realization of coherent opto-mechanical interfaces. These are the objectives of the ANR project "AQOUSTIQS", which gathers the above-mentioned partners and will be launched early 2025.

Fundings
• European Union's Horizon 2020 research and innovation program, Marie Skłodowska-Curie grant "QUDOT-TECH"
• French Agence Nationale de la Recherche, grant "IPOD"

REFERENCES

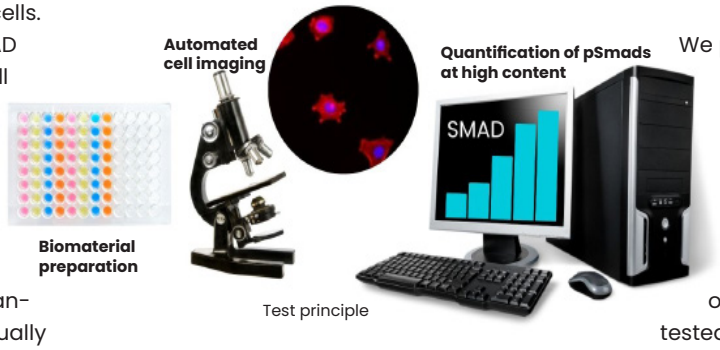
[1] R. Tanos, H. Tlili, Y. Curé, M. Finazzer, A. Artioli, S. Kotal, Y. Genuist, P. Verlot, J. Bleuse, J-M. Gérard and J. Claudon
High-order nanowire resonances for high-frequency, large coupling strength quantum dot hybrid nanomechanics
ACS Photonics 2024

[2] M. Finazzer, R. Tanos, Y. Curé, A. Artioli, S. Kotal, J. Bleuse, Y. Genuist, J.-M. Gérard, F. Donatini and J. Claudon
On-Chip Electrostatic Actuation of a Photonic Wire Antenna Embedding Quantum Dots
Nanoletters 2023

Biological signal quantified by automated test based on fluorescence microscopy

Catherine Picart Biosanté Biology and Biotechnology for Health Laboratory

Bone morphogenetic proteins (BMPs) and transforming growth factor beta TGFβ play a key role in various physiological and pathological processes, such as organ development and cancer. The biological signal induced by these proteins results in the expression of the pSMAD factor in the cell nucleus. Typically, this signal activation is measured by the Western blot assay, which provides average information for all cells.
In order to monitor the pSMAD biological signal for each cell and for a wide range of conditions, we have developed an assay based on fluorescence microscopy. This automated assay makes it possible to analyze cell images and quantify the pSMAD factor individually within each cell.The immuno-fluorescence test meets the same requirements as the Western blot test.



We performed a kinetic study of pSmad activity in response to its activation by BMP/TGFβ proteins, using 96-well microplates. Proteins are presented either directly in solution in the culture medium, or *via* a biomaterial deposited at the bottom of each well.In addition, we have tested drugs targeting the biological signal induced by BMP/TGFβ proteins.

This imaging technique can be applied to the study of other biological signals within cells, in response to stimulation by various proteins playing a physiological or pathological role.

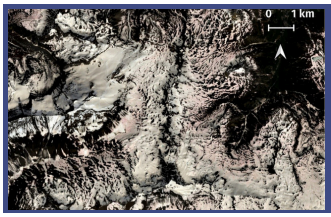
REFERENCE

Khodr V, Clauzier L, Machillot P, Sales A, Migliorini E and Picart C.
Development of an automated high-content immunofluorescence assay of pSmads quantification: Proof-of-concept with drugs inhibiting the BMP/TGFβ pathways
Biotechnology Journal 2024

Press releases - Prizes

Inauguration of a state-of-the-art cryo-electron microscope dedicated to biology

on IRIG website



Glacier blood mapped by satellite detection

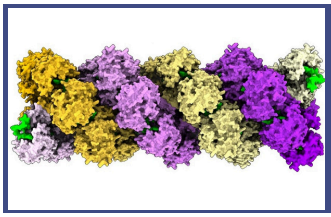
on IRIG website

The Cryonext program for quantum technologies

on IRIG website

Peter Reiss awarded the Prize Clément Codron 2024

on IRIG website



Targeting the genome of the influenza virus encapsidated by nucleoprotein

on IRIG website

Yvain Nicolet - Winner of the 2024 Docteur Henri Labbé and Madame Henri Labbé Prize

on IRIG website

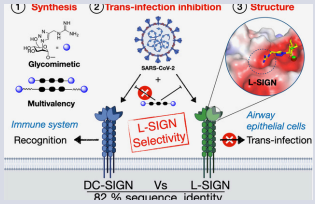
Scientific news from laboratories

A unified nomenclature for tissues near tumors to accelerate cancer research

On BIOSANTE website

Quantum mechanics of poisoned superconducting junctions

On PHELIQS website

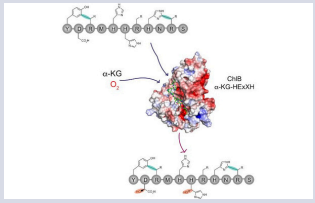


Development of a Specific Antagonist for One of the Two Lectin Receptors of Ebola and SARS-CoV-2 Viruses: Exploiting a Difference of a Single Amino Acid in the Active Site

On IBS website

Dai Aoki awarded 2024 Nishina Memorial Prize

On PHELIQS website

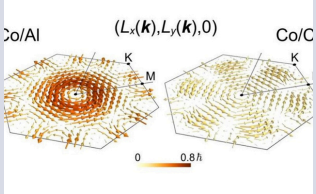


Fused-radical SAM and novel αKG-HExxH oxygenase catalyse cyclophane formation and β-hydroxylation

On IBS website

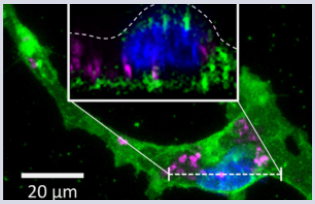
|Hop⟩ the Quantum Game

On PHELIQS website



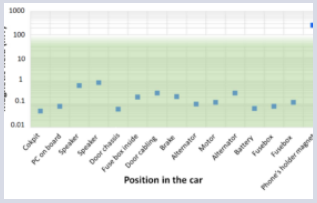
Large chiral orbital texture and orbital Edelstein effect in Co/Al heterostructure

On SPINTEC website



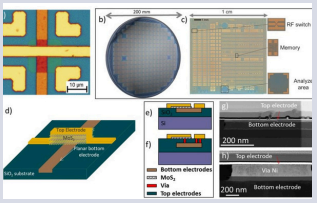
Substrate softness-dependent vortex microdiscs induced cytotoxicity

On SPINTEC website



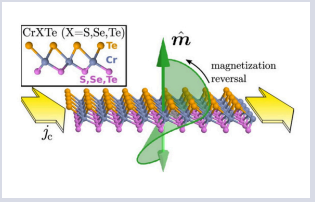
Impact of external magnetic field on Spin Transfer Torque magnetic memory operation

On SPINTEC website



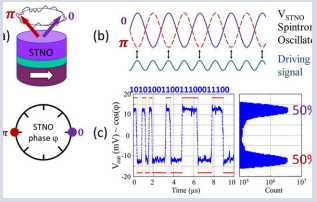
Development and optimization of large-scale integration of 2D material in memristors

On SPINTEC website



Field-Free Spin–Orbit Torque Switching in Janus Chromium Dichalcogenides

On SPINTEC website



Thermal noise, binary phase states and how this can be used for data encryption

On SPINTEC website

Biology and Biotechnology for Health
Unité Inserm
CEA-INSERM-UGA
www.BGE-lab.fr

Biosciences and Bioengineering for Health
UMR
CEA-INSERM-UGA
biosante-lab.fr

Chemistry and Biology of Metals
UMR
CEA-CNRS-UGA
www.CBM-lab.fr

Institut de Biologie Structurale
UMR
CEA-CNRS-UGA
www.IBS.fr

Modeling and Exploration of Materials
UMR
CEA- UGA
www.MEM-lab.fr

Quantum Photonics, Electronics and Engineering
UMR
CEA-UGA
www.pheliqs.fr

Cell & Plant Physiology
UMR
CEA-CNRS-UGA-INRAE
www.LPCV.fr

Low Temperature Systems
Department
UMR
CEA-UGA
www.d-SBT.fr

Spintronics and Component Technology
UMR
CEA-CNRS-UGA-G INP
www.Spintec.fr

Molecular Systems and nanoMaterials for Energy and Health
UMR
CEA-CNRS-UGA
www.Symmes.fr

irig.cea.fr

Interdisciplinary Research Institute of Grenoble
CEA
38054 Grenoble cedex 9

Head
Pascale Bayle-Guillemaud
Annie Andrieux

Publishing Director
Pascale Bayle-Guillemaud

Editor and electronic format
Alain Farchi

Comité de rédaction
Quentin Berrod, Julien Claudon, Marie-Odile Fauvarque, Giovanni Finazzi, Luigi Genovese, Sandrine Ollagnier, Manuel Théry, Joanna Timmins, Alain Farchi