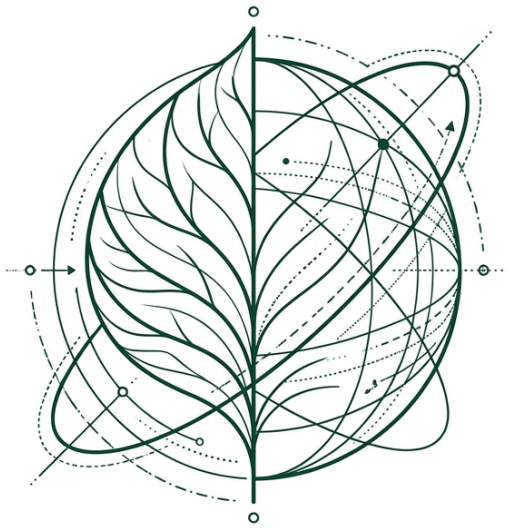
Fundusze Europejskie dla Rozwoju Społecznego | Rzeczpospolita Polska | Dofinansowane przez Unię Europejską | NAWA Narodowa Agencja Wymiany Akademickiej

International Mobility Guide



RESEARCH INTERNSHIPS, STUDY VISITS & ADVANCED WORKSHOPS
PRACTICAL HOST LABORATORY PROFILES, PEER EVALUATIONS, AND ACTIONABLE INSIGHTS FOR EARLY-CAREER RESEARCHERS

Edition: Version 1.0
Publisher: Institute of Biochemistry and Biophysics, Polish Academy of Sciences (IBB PAS)

INTRODUCTION & USER GUIDE

PREFACE: NAVIGATING INTERNATIONAL ACADEMIC MOBILITY AT IBB PAS

The International Mobility Guide is a peer-driven, practical resource designed to assist doctoral candidates and early-career researchers at the Institute of Biochemistry and Biophysics, Polish Academy of Sciences (IBB PAS) in identifying, planning, and executing high-impact foreign academic exchanges.

International research visits and advanced training workshops are pivotal for scientific independence, method diversification, and international networking. This guide consolidates first-hand knowledge, institutional evaluations, and practical recommendations from past mobility participants into a structured roadmap for future applicants.

Origin and Creation of the Guide

This guide was developed through a comprehensive synthesis of participant data collected following foreign mobilities undertaken by IBB PAS researchers. The entries are constructed from two primary data sources:

1. Substantive Foreign Trip Reports & Manuscript Abstracts: Technical descriptions detailing research objectives, host laboratory profiles, scientific supervisors (PIs), experimental methodologies, and collaborative outcomes.
2. Participant Evaluation Surveys: Quantitative ratings and qualitative feedback submitted anonymously by participants, covering host institution infrastructure, mentorship quality, administrative support, team integration, and logistical conditions.
3. To maximise long-term utility, host institution profiles have been expanded to reflect the broader research scope and real-world scientific focus of each laboratory and principal investigator.

HOW TO USE THIS GUIDE

The guide is organised into thematic entries categorised by mobility type:

- [RESEARCH INTERNSHIP] – Medium- to long-term collaborative research placements.
- [STUDY VISIT] – Short-term targeted laboratory visits for method acquisition or preliminary data collection.
- [WORKSHOP / SUMMER SCHOOL] – Intensive practical training courses and specialised methodology schools.

Each entry contains the following standardised sections:

- Participant & Host Information: Key details including participant status, keywords, host institution, department, exact address, and scientific supervisor.

- Host Institution Profile & General Research Areas: An overview of the host unit’s broader scientific scope, expertise, and ongoing research lines.
- Host Institution Evaluation Dashboard: A visual summary rating host performance across five core categories (Scientific Support & Mentoring, Research Infrastructure & Equipment, Administrative & Onboarding Support, Team Integration & Work Atmosphere, and Logistics & Accommodation Assistance), alongside an overall recommendation score derived from participant surveys.
- Practical Tips for Applicants: Actionable advice covering protocol optimizations, safety compliance, housing logistics, language considerations, and computational/AI tool usage.
- "Why You Should Choose This Laboratory / Mobility": A summary outlining the unique scientific value and career benefits of selecting the specific host center.

FUNDING & ACKNOWLEDGMENTS

The foreign mobilities documented in this publication, as well as the creation and publication of this guide, were made possible through financial support from the Polish National Agency for Academic Exchange (NAWA) under the PROM Programme (International Scholarship Exchange of PhD Students and Academic Staff).

OFFICIAL FUNDING STATEMENT:

This publication and the international academic mobilities described herein were funded by the Polish National Agency for Academic Exchange (NAWA) as part of the PROM Programme – International Scholarship Exchange of PhD Students and Academic Staff.

RESEARCH INTERNSHIPS AND STUDY VISITS

INSTITUTO DE BIOLOGÍA MOLECULAR Y CELULAR DE PLANTAS (IBMCP) – UPV/CSIC

Keywords: Artificial microRNAs, Gene silencing, Plant stress signalling, Agroinfiltration, Functional genomics.

Host Institution & Laboratory: Instituto de Biología Molecular y Celular de Plantas (IBMCP), Joint Institute UPV-CSIC, Valencia, Spain.
Scientific Supervisor: Dr. Alberto Carbonell (acarbonell@ibmcp.upv.es).

HOST INSTITUTION OVERVIEW:

The Instituto de Biología Molecular y Celular de Plantas (IBMCP) is a premier joint research centre of the Spanish National Research Council (CSIC) and the Universitat Politècnica de València (UPV). Located on the UPV campus in Valencia, IBMCP is a leading European hub for plant science, focusing on molecular genetics, cell biology, and crop biotechnology under adverse environmental conditions.

GENERAL RESEARCH AREAS:

Plant small RNA biotechnology, design and optimisation of artificial small RNAs (amiRNAs and syn-tasiRNAs) for crop protection, RNA silencing pathways against plant viral pathogens, molecular mechanisms of small RNA biogenesis and Argonaute loading, and functional genomics tools for transgene-free gene knockdown.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★☆
Administrative & Onboarding Support	★★★★☆
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★☆

Overall Recommendation **Definitely Recommended**

PRACTICAL TIPS FOR APPLICANTS

- Experimental Workflows: High-throughput design and screening of artificial microRNA (amiRNA) constructs using TargetFinder and p-sams computational pipelines. Practical execution includes transient transformation of tomato (Solanum lycopersicum) and non-radioactive sRNA Northern blots.

- Genomic Resources: Access to updated Telomere-to-Telomere (T2T) Nicotiana benthamiana genome annotations to minimise off-target silencing effects.
- Lab Culture & Onboarding: Exceptionally well-organised laboratory culture with open-access protocols, shared electronic lab notebooks, meticulously catalogued plasmid/bacterial repositories, and structured mentoring. Pre-arrival communication with the host PI is highly proactive.

WHY YOU SHOULD CONSIDER THIS LABORATORY

If you aim to master precise molecular tools for fine-tuning gene expression in plants to tackle environmental challenges like drought stress. The host facility provides an ideal setting to integrate bioinformatic workflows (such as designing artificial microRNAs via the P-SAMS platform) with experimental molecular cloning and functional validation via Agrobacterium-mediated transient expression (agroinfiltration) in crop models such as Solanum lycopersicum. This placement is particularly suited for researchers interested in stress signalling mechanisms, post-transcriptional regulation, and adopting modern team-management practices such as shared electronic laboratory notebooks within a dynamic international team.

[RESEARCH INTERNSHIP] UNIVERSITY OF EDINBURGH – GILBERT LABORATORY

Keywords: DNA supercoiling, Trimethylpsoralen cross-linking, Genome architecture, Transcriptional stress, RNAPIII mutants

- Host & Location: University of Edinburgh, Edinburgh, Scotland, UK (Crewe Rd, EH4 2XU)
- Scientific Supervisor: Prof. Nick Gilbert (nick.gilbert@ed.ac.uk)

HOST INSTITUTION PROFILE

The University of Edinburgh (Institute of Genetics and Cancer / MRC Human Genetics Unit) is a world-leading biomedical research center specializing in human genetics, chromatin structure, and genome biology. The Gilbert Laboratory focuses on understanding how chromatin architecture and physical DNA topology (such as supercoiling) regulate gene expression and genome stability.

GENERAL RESEARCH AREAS

Microbial biodiversity and comparative genomics, structural biochemistry of extremophilic bacterial enzymes, isolation and biophysical characterisation of novel natural products, high-throughput protein crystallisation pipelines, and microbial strain preservation, 3D genome architecture, physical DNA supercoiling and torsional stress, transcriptional dynamics (RNAPII and RNAPIII), epigenomics, and integration of high-throughput sequencing with computational modelling.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★☆

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Lab Layout & Collaboration: A shared open-plan laboratory and office design strongly facilitates casual cross-group knowledge exchange and interdisciplinary collaboration.

- Protocol Optimisation: Biotinylated trimethylpsoralen cross-linking protocol requires careful optimisation for specific mammalian cell lines.
- Computational & Wet-Lab Synergy: Excellent environment for combining wet-lab epigenomic mapping with AI/machine learning tools for analysing torsional stress datasets.

WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY:

You should consider this laboratory if you aim to master advanced experimental and computational techniques for mapping physical DNA topology and 3D genome organisation. The host facility provides state-of-the-art infrastructure for genome-wide mapping of negative DNA supercoiling using biotinylated trimethylpsoralen cross-linking combined with high-throughput sequencing. This placement is particularly suited for researchers interested in understanding how transcriptional machinery generates mechanical forces that regulate neighbouring genes during cellular stress responses, as well as those seeking to integrate experimental mapping datasets with machine learning models within an open, highly collaborative international research environment.

RESEARCH INTERNSHIP UNIVERSITY OF OSLO – VALEN GROUP (DEPARTMENT OF BIOSCIENCES)

Keywords: Nanopore sequencing, Nano3P-seq, Mitochondrial transcriptome, RNA surveillance, Long-read sequencing

- Host & Location: Department of Biosciences, University of Oslo, Oslo, Norway (Kristine Bonnevies Hus, Blindernveien 31, 0371 Oslo)
- Scientific Supervisor: Prof. Eivind Valen (eivind.valen@ibv.uio.no)

HOST INSTITUTION PROFILE

The Department of Biosciences at the University of Oslo (UiO) is a premier Scandinavian life science research centre. The Valen Laboratory specialises in computational biology, genome-wide RNA regulation, and the co-development of cutting-edge Oxford Nanopore sequencing (ONT) protocols and bioinformatic pipelines.

GENERAL RESEARCH AREAS

Mitochondrial transcriptome dynamics, post-transcriptional RNA processing, non-coding RNA surveillance, long-read sequencing protocol design (Nano3P-seq), and bioinformatic tool development.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★☆

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Protocol Co-Authors: Direct collaboration with co-authors of the Nano3P-seq protocol enables hands-on wet-lab troubleshooting and bioinformatics guidance.
- Local AI Infrastructure: UiO offers a secure local AI infrastructure (GPT UiO) where data are kept strictly on internal university servers, ensuring complete data security.

- Bring Your Own Samples: Excellent opportunity for PhD candidates to bring pre-extracted RNA/cDNA samples to generate core dissertation long-read sequencing datasets.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY

You should consider this laboratory if you aim to master state-of-the-art long-read Oxford Nanopore sequencing (ONT) techniques, particularly Nano3P-seq protocols, for analysing complex cellular RNA populations. The host facility provides specialised expertise for both wet-lab library preparation troubleshooting and dedicated bioinformatic processing of direct cDNA sequencing datasets. This placement is ideal for researchers seeking to investigate post-transcriptional RNA processing, mitochondrial transcriptome regulation, or host-pathogen interactions using long-read sequencing technologies under the guidance of leading pioneers in nanopore data analysis.

[RESEARCH INTERNSHIP] HEALTH RESEARCH INSTITUTE HOSPITAL LA FE (IIS LA FE) – NEONATAL RESEARCH GROUP

Keywords: Extracellular vesicles (EVs), Human milk lipidomics, Size Exclusion Chromatography, GC-MS metabolomics, ExoView characterisation

- Host & Location: Health Research Institute Hospital La Fe (IIS La Fe), Valencia, Spain (Fernando Abril Martorell 106, Torre A, 46026 Valencia)
- Scientific Supervisor: Dr. Julia Kuligowski (julia.kuligowski@uv.es)

HOST INSTITUTION PROFILE

The Health Research Institute Hospital La Fe (IIS La Fe) is a top-tier Spanish biomedical research centre directly integrated with the La Fe University and Polytechnic Hospital in Valencia. It provides state-of-the-art translational research infrastructure, specialising in neonatal health, biochemical analysis of human milk, and advanced extracellular vesicle profiling.

GENERAL RESEARCH AREAS

High-throughput sequencing bioinformatics, multi-omics data integration algorithms, scalable and reproducible workflow engineering (Nextflow/Snakemake), population genomics, and structural variant annotation.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★☆
Research Infrastructure & Equipment	★★★☆☆
Administrative & Onboarding Support	★☆☆☆☆
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★☆☆☆

Overall Recommendation **Recommended with Planning**

💡 PRACTICAL TIPS FOR APPLICANTS

- Direct integration with Hospital La Fe enables close collaboration with local human milk bank networks and clinical sample pipelines.
- Robust AI and data governance environment adhering to the European AI Act and Spain's Esquema Nacional de Seguridad (ENS).

- Language Barrier Alert: Local hospital administrative staff frequently communicate exclusively in Spanish; develop strong soft skills and patience when completing local paperwork.
- Vesicle Standards: Strict application of International Society for Extracellular Vesicles (ISEV) standards using SEC, UC, TRPS, and ExoView platforms.
- Warm Team Culture: Despite administrative hurdles, the scientific research team is exceptionally welcoming, fostering long-term collaborative project opportunities.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY

You should consider this institute if you aim to master comprehensive workflows for the isolation, characterisation, and profiling of extracellular vesicles (EVs) from complex biological fluids. The Neonatal Research Group at IIS La Fe provides an outstanding multi-platform facility combining Size Exclusion Chromatography (SEC), ultracentrifugation, ExoView protein colocalization, TRPS, ATR-FTIR spectroscopy, and GC-MS metabolomics/lipidomics. This placement is ideal for researchers focused on vesicle-based therapeutics, bioactive dietary supplements, or clinical translational studies seeking to establish high-purity standardised methodologies within an international biomedical centre.

[RESEARCH INTERNSHIP] UNIVERSITY OF IOWA – KEHL-FIE LABORATORY (DEPARTMENT OF MICROBIOLOGY AND IMMUNOLOGY)

Keywords: Staphylococcus aureus, Nutritional immunity, Superoxide dismutases, pKOR knockout system, Manganese homeostasis

- Host & Location: Department of Microbiology and Immunology, Carver College of Medicine, University of Iowa, Iowa City, IA, USA
- Scientific Supervisor: Prof. Thomas Kehl-Fie

HOST INSTITUTION PROFILE

The Department of Microbiology and Immunology at the University of Iowa is a top-tier US research centre specialising in the mechanisms of infectious diseases and host-pathogen interactions. The Kehl-Fie Laboratory is a renowned hub for nutritional immunity, investigating how bacterial pathogens resist host-mediated starvation of transition metals (such as manganese and zinc) and oxidative stress during infection.

GENERAL RESEARCH AREAS

Microbial synthetic biology, genetic tool development for non-conventional chassis, metabolic flux optimization for bio-based production, synthetic promoter library construction, and fermentation bioprocess engineering. Bacterial pathogenesis, nutritional immunity, trace metal homeostasis, functional divergence of superoxide dismutase (SodFM) enzyme families, oxidative stress defence, and genetic engineering of BSL-2 bacterial pathogens.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★☆

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- BSL-2 Compliance: Requires strict BSL-2 biosafety compliance and specialised handling protocols for pathogenic Staphylococcus aureus strains.
- Staphylococcal Genetics: Direct practical experience with staphylococcal genetic tools, including pKOR allelic replacement, phage transduction, and calprotectin-supplemented growth assays.
- Network Expansion: Excellent host environment for establishing international research connections that support future joint grant applications and high-impact co-publications.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY

You should consider this laboratory if you aim to investigate how bacterial pathogens adapt to hostile host environments, specifically overcoming metal starvation and oxidative stress. The Kehl-Fie Laboratory offers a premier BSL-2 setting to master advanced staphylococcal genetics, including the construction of knockout strains via pKOR allelic replacement, phage transduction, and bacterial growth assays in chemically defined media supplemented with calprotectin. This placement is ideally suited for researchers exploring superoxide dismutases (SodFMs), metal homeostasis, and host-pathogen dynamics within a highly structured and collaborative academic environment.

RESEARCH INTERNSHIP IN WEILL CORNELL MEDICINE USA

Keywords: Polyisoprenoids, Membrane biophysics, Lipid flip-flop, C-Laurdan spectroscopy, Dynamic Light Scattering (DLS)

- Host Institution & Department: Weill Cornell Medicine – Department of Biochemistry & Biophysics (Menon Laboratory)
- Host & Location: Weill Cornell Medicine, New York, NY, USA (1300 York Ave, Box 65)
- Scientific Supervisor: Prof. Anant Menon (akm2003@med.cornell.edu)

HOST INSTITUTION PROFILE

Weill Cornell Medicine (Department of Biochemistry & Biophysics) in New York City is a world-renowned biomedical academic centre. The Menon Laboratory is an international authority in membrane biophysics, investigating lipid dynamics, lipid translocation (flippases/scramblases), and the structural role of polyisoprenoid lipids in cellular membranes.

GENERAL RESEARCH AREAS

Plant physiological responses to environmental stress, transcriptional networks controlling drought and salinity tolerance, membrane transport mechanisms, post-translational regulation under oxidative stress, and translational crop biology.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★★

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Biophysical Spectroscopy: Hands-on training in preparing model liposomes and performing NBD-labeled assays and C-Laurdan spectroscopy.
- Data Analysis: Excellent environment for learning Generalised Polarisation (GP) calculations and Dynamic Light Scattering (DLS) data analysis.

- High-Value Data: Obtaining high-quality biophysical datasets that significantly enhance doctoral thesis quality and manuscript preparation.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY

You should consider this laboratory if you aim to gain deep expertise in membrane biophysics and state-of-the-art lipid dynamics methodologies. The Menon Laboratory at Weill Cornell Medicine offers a premier biophysical setup to investigate how specialised lipids (such as polyisoprenoids) regulate membrane fluidity, lipid packing, and flip-flop mechanisms using advanced fluorescence spectroscopy and Dynamic Light Scattering (DLS). This internship is exceptionally valuable for researchers investigating cellular stress adaptation, membrane organisation, and lipid-protein interactions within an inspiring, top-tier international biomedical research environment.

RESEARCH INTERNSHIP – LEIBNIZ INSTITUTE

Keywords: Bacteriophage preservation, Lyophilization / Freeze-drying, Biological Resource Centre (BRC), Phage collection management, Host strain preservation

- Host Institution & Department: Leibniz Institute DSMZ – German Collection of Microorganisms and Cell Cultures GmbH
- Host & Location: Science Campus Braunschweig-Süd, Braunschweig, Germany (Inhoffenstraße 7B, 38124 Braunschweig)
- Scientific Supervisor: Dr. Ana Filipa Moreira Martins (ana.filipa.moreira.martins@dsmz.de)

HOST INSTITUTION PROFILE

The Leibniz Institute DSMZ (German Collection of Microorganisms and Cell Cultures GmbH) is one of Europe's largest biological resource centres (BRCs). Located on the Science Campus Braunschweig-Süd, DSMZ sets international quality standards and regulatory frameworks for the long-term collection, preservation, and global distribution of high-quality microbial resources, bacteriophages, and cell lines.

GENERAL RESEARCH AREAS

Microbial biodiversity and comparative genomics, structural biochemistry of extremophilic bacterial enzymes, isolation and biophysical characterisation of novel natural products, high-throughput protein crystallisation pipelines, and microbial strain preservation

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★☆

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Visitors receive a concise 4-page standardised onboarding guide covering safety rules, emergency procedures, and facility navigation.

- Outstanding environment to learn strict European guidelines, Standard Operating Procedures (SOPs), and regulatory requirements for Biological Resource Centers.
- Great opportunity to gain access to historical phage lysates and build collaborative projects for long-term strain banking.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY

You should consider this laboratory if you aim to master standardised, long-term preservation techniques for bacteriophages and their bacterial host strains. The Leibniz Institute DSMZ provides world-class infrastructure and expert training in lyophilization (vacuum freeze-drying on discs and in skim milk ampoules), capillary tube storage in liquid nitrogen, and reactivation assays. This placement is uniquely suited for researchers establishing or managing phage collections, seeking hands-on biological resource-banking experience, and adopting strict BRC quality standards to ensure sample viability and reproducibility for long-term microbiological research.

RESEARCH INTERNSHIP - SYNTHETIC GENOMICS & PASSIVE GENE REGULATION IN YEAST

Keywords: Synthetic genomics, Passive gene regulation, Engineered yeast strains, Genomic architecture, Quantitative growth assays

- Host Institution & Department: Zentrum für Molekulare Biologie der Universität Heidelberg (ZMBH) – Schindler Laboratory (Synthetic Genomics)
- Host & Location: Heidelberg University, Heidelberg, Germany (Laboratory of Synthetic Genomics, ZMBH)
- Scientific Supervisor: Prof. Daniel Schindler

HOST INSTITUTION PROFILE

The Zentrum für Molekulare Biologie der Universität Heidelberg (ZMBH) is a premier European center for basic research in molecular and cellular biology. The Schindler Laboratory (Synthetic Genomics) specialises in engineering fungal genomes to investigate passive regulatory mechanisms, genomic architecture, and how sequence context dictates cellular fitness and gene expression.

GENERAL RESEARCH AREAS

Microbial synthetic genomics, de novo design and synthesis of eukaryotic and bacterial chromosomes, passive regulatory principles of genome organisation, high-throughput automated yeast phenotyping, and engineering microbial chassis for industrial biotechnology.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★☆

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Hands-on characterisation of tagged and gene-deletion yeast strains using quantitative phenotypic assays.

- Excellent setting for using AI assistance responsibly (e.g., Python/R plotting scripts) to enhance data visualisation workflows.
- Strong collaborative lab culture with regular group meetings, joint troubleshooting, and active involvement of visiting researchers.
- Direct interaction and skills acquisition from leading scientists in synthetic genomics and chromosome engineering.
- Onboarding & Support: Swift processing of official documents and continuous host assistance throughout the stay.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY/ MOBILITY:

You should consider this laboratory if you aim to explore how genomic architecture and passive regulatory mechanisms shape gene activity and cellular adaptation. The Schindler Laboratory at ZMBH Heidelberg provides an ideal synthetic biology environment for working with engineered yeast models, performing high-precision growth measurements, and analysing context-dependent gene regulation. This placement is particularly valuable for researchers seeking to combine molecular genetics with quantitative phenotypic profiling and computational data visualisation within a world-class molecular biology institute.

[RESEARCH INTERNSHIP] AUTOMATED PHENOTYPING & INTERGENERATIONAL STRESS RESPONSES IN C. ELEGANS

Keywords: C. elegans phenotyping, Exopher production, Automated longitudinal imaging, Intergenerational stress, Deep learning image analysis

- Host Institution & Department: Institute of Cell Biology, University of Bern – Organismal Systems Biology Laboratory (Towbin Lab)
- Host & Location: University of Bern, Bern, Switzerland (Baltzerstrasse 4, CH-3012 Bern)
- Scientific Supervisor: Dr. Benjamin Towbin (benjamin.towbin@unibe.ch)

HOST INSTITUTION PROFILE

The Institute of Cell Biology at the University of Bern is a leading Swiss research center specializing in cell biology and developmental genetics. The Organismal Systems Biology Laboratory, led by Dr. Benjamin Towbin, focuses on quantitative developmental biology, combining Caenorhabditis elegans genetics with automated longitudinal phenotyping, image-based growth analysis, and deep learning computational pipelines.

GENERAL RESEARCH AREAS

Quantitative developmental biology, system-level design principles of multicellular genetic circuits, developmental robustness and body-size scaling across tissues, quantitative live-cell imaging and microfluidic automation, and intergenerational environmental stress adaptation in C. elegans.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★★

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Utilises established, validated deep learning models for processing automated longitudinal imaging datasets.
- High level of lab automation, including automated plate-pouring machines, streamlining routine preparation tasks.
- Inspiring research environment with supportive academic culture and regular constructive feedback sessions.
- High-Throughput Paradigm: Learn a quantitative approach to the life sciences using automated longitudinal imaging and computational deep learning tools for big-data extraction.
- Paperless Administration: The administrative onboarding process is entirely digital, paperless, and exceptionally smooth for visiting scientists.
- Lab Automation: High level of routine automation, including automated plate-pouring machines and high-content bioimaging systems.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY:

You should consider this laboratory if you aim to master automated, high-throughput quantitative phenotyping and longitudinal growth tracking in Caenorhabditis elegans. The Towbin Laboratory at the University of Bern provides an advanced experimental and computational setup that integrates automated imaging, deep-learning analysis pipelines, and developmental genetics. This placement is particularly valuable for researchers investigating intergenerational stress communication, developmental dynamics, and body-size scaling relationships within a highly automated and collaborative Swiss research environment.

[RESEARCH INTERNSHIP] PROXIMITY LABELING & STRESS GRANULE PROTEOMICS IN PLANT IMMUNITY

Keywords: Proximity biotinylation, APEAL / TurboID, Stress granules, Type III effectors, Biomolecular condensates

- Host Institution & Department: Institute of Molecular Biology and Biotechnology (IMBB-FORTH) & University of Crete – Department of Plant and Plant-Microbe Biology (Moschou Lab)
- Host & Location: IMBB-FORTH / University of Crete, Heraklion, Greece
- Scientific Supervisor: Prof. Panagiotis Moschou (panagiotis.moschou@uoc.gr)

HOST INSTITUTION PROFILE

The Institute of Molecular Biology and Biotechnology (IMBB-FORTH) at the University of Crete in Heraklion is a top-tier European research centre in molecular plant sciences, biotechnology, and cellular biology. The Moschou Laboratory focuses on biomolecular condensates (processing bodies and stress granules), RNA/protein homeostasis, cell polarity, and host-microbe interactions, and has pioneered advanced proximity-labelling methodologies, with publications in leading journals such as The Plant Cell.

GENERAL RESEARCH AREAS

Plant cell and developmental biology, spatial proteolytic control and polyamine catabolism, mechanisms of liquid-liquid phase separation (LLPS) in plant development, cellular signalling driving stress-induced stem cell transitions, and RNA/protein quality control networks during environmental adaptation.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★☆
Research Infrastructure & Equipment	★★★★☆
Administrative & Onboarding Support	★★★☆☆
Team Integration & Work Atmosphere	★★★★☆
Logistics & Accommodation Assistance	★☆☆☆☆

Overall Recommendation **Recommended with Planning**

💡 PRACTICAL TIPS FOR APPLICANTS

- Strict protocol design: complete all essential control experiments before committing samples to costly mass spectrometry pipelines.

- Hands-on training provided for two-arm affinity purification (anti-FLAG capture, free-biotin removal, streptavidin capture) and Western blot normalisation.
- Laboratory protocols are treated as "living documents" and are constantly updated after experimental runs to maximise reproducibility.
- Experimental Controls: Complete all essential control experiments (non-biotin control, wild-type plant controls) before committing samples to mass spectrometry.
- Housing Warning: Finding accommodation in Heraklion during peak tourist/summer seasons is very challenging; arrange housing several months in advance of arrival.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY:

You should consider this laboratory if you aim to master cutting-edge proximity-biotinylation techniques (such as APEAL and TurboID) to map proteomic and transcriptomic microenvironments inside living plant cells. The Moschou Laboratory at IMBB-FORTH provides an outstanding research environment for studying stress granules, processing bodies, and host-pathogen interactions. This placement is particularly ideal for researchers investigating how environmental stress or bacterial effectors alter biomolecular condensates, offering hands-on expertise in in vivo biotin feeding, complex affinity purification, and control optimisation within a highly collaborative international setting.

[RESEARCH INTERNSHIP] VIRAL NUCLEOPROTEIN & HOST PABPC1 INTERACTIONS IN MRNA DECAY

Keywords: La Crosse virus (LACV), Poly(A)-binding protein (PABPC1), Yeast Two-Hybrid (Y2H), In vitro deadenylation assay, AlphaFold structure prediction

- Host Institution & Department: Institut de Génétique et de Biologie Moléculaire et Cellulaire (IGBMC) – Séraphin Laboratory
- Host & Location: IGBMC, Illkirch-Graffenstaden / Strasbourg, France (1 Rue Laurent Fries, 67400 Illkirch-Graffenstaden)
- Scientific Supervisor: Dr. Bertrand Séraphin (seraphin@igbmc.fr)

HOST INSTITUTION PROFILE

The Institut de Génétique et de Biologie Moléculaire et Cellulaire (IGBMC) in Illkirch-Graffenstaden (Strasbourg) is one of Europe's premier biomedical research centres. The Séraphin Laboratory is an internationally renowned authority on mRNA metabolism, post-transcriptional regulation of gene expression, deadenylation mechanisms, and ribonucleoprotein complex dynamics.

GENERAL RESEARCH AREAS

Eukaryotic post-transcriptional gene regulation, molecular architecture and enzymatic regulation of mRNA deadenylation complexes (CCR4-NOT, PAN2-PAN3), cytoplasmic and nuclear RNA degradation pathways, structural biology of ribonucleoprotein complexes (RNPs), and human genetic pathologies linked to RNA decay defects.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★☆
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★★

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Integrated usage of AlphaFold3 / AlphaFold-Multimer as a hypothesis-generating step to narrow candidate interaction surfaces before designing Y2H truncations and EMSA experiments.

- Institute-wide centralised plasmid/protein repositories and barcoded buffer facilities significantly accelerate the start times of short-term projects.
- Open technology platforms (e.g., Instruct-ERIC facilities) staffed by dedicated scientists enable rapid onboarding of advanced biophysical instrumentation during one-month stays.
- Multi-Lab Networking: High exposure to multiple adjacent specialized laboratories in the Strasbourg life science cluster, creating immediate opportunities for broader scientific networking.
- In Silico Modelling: Integrated usage of AlphaFold3 / AlphaFold-Multimer as a hypothesis-generating step to narrow candidate interaction surfaces before designing Y2H truncations and EMSA experiments.
- Funding Timing: Prompt scholarship disbursement allows researchers to comfortably pre-book flights and initial month accommodation without out-of-pocket delays.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY:

You should consider this laboratory if you aim to investigate the molecular mechanisms of post-transcriptional gene regulation, mRNA decay pathways, and viral-host interactions. The Séraphin Laboratory at IGBMC provides world-class expertise and infrastructure for combining yeast genetic screens (Y2H), in vitro deadenylation assays, EMSA, and AlphaFold-driven structural modelling. This placement is particularly valuable for researchers seeking to decipher how viral nucleoproteins manipulate host-cell mRNA stability and the translation machinery within a highly organised and supportive international research institute.

[RESEARCH INTERNSHIP] PROXIMITY BIOTINYLATION (BIOE3) & RNF2 LIGASE SUBSTRATE PROFILING

Keywords: BioE3 technology, RNF2 E3 ubiquitin ligase, DNA polymerase iota (Polι), Proximity biotinylation, LC-MS/MS proteomics

- Host Institution & Department: Center for Cooperative Research in Biosciences (CIC bioGUNE) – Ubiquitin-likes and Development Laboratory
- Host & Location: CIC bioGUNE (Basque Research and Technology Alliance), Derio/Bilbao, Spain
- Scientific Supervisors: Prof. Rosa Barrio (rbarrio@cicbiogune.es) & Dr. James D. Sutherland

HOST INSTITUTION PROFILE

The Centre for Cooperative Research in Biosciences (CIC bioGUNE) near Bilbao is a leading Spanish biomedical research institute within the Basque Research and Technology Alliance (BRTA). The Barrio Laboratory (Ubiquitin-likes and Development Lab) specialises in ubiquitin and SUMO pathway dynamics, pioneering the BioE3 proximity labelling technology to identify substrate networks and regulatory interactomes of E3 ubiquitin ligases.

GENERAL RESEARCH AREAS

Ubiquitin and SUMO pathway dynamics in development and disease, targeted protein degradation (PROTACs and molecular glues), molecular mechanisms of ubiquitin-like modifications in rare developmental disorders and tumorigenesis, Drosophila developmental genetics, and bioengineering of proximity-labelling methodologies for proteome proofreading.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★☆☆

Overall Recommendation **Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Hands-on implementation of BioE3 technology (E3 ligase-BirA fusion coupled with engineered biotinylated ubiquitin) for marking proximal targets.
- Integrates nuclear confocal microscopy with biochemical purification to verify spatial localisation and filter out non-specific background.
- Structured mentoring pipeline with Dr. James D. Sutherland for construct design, experimental induction, troubleshooting, and MS sample preparation.
- Methodology Mastery: Rapid progression from guided training to independently executing major parts of the BioE3 proximity labelling workflow for RNF2 ligase substrate identification.
- Imaging & Proteomics: Integrates nuclear confocal microscopy with biochemical purification to verify spatial localisation and filter out non-specific background.
- Housing Warning: Accommodation search in Bilbao/Derio can be variable in price and availability; start housing arrangements well in advance of the trip.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY:

You should consider this laboratory if you aim to master novel proximity biotinylation methodologies (BioE3) for identifying E3 ubiquitin ligase substrates and regulatory networks. The Barrio Laboratory at CIC bioGUNE offers an exceptional research setting combining cell culture biotinylation, nuclear confocal imaging, biochemical purification, and LC-MS/MS quantitative proteomics. This placement is ideally suited for researchers studying ubiquitin signalling, proteostasis, or DNA damage tolerance mechanisms who want to adapt state-of-the-art proximity labelling to discover novel protein interactomes under expert international guidance.

[RESEARCH INTERNSHIP] HIGH-FIELD EPR SPECTROSCOPY OF MANGANESE SUPEROXIDE DISMUTASES IN STAPHYLOCOCCUS AUREUS

Keywords: High-Field EPR (HFEPR), Superoxide dismutase (SodFM), Staphylococcus aureus, Manganese coordination sphere, Metal cofactor specificity

- Host Institution & Department: CEA-Saclay – Interdisciplinary Research Institute / Bioenergetics, Structural Biology & Biophysics
- Host & Location: CEA-Saclay, Gif-sur-Yvette, France (Bâtiment 532, CEA-Saclay, 91191 Gif-sur-Yvette)
- Scientific Supervisor: Dr. Sun Un (sun.un@cea.fr)

HOST INSTITUTION PROFILE

CEA-Saclay (Commissariat à l'énergie atomique et aux énergies alternatives) in Gif-sur-Yvette, France, is a premier European scientific research complex. The biophysics infrastructure at CEA-Saclay features specialised high-field high-frequency electron paramagnetic resonance (HFEPR) facilities designed for high-resolution analysis of metalloprotein active sites and paramagnetic centres.

GENERAL RESEARCH AREAS

Advanced biophysical spectroscopy, high-field, high-frequency electron paramagnetic resonance (HFEPR), active-site coordination chemistry of metalloproteins, radical dynamics in enzymology, electron-transfer mechanisms, and structural biophysics of membrane protein complexes and photosynthetic reaction centres.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★☆
Overall Recommendation	**Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Direct access to expert guidance for modelling complex paramagnetic centres and analysing second-shell coordination sphere mutations.

- Excellent opportunities for collaborative biophysical projects complementing molecular genetics and biochemistry research conducted at home institutions.
- Instrumentation Access: Specialised facility for conducting high-field high-frequency EPR (HFEPR) measurements on manganese-loaded protein samples.
- Dataset Synergy: Seamless integration of HFEPR data from multi-site mutant variants with home biochemical assays to generate publication-quality datasets.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY:

You should consider this laboratory if you aim to gain hands-on expertise in advanced high-field EPR spectroscopy applied to metalloenzymes and paramagnetic metal centres. The biophysics division at CEA-Saclay offers world-class HFEPR instrumentation and specialised technical knowledge to resolve subtle changes in metal coordination, cofactor loading, and active-site electronic structures. This placement is ideal for researchers studying superoxide dismutases (SodFMs), host-pathogen metal homeostasis, or enzyme catalysis who wish to combine site-directed mutagenesis with high-resolution biophysical characterisation.

[STUDY VISIT] BIOMOLECULAR NMR SPECTROSCOPY OF SOD HETERODIMERS IN STAPHYLOCOCCUS AUREUS

Keywords: Biomolecular NMR spectroscopy, Superoxide dismutase (SOD), Staphylococcus aureus, Mixed-metal heterodimers, Metalloprotein active sites

- Host Institution & Department: Centro Risonanze Magnetiche (CERM) & Department of Chemistry, University of Florence
- Host & Location: CERM, Sesto Fiorentino (Florence), Italy (Via Luigi Sacconi 6, 50019 Sesto Fiorentino)
- Scientific Supervisor: Prof. Simone Ciofi Baffoni (simone.ciofibaffoni@unifi.it)

HOST INSTITUTION PROFILE

Centro Risonanze Magnetiche (CERM) at the University of Florence is an internationally renowned European research centre for bio-NMR spectroscopy and structural biology. CERM houses state-of-the-art high-field NMR instrumentation and advanced software infrastructure, offering high-resolution biophysical characterisation of biomacromolecules, metalloproteins, and transient protein complexes.

GENERAL RESEARCH AREAS

Structural biology of metalloproteins, high-field bio-NMR spectroscopy of paramagnetic biological systems, mitochondrial iron-sulfur cluster biogenesis and maturation pathways, cellular copper trafficking and homeostasis, and structural characterisation of protein-protein interaction networks in human diseases and bacterial pathogens.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★☆

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Hands-on training on high-field NMR spectrometers, including parameter optimisation, machine operation, and spectral data collection.

- Data Integration: Direct guidance on comparative spectral analysis against wild-type/mutant protein homodimers and literature benchmarks.
- Dissertation Output: The short stay provides immediate high-value spectral datasets directly suitable for core PhD dissertation chapters and manuscript preparation.
- Highly structured facility management with open, collaborative workflows that facilitate high-quality experimental output for visiting researchers.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY:

You should consider this laboratory if you seek to master biomolecular NMR spectroscopy and investigate metalloprotein active sites at a proton-level resolution. CERM at the University of Florence provides unmatched expertise and world-class NMR facilities to probe metal coordination environments, mixed-metal heterodimers, and subatomic structural dynamics. This placement is exceptionally valuable for PhD candidates and researchers studying bacterial stress responses, host-imposed nutrient starvation, or metalloenzyme catalysis who wish to integrate biochemical sample preparation with state-of-the-art structural biophysics.

[RESEARCH INTERNSHIP] BIOINFORMATIC & EXPERIMENTAL PROFILING OF MINOR SPLICEOSOME KINETICS IN NEURAL DEVELOPMENT

Keywords: Minor spliceosome, Minor splice-sites (U12-type introns), RNA-seq splicing kinetics, RT-PCR transcript validation, AI-assisted splicing prediction

- Host Institution & Department: The University of Edinburgh – Institute of Genetics and Cancer (Western General Hospital)
- Host & Location: The University of Edinburgh, Edinburgh, United Kingdom (Western General Hospital, Crewe Rd S, Edinburgh EH4 1QY)
- Scientific Supervisor: Nic Robertson (nic.robertson@ed.ac.uk)

HOST INSTITUTION PROFILE

The Institute of Genetics and Cancer at the University of Edinburgh's Western General Hospital campus is a global leader in medical genetics, genomic medicine, and quantitative RNA biology. The research environment integrates high-performance bioinformatics infrastructure with experimental molecular biology laboratories to investigate the control of eukaryotic gene expression, pre-mRNA processing, developmental neurobiology, and human genetic disorders.

GENERAL RESEARCH AREAS

Pre-mRNA splicing mechanisms and spliceosome regulation, minor (U12-dependent) spliceosome kinetics during mammalian neurodevelopment, transcriptome-wide bioinformatic profiling of alternative splicing in embryonic mouse brain models, algorithmic tool development for splicing event detection, and experimental validation of candidate disease-associated transcripts (including RECQL4, UBA7, RAF1, RFX5, DISC1, and USP9X).

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★☆

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Access to well-documented, intuitive in-house computational servers and shared high-performance computing resources optimised for RNA-seq dataset processing.
- Combines computational splicing kinetics analysis with established laboratory protocols for RT-PCR gel band quantification and transcript verification.
- Implementation of a supervised, AI-assisted workflow to predict minor splicing events and functional gene associations, ensuring that all AI-generated predictions are independently verified against the literature before inclusion.
- Structured lab organisation with regular progress presentations, group feedback sessions, and final seminar discussions that facilitate interdisciplinary knowledge exchange.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY:

You should consider this laboratory if you aim to combine bioinformatic analysis of RNA splicing kinetics with experimental transcript validation in developmental biology models. The research group at The University of Edinburgh provides an outstanding environment for studying minor spliceosome dynamics, offering robust in-house bioinformatic servers, validated RT-PCR protocols, and supportive supervision. This placement is particularly valuable for PhD candidates developing bioinformatic tools for alternative splicing detection who wish to integrate supervised AI prediction models with hands-on laboratory verification within an international research centre.

[STUDY VISIT] SPATIAL TRANSCRIPTOMICS & FFPE/FROZEN TISSUE HANDLING PIPELINES IN TUMOR PATHOLOGY

Keywords: 10x Genomics Visium, Spatial transcriptomics, Tissue sectioning, FFPE & frozen tumour samples, Spatial gene mapping

- Host Institution & Department: Institut Curie – Department of Pathology / Bioimaging & Spatial Omics Platform
- Host & Location: Institut Curie, Paris, France (26 rue d'Ulm, 75248 Paris)
- Scientific Supervisor: Renaud Leclere (messagerie.pathex@curie.fr)

HOST INSTITUTION PROFILE

Institut Curie in Paris is a world-renowned European biomedical research center and clinical hospital specialising in cancer biology and oncology. Its pathology department and molecular platforms integrate diagnostic histology with state-of-the-art bioimaging, tissue biobanking, and spatial transcriptomics technologies.

GENERAL RESEARCH AREAS

Clinical and translational cancer biology, cellular and molecular characterisation of the tumour microenvironment, epigenomic regulation and chromatin dynamics in oncogenesis, integration of high-resolution spatial transcriptomics with diagnostic histopathology on FFPE and fresh-frozen clinical specimens, and spatial multi-omics platforms.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★☆
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★★

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Hands-on practical training in upstream tissue handling, sample preparation, and manual sectioning protocols for both FFPE (formalin-fixed paraffin-embedded) and fresh-frozen tumour specimens.
- Direct protocol implementation using the 10x Genomics Visium spatial transcriptomics platform.
- Methodology focused on mapping gene expression directly within intact anatomical tissue structures to resolve spatial biological patterns.
- Network Exposure: Broad exposure to several pathology and bioimaging laboratories working on cancer multi-omics, fostering new international contacts

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY:

You should consider this mobility if you want to gain hands-on experience with advanced spatial transcriptomics technologies in an international scientific environment. Renaud Leclere's group at Institut Curie provides specialised training in upstream tissue handling, manual sectioning of FFPE and frozen tumour samples, and processing workflows using the 10x Genomics Visium platform. This visit is ideal for researchers seeking to learn how to map gene activity directly within tissue structures to better understand disease mechanisms and spatial biological processes.

[RESEARCH INTERNSHIP] MASS SPECTROMETRY PROFILING OF COPPER-GLUTATHIONE COMPLEXATION & SILVER ION INTERFERENCE

Keywords: ESI-MS mass spectrometry, Copper-glutathione complexes, Metal-ligand stoichiometry, Silver ion interference, Bioinorganic coordination chemistry

- Host Institution & Department: Institute of Analytical Sciences and Physico-Chemistry for Environment and Materials (IPREM) – CNRS / Université de Pau et des Pays de l'Adour (UMR 5254)
- Host & Location: IPREM, Pau, France (Technopôle Hélioparc, 2 Av. du Président Pierre Angot, 64053 Pau Cedex 9)
- Scientific Supervisor: Prof. dr hab. Joanna Szpunar (joanna.szpunar@univ-pau.fr)

HOST INSTITUTION PROFILE

The Institute of Analytical Sciences and Physico-Chemistry for Environment and Materials (IPREM) in Pau, France, operated jointly by CNRS and the Université de Pau et des Pays de l'Adour (UMR 5254), is a world-renowned research centre for analytical chemistry, metallomics, and environmental physico-chemistry. The institute features advanced mass spectrometry infrastructure dedicated to bio-inorganic speciation analysis, trace metal characterisation, and the study of metal-biomolecule interaction networks.

GENERAL RESEARCH AREAS

Bioinorganic speciation analysis, metallomics, hyphenated analytical techniques (HPLC-ICP-MS, ESI-MS/MS), metal-biomolecule interaction mechanisms, trace and ultratrace elemental analysis in biological matrices, computational strategies for speciation data processing, and high-resolution mass spectrometry for inorganic and organometallic species identification.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★☆
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★☆
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★☆

Overall Recommendation **Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Hands-on preparation of biological metal-ligand samples across varying metal-to-ligand molar ratios.
- Short onboarding training session on electrospray ionization mass spectrometry (ESI-MS) followed by independent sample analysis and data interpretation.
- Collaborative optimisation of analytical measurement conditions, spectral interpretation, and problem-solving alongside host lab researchers.
- Analytical Skills: High-value analytical experience in sample preparation across a range of metal-to-ligand molar ratios.
- Scientific Discussion: Active emphasis on data interpretation, analytical condition optimisation, and critical scientific problem-solving with host team members.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY:

You should consider this laboratory if you aim to investigate metal ion interactions with key biological molecules such as glutathione using electrospray ionisation mass spectrometry (ESI-MS). Prof. Joanna Szpunar's team at IPREM Pau provides expert scientific supervision, guidance on analytical method optimisation, and a collaborative environment for studying the stability of metal-ligand complexes and competitive ion interference. This internship is ideal for PhD candidates seeking to expand their practical skills in sample preparation, analytical measurements, and ESI-MS data analysis within an international research group.

[RESEARCH INTERNSHIP] ADP-RIBOSYLATION PROFILING & PLANT HOST TARGET IDENTIFICATION OF PSEUDOMONAS SYRINGAE TYPE THREE EFFECTORS

Keywords: Pseudomonas syringae, type three secretion system effectors, ADP-ribosylation profiling, Macro domain affinity resin enrichment, Anti-ADP-ribose immunoblotting

- Host Institution & Department: Leibniz Institute of Plant Biochemistry (IPB) – Department of Biochemistry of Plant Interactions
- Host & Location: Leibniz Institute of Plant Biochemistry (IPB), Halle (Saale), Germany (Weinberg 3, 06120 Halle (Saale))
- Scientific Supervisor: Dr. Lennart Wirthmüller (Lennart.Wirthmueller@ipb-halle.de)

HOST INSTITUTION PROFILE

The Leibniz Institute of Plant Biochemistry (IPB) in Halle (Saale), Germany, is a European centre of excellence in plant biochemistry and molecular biology. The Department of Biochemistry of Plant Interactions focuses on molecular plant-microbe interactions, investigating the structure, function, and intracellular signalling cascades of plant proteins that mediate developmental processes and immune responses upon pathogen infection.

GENERAL RESEARCH AREAS

Plant biochemistry and molecular plant-microbe interactions, biosynthesis and chemical diversity of plant and fungal secondary metabolites, molecular mechanisms of plant immunity and bacterial effector action, post-translational modifications (including ADP-ribosylation) in host-pathogen crosstalk, and intracellular signalling cascades regulating plant development and defence.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★★

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Practical implementation of Agrobacterium-mediated transient overexpression in Nicotiana benthamiana, plant cell extract preparation, anti-ADP-ribose immunoblotting, and affinity enrichment of modified proteins using GST-tagged Macro domain resins.
- Direct sample preparation and processing for LC-MS/MS quantitative mass spectrometry analysis to identify specific host substrate proteins and exact modification sites.
- Well-organised infrastructure with online booking for FPLC systems, institute-wide IT integration for raw data access, and automated 24/7 electronic monitoring for -80°C freezers.
- Seminar Defence: Opportunities to present PhD dissertation at departmental seminars, receiving direct, constructive feedback from field leaders.
- Shared Equipment: Online reservation for shared FPLC systems and centralised access to instrument data from any authorized computer.
- Structured mentoring with continuous scientific supervision, organisational support, and opportunities to present PhD results at departmental seminars for interdisciplinary feedback.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY:

You should consider this laboratory if you aim to master advanced molecular plant biology methodologies, particularly for investigating bacterial effector virulence mechanisms and post-translational host protein modifications such as ADP-ribosylation. The Department of Biochemistry of Plant Interactions at IPB Halle provides excellent scientific guidance, modern laboratory infrastructure with shared analytical facilities, and strong institutional support. This internship is ideal for PhD candidates seeking to refine practical skills in plant cell extract preparation, affinity chromatography, mass spectrometry sample preparation, and scientific communication within an international research centre.

[RESEARCH INTERNSHIP] MASS SPECTROMETRY PROTEOMICS OF THE MLK4-DRIVEN TNBC SECRETOME & TUMOR MICROENVIRONMENT

Keywords: MLK4 kinase, Triple-negative breast cancer (TNBC), Secretome mass spectrometry, Tumour microenvironment (TME), LAMC2, Macrophage-cancer cell co-culture

- Host Institution & Department: Multidisciplinary Group of Translational Oncology (GMOT) – University of the Balearic Islands (UIB)
- Host & Location: GMOT, UIB, Palma, Balearic Islands, Spain (Cra. Valldemossa km 7.5, 07122 Palma)
- Scientific Supervisor: Dr. Mercedes Nadal Serrano (mercedes.nadal@uib.es)

HOST INSTITUTION PROFILE

The Multidisciplinary Group of Translational Oncology (GMOT) at the University of the Balearic Islands (UIB) and the Health Research Institute of the Balearic Islands (IdISBa) is a specialised Spanish research team in translational cancer biology. GMOT focuses on the cellular and molecular dynamics of the tumour microenvironment, combining mass spectrometry secretomics, flow cytometry, and 3D co-culture models to decipher cancer-immune interactions.

GENERAL RESEARCH AREAS

Translational oncology and cancer biomarker discovery, molecular mechanisms of breast cancer chemoresistance and invasion, tumour microenvironment (TME) remodelling and extracellular matrix architecture, cancer cell secretomics and paracrine signalling networks, and 3D tumour-immune co-culture modelling.

★ RATING & EVALUATION

Evaluation Category	Score / Rating
Scientific Support & Mentoring	★★★★★
Research Infrastructure & Equipment	★★★★★
Administrative & Onboarding Support	★★★★★
Team Integration & Work Atmosphere	★★★★★
Logistics & Accommodation Assistance	★★★★★

Overall Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Hands-on protein precipitation, enzymatic digestion, and mass spectrometry proteomic analysis of cancer cell conditioned media.
- Knowledge transfer for setting up 3D macrophage–breast cancer cell co-cultures to evaluate immune cell recruitment and paracrine cross-talk.
- Highly supportive research environment featuring a structured onboarding process, weekly progress updates, 1-on-1 supervisory sessions, and regular team integration activities.

💬 WHY YOU SHOULD CONSIDER THIS LABORATORY / MOBILITY:

You should consider this laboratory if you aim to master mass spectrometry-based secretome proteomics and 3D co-culture methodologies for characterising the tumour microenvironment. Under the mentorship of Dr. Mercedes Nadal Serrano and the GMOT team at UIB, participants gain practical experience in analysing conditioned media, performing proteomic workflows, and evaluating cancer-immune cell cross-talk. This internship is particularly valuable for researchers investigating kinase signalling (such as MLK4), extracellular matrix remodelling, and immunosuppressive niche formation who wish to combine analytical proteomic pipelines with cell culture models in a supportive international research group.

WORKSHOPS/TRAININGS

[WORKSHOP / SUMMER SCHOOL] 10TH BERLIN SUMMER SCHOOL IN NGS DATA ANALYSIS

Keywords: NGS Data Analysis, RNA-Seq, Variant Calling, Linux Bioinformatics, Differential Expression

- Event & Location: ECSEQ Bioinformatics at PC-college, Berlin, Germany
- Organising Body: ECSEQ Bioinformatics (Specialised German training provider for hands-on NGS bioinformatics and computational life science workshops)

EVENT & ORGANIZER PROFILE

ECSEQ Bioinformatics provides intensive, practice-oriented training courses in high-throughput sequencing data analysis for life science researchers. The Berlin Summer School is a well-established annual training event designed to bridge the gap between theoretical genomics and practical command-line bioinformatics.

PROGRAM & LEARNING OUTCOMES

The one-week intensive curriculum covers foundational Linux command-line operations, quality control of raw reads (FastQC), read mapping and alignment (STAR, samtools), RNA-seq quantification (Salmon), differential gene expression analysis (DESeq2), visualisation (IGV), and DNA variant calling pipelines applied to real Illumina datasets.

★ RATING & EVALUATION

Workshop Evaluation Category	Score / Rating
Course Curriculum & Lecture Quality	★★★★★
Hands-on Practice & Workstation Setup	★★★★★
Course Materials & Computational Workflows	★★★★★
Networking & Expert Consultations	★★★★★
Course Logistics & Organization	★★★★☆

Overall Course Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Practical computational sessions are held on dedicated high-performance workstations using real RNA-seq datasets.
- Reviewing basic Linux terminal commands before arrival helps maximise progress during hands-on modules.
- Guest lectures by field experts and organised social activities provide strong international networking opportunities.

WHY YOU SHOULD ATTEND THIS WORKSHOP:

You should consider this summer school if you want to gain comprehensive, hands-on proficiency in processing and interpreting Next-Generation Sequencing (NGS) raw data. The course offers an ideal blend of theoretical lectures and intensive computational exercises on high-performance workstations using real Illumina RNA-seq datasets. Participants acquire direct, practical experience with industry-standard command-line tools (including FastQC, STAR, Salmon, samtools, DESeq2, and IGV), covering the entire analytical workflow from quality control to RNA-seq differential gene expression and DNA variant calling. This training is particularly valuable for PhD students and researchers in microbial genomics, transcriptomics, or evolutionary biology looking to independently build and execute robust bioinformatics pipelines.

[WORKSHOP] QUANTITATIVE APPROACHES TO DNA DAMAGE, REPAIR & GENOME INSTABILITY

Keywords: Quantitative biology, DNA damage & repair, Single-molecule imaging, Machine learning in DSBs, Chromatin dynamics

- Host Institution & Organisers: École Normale Supérieure – PSL University (Q-Life Institute)
- Event & Location: PSL-Qlife Winter School, Paris, France (46 rue d'Ulm, 75005 Paris)
- Scientific Coordinators & Contact: Prof. Patrick Charnay (qlife.events@psl.eu)

EVENT & ORGANIZER PROFILE

The Q-Life Institute at Ecole Normale Supérieure – PSL University (Paris) is a premier European interdisciplinary centre dedicated to quantitative biology. The PSL-Qlife Winter School brings together world-leading biophysicists, bioinformaticians, and molecular geneticists to train early-career researchers in cutting-edge quantitative and computational approaches to genome stability.

PROGRAM & LEARNING OUTCOMES

The intensive one-week curriculum covers quantitative mechanisms of DNA double-strand break (DSB) repair, replication stress, telomere dynamics, and genome instability during cellular ageing. Participants receive advanced training in fluorescence microscopy, single-molecule imaging, electron microscopy, polymer modelling, and machine learning (ML) bioinformatic pipelines in Python/R for predicting DNA break sites and clustering genomic mutations.

★ RATING & EVALUATION

Workshop Evaluation Category	Score / Rating
Course Curriculum & Interdisciplinary Depth	★★★★★
Hands-on Practice & Quantitative Workshops	★★★★★
Course Materials & Computational Pipelines	★★★★★
Poster Sessions & Expert Discussions	★★★★★
Event Logistics & Accommodation	★★★★★

Overall Course Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Features poster presentation sessions with direct, informal feedback from top international authorities (e.g., Dana Branzei, Leonid Mirny).
- Combines theoretical physical/computational lectures with practical data analysis modules using ML tools for genomic datasets.
- Highly interdisciplinary format that fosters networking across biophysics, cell biology, and bioinformatics disciplines.

💬 WHY YOU SHOULD ATTEND THIS WORKSHOP:

You should consider this winter school if you want to acquire quantitative, biophysical, and computational skills for studying DNA damage, repair, and genome architecture. The PSL-Qlife program provides a unique interdisciplinary learning environment led by world-class experts, bridging advanced imaging techniques (single-molecule and fluorescence microscopy) with machine learning workflows for analysing double-strand breaks and chromatin dynamics. This training is exceptionally valuable for PhD students and postdocs working on cellular ageing, stress responses, or genomic stability who wish to integrate rigorous quantitative modelling and bioinformatic pipelines into their experimental biological research.

[WORKSHOP] EPIGENOMICS, CHROMATIN DYNAMICS & TRANSPOSABLE ELEMENT REGULATION

Keywords: Epigenomics, Genome dynamics, Transposable elements, Single-cell CUT&Tag, Long non-coding RNA (lncRNA)

- Host Institution & Organisers: Institut Curie Research Centre & Sorbonne University
- Event & Location: Genome Dynamics International Course, Paris, France (Institut Curie, 12 rue Lhomond, 75005 Paris)
- Scientific Coordinators & Contact: Organising Committee at Institut Curie & Sorbonne University

EVENT & ORGANIZER PROFILE

The Institut Curie Research Centre, in collaboration with Sorbonne University, hosts the international "Genome Dynamics: Cell Identity, Regulation and Evolution" advanced course in Paris. This prestigious training initiative brings together internationally recognised leaders to explore genome architecture, epigenomics, transposable element biology, and single-cell genomics.

PROGRAM & LEARNING OUTCOMES

The intensive eight-day course covers six core thematic modules: Genome Architecture, Epigenomics & Gene Regulation, Translational Genomics, Mobile DNA, Cell Identity & Clonality, and Genome Evolution. Participants gain theoretical and analytical insights into lncRNA-guided chromatin complexes, single-cell CUT&Tag profiling, single-cell long-read sequencing (CELLO-seq), TE silencing mechanisms, multi-omics data integration, and green laboratory practices.

★ RATING & EVALUATION

Workshop Evaluation Category	Score / Rating
Course Curriculum & Evolutionary Depth	★★★★★
Interactive Sessions & Single-Cell Omics	★★★★★
Course Materials & Methodological Scope	★★★★★
Networking & Career Panels	★★★★★
Administrative Support & Efficiency	★★★★★

Overall Course Recommendation **Definitely Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Features active participation formats, including elevator pitches, poster sessions, and career development panels.
- Provides practical experience in interpreting single-cell omics data (UMAP plots, clustering outputs, multi-omics integration).
- Excellent venue for networking with early-career researchers and top principal investigators across European institutions.

💬 WHY YOU SHOULD ATTEND THIS WORKSHOP:

You should consider this international course if you want to gain cutting-edge insights into chromatin regulation, epigenomics, and transposable element biology across eukaryotic systems. Held at the historic Institut Curie in Paris, the program offers a masterclass in how non-coding RNAs, histone modifications, and mobile DNA shape genome stability and cell identity. Participants benefit from exposure to novel single-cell omics technologies (such as single-cell CUT&Tag and long-read TE profiling), multidisciplinary workshops on scientific presentation and green lab transitions, and outstanding networking opportunities with leading European experts and international peers.

[WORKSHOP] LIGHT & CONFOCAL MICROSCOPY: FUNDAMENTALS, IMAGING & PLA QUANTIFICATION

Keywords: Confocal microscopy, Proximity Ligation Assay (PLA), Light microscopy, Image segmentation, Fluorescence imaging

- Host Institution & Organisers: Cellular Imaging Core Facility (CELLIM CF), CEITEC – Masaryk University
- Event & Location: Fundamentals of Light Microscopy, Brno, Czech Republic (Masaryk University Campus, Kamenice 5, 625 00 Brno-Bohunice)
- Scientific Coordinators & Contact: CELLIM Core Facility Team (Milan Esner, Sona Legartová; cellim@ceitec.muni.cz)

EVENT & ORGANIZER PROFILE

The Cellular Imaging Core Facility (CELLIM CF) at CEITEC, Masaryk University in Brno, Czech Republic, is a leading European core facility for bioimaging. CELLIM provides state-of-the-art light and confocal microscopy infrastructure, structured hands-on training programs, and expert scientific consultation for high-resolution imaging and quantitative data analysis.

PROGRAM & LEARNING OUTCOMES

The intensive five-day practical course covers the physical and biological principles of light and fluorescence microscopy, optical resolution, transmitted light, widefield versus confocal microscopy (Zeiss LSM880/LSM800 systems), image processing, quantitative software analysis, Proximity Ligation Assay (PLA) optimisation, and AI-assisted image segmentation and denoising.

★ RATING & EVALUATION

Workshop Evaluation Category	Score / Rating
Course Curriculum & Optical Fundamentals	★★★★☆
Hands-on Practice & Confocal Systems	★★★★★
Course Materials & Image Processing Tools	★★★★☆
Technical Consultations & PLA Optimization	★★★★☆
Core Facility Infrastructure & Equipment	★★★★★

Overall Course Recommendation **Recommended**

💡 PRACTICAL TIPS FOR APPLICANTS

- Practical training on Zeiss LSM880 confocal systems translates directly to workflows on local Zeiss LSM800 equipment.
- Explores AI-based computational tools for automated image segmentation, object detection, and deep learning restoration under low-light conditions.
- Provides direct consultation with CELLIM specialists (Milan Esner, Sona Legartová) for troubleshooting Proximity Ligation Assay (PLA) imaging protocols.

💬 WHY YOU SHOULD ATTEND THIS WORKSHOP:

You should consider this workshop if you aim to master fundamental and advanced confocal light microscopy techniques, particularly for visualising and quantifying protein-protein interactions via Proximity Ligation Assay (PLA). Held at the state-of-the-art CELLIM Core Facility at CEITEC Masaryk University, the course offers comprehensive hands-on training on Zeiss confocal platforms, image acquisition optimisation, and quantitative image analysis software. It is ideal for PhD candidates investigating DNA damage tolerance, genome stability, or cellular stress responses who want to integrate quantitative fluorescence imaging and AI-assisted image processing into their research pipelines.