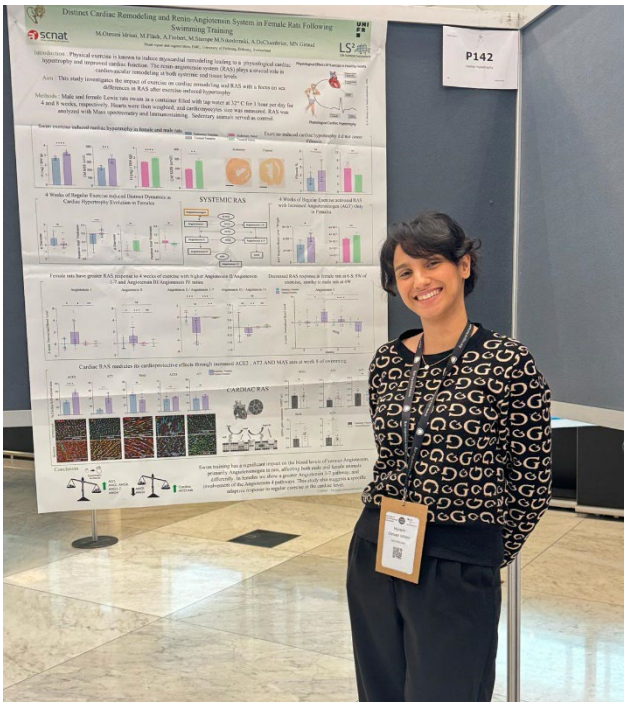
LS2 Travel Grant report

12-14 April 2024, Rai Amsterdam, Amsterdam, The Netherlands.

This year, I was fortunate to receive a travel grant from Life Sciences Switzerland (LS2) and the Swiss Academy of Sciences (SCNAT). This grant enabled me to participate in the Frontiers in Cardiovascular Biomedicine 2024 European congress. The congress was a rewarding experience. I found the sessions to be very informative and the opportunity to connect with other cardiovascular scientists was invaluable.

My poster drew the attention of some other attendees, allowing me to engage in some truly interesting conversations. As a PhD Student committed to my research, these moments of connection with fellow researchers are highly appreciated.

I had engaging discussions with a pediatrician who expressed interest in the importance of incorporating physical activity into the therapeutic approach for children diagnosed with hypertension. It was yet again another confirmation of the impact and the importance of our research in guiding and improving the choice of therapy in this field. The poster session has boosted my motivation and curiosity. Currently, I am in the process of implementing a suggestion that emerged during the congress into my work.



The congress lasted 3 days and completed 51 scientific sessions. It was important for my learning to attend lectures centered around pathological cardiac hypertrophy. A particular one was delivered by Professor Jolanda van der Velden who provided insights into the genetic basis and molecular mechanisms involved in dilated cardiomyopathy (DCM). This talk improved my understanding of the subject.

To finish, I would like to again thank the sponsors for their funding, I encourage everyone to apply for this opportunity because it really provides students with great chance to discover, communicate and network.

Conference report

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Affiliation: Laboratory of the Physics of Biological Systems, Institute of Physics, École polytechnique fédérale de Lausanne (EPFL), Lausanne, Switzerland

PI: Sahand Rahi

Conference: American Physical Society March Meeting

Talk: Continuous evolution of dynamic, multi-state, and computational protein functionalities

LS^2 section: Systems Biology

From 03 to 08 March 2024, I attended the March meeting of the American Physical Society (APS) in Minneapolis. I am very grateful for the support of LS2 to attend this meeting.

In the "Synthetic Biology" session, I gave a talk on one of my main PhD projects. In this work, we propose and experimentally demonstrate a new paradigm for the directed evolution of switchable and computational proteins. By coupling the protein of interest to the cell cycle control in budding yeast, we achieve simultaneous selection for both its high "on" and low "off" activity. Using this method, we evolved new optogenetic tools and new logic gates.

The meeting hosted a wide range of topics in physics. I mostly attended the biophysics talks, but even among these, it was impossible to go to all of them, as there were typically three parallel sessions ongoing. The evolutionary dynamics sessions were particularly thought-provoking, but I was also intrigued by the developments in some fields I had very little knowledge of, such as the effects of magnetic fields on proteins in vitro and wound healing in animals. I enjoyed discussing science with other people in the field of experimental evolution and synthetic biology, as well as a few who worked in completely unrelated fields.

Unfortunately, the conference was just three days after the travel grant submission deadline, so I did not get a picture of myself while presenting. Instead, I have a picture of my conference ID (Fig. 1). I had never visited Minneapolis before (in fact, it was only my second time in the US), but I found the city very nice, with numerous skyways connecting the buildings in downtown. An Uber driver claimed you could visit the whole downtown without touching the soil this way. Just before catching the flight to Europe, I visited one of the main museums in the area—the Minneapolis Institute of Art, which hosted pieces from diverse artists (see one of my favorites in Fig. 2).

Overall, the conference was very scientifically enriching and I am thankful to LS^2 for generously supporting me through a travel grant.

Figure 1. ID from APS March meeting

Figure 2. Excerpt from Sir Edwin Henry Landseer's *The Cat's Paw*

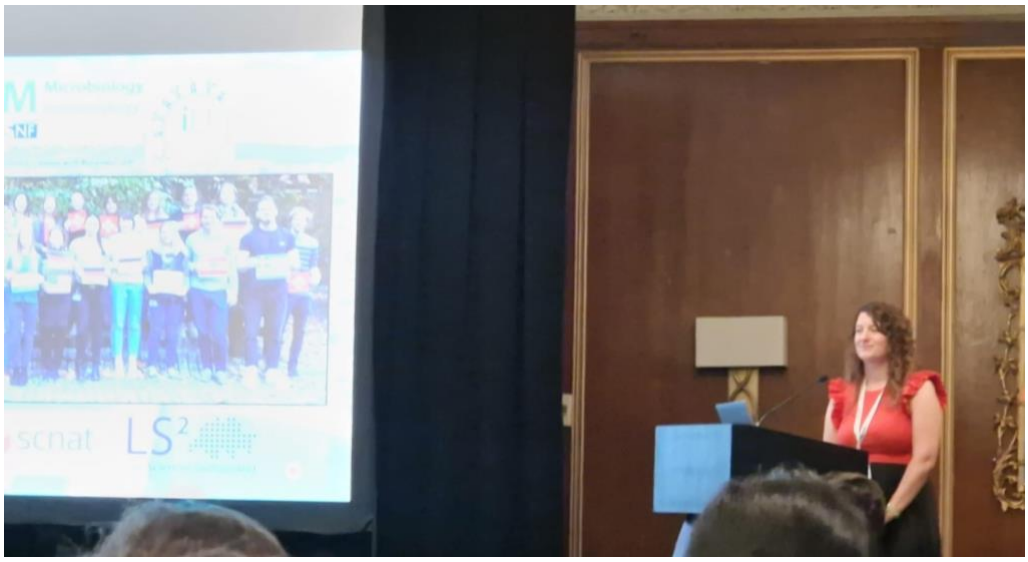
L2S Travel Grant 2024 for PhD Students – Meeting Report
Katarina Schmidt, Institute of Experimental Immunology, University of Zurich

It was a pleasure attending the International Symposium on Epstein Barr Virus (EBV) & Kaposi Sarcoma Associated Virus (KSHV) & related Agents and Diseases (3rd joint meeting) in Boston on June 29-July 3, 2024 in Boston, Massachusetts, USA. Thanks to the support of the Swiss Academy of Sciences (SCNAT) and Life Sciences Switzerland (LS2), I could present my data during as a 12-minute talk during the virus/host interactions parallel session I. This conference took place on the 60th and 30th anniversaries of the discoveries of EBV and KSHV, respectively. There were over 400 participants from over 26 countries and overall the tone of the conference was welcoming and inclusive, focused on scientific exchange.

EBV and KSHV are gamma-herpesviruses that can cause cancer. My research focuses on the interaction between autophagy and KSHV entry. We found that autophagy restricts KSHV infection and that KSHV could be causing endosomal membrane damage that triggers the autophagy response. Although this type of endosomal membrane damage is common among invading bacteria and non-enveloped viruses, this is the first time that is has been described for an enveloped virus. I had took two questions after my talk which asked about lysosomal acidification and colocalization with Rab proteins, both of which I was able to address. The logos of LS2 and SCNAT were placed on my acknowledgment slide.

The other sessions had quite diverse topics for example: epigenetics, gene expression, viral re-activation, tumor microenvironment, viral replication, oncogenesis, autoimmunity including multiple sclerosis, vaccination strategies, noncoding RNA, RNA degradation, structure, therapeutics, clinical care, viral egress, assembly, cancer risk variants, pathogenesis. In addition, there were two poster sessions in the evenings to encourage more discussion.

Attending this conference was an exciting and enriching experience and helped me define my next professional steps. Thus, I would like to thank LS2 and SCNAT again for their kind and generous support.



LS2 Travel Grant Report
HypoxEU Conference, Dresden, Germany
June 9-12, 2024

Thanks to the generous support of Life Sciences Switzerland (LS2) and the Swiss Academy of Sciences (SCNAT), I had the invaluable opportunity to attend the HypoxEU conference, held in Dresden from June 9-12, 2024. This annual conference is a key event for researchers working in the field of hypoxia and its impact on health and disease.

One of the highlights of the conference was the presence of Nobel laureate Sir Peter J. Ratcliffe, whose work on oxygen sensing has significantly advanced our understanding of hypoxia pathways. The presenting scientists were both insightful and inspiring, offering a deep dive into the molecular mechanisms underlying hypoxia, with applications ranging from cancer to cardiovascular diseases. I also had an opportunity to meet other PhD students and share my experiences.

I was privileged to present my own research during both an oral presentation and a poster session. My work, titled *"Single-cell variability of hypoxia-inducible gene expression"*, was well-received by attendees. Engaging in discussions with other scientists in the field provided valuable feedback that will undoubtedly enhance the direction of my project. The poster session led to potential collaborations with other researchers interested in the heterogeneity of hypoxia responses at the cellular level and gave me some ideas for how to answer my scientific questions.

Izabela Smok (ETH Zurich, D-BIOL, Institute of Molecular Systems Biology)
29th RNA Society Annual Meeting 2024; Edinburgh, Scotland; May 28 to June 2, 2024

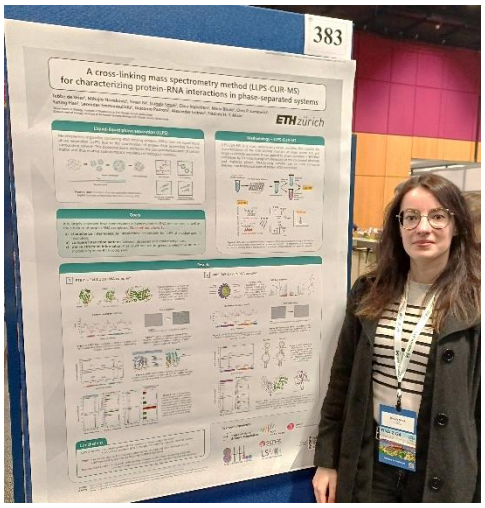
Thanks to the financial support of the Life Sciences Switzerland (LS^2) and the Swiss Academy of Sciences (SCNAT) I was given a chance to attend the 29th RNA Society Annual Meeting 2024 in Edinburgh, Scotland. The meeting took place at the Edinburgh International Conference Centre (EICC) from May 28 to June 2, 2024. As one of the biggest and the most influential RNA meetings, the conference gathered several thousands of scientists involved in the RNA biology research.

Due to the size of the meeting, the oral sessions were run in parallel, covering many aspects of RNA research, including the compartmentalization, method development and structural biology seminars, which were of interest to me. Additionally, a voluntary "Public engagement in RNA research workshop" addressed science communication and common misconceptions of RNA science, also in the context of RNA vaccines.

One of the highlights was a "Mentor-mentee dinner". I have participated in the "academia-to-industry" table discussion, where the industrial scientists, entrepreneurs and consultants casually shared their own experiences and pieces of advice with the young researchers willing to enter the industrial branches. The meeting was also a great chance to network with the fellow scientists, as a part of the organized city tours, dinners and the poster sessions.

The conference organizers gave me the opportunity to present a scientific poster that summarizes the method developed in collaboration with the Allain group at ETH Zurich, titled "*A cross-linking mass spectrometry method (LLPS-CLIR-MS) for characterizing protein-RNA interactions in phase-separated systems*". This method can provide insight into protein-RNA interaction interfaces in various biophysical states of the protein-RNA complexes. It was an important experience for me to present my own work in front of a massive audience, with diverging backgrounds, which helped me to get a "bigger picture" perspective of my own work. My poster presentation allowed me to meet and connect with other researchers who deal with structural proteomics, as well as with the structural biologists who saw our method as a complimentary tool to their own techniques.

Eventually, I was awarded the Best Poster Presentation Award. Taking into account the importance and influence of the RNA Society Meetings, it is one of the most appreciative merits I have received. This would not be possible without the LS^2/SCNAT travel grant; therefore, I would like to express my appreciation and gratitude once again!



European Phagocyte Workshop

March 20 - 23, 2024 | Visegrád, Hungary

CERTIFICATE OF ATTENDANCE

This certificate is to confirm that

Maria Cruz Cobo

Genève, Switzerland

participated in the

EUROPEAN PHAGOCYTE WORKSHOP 2024

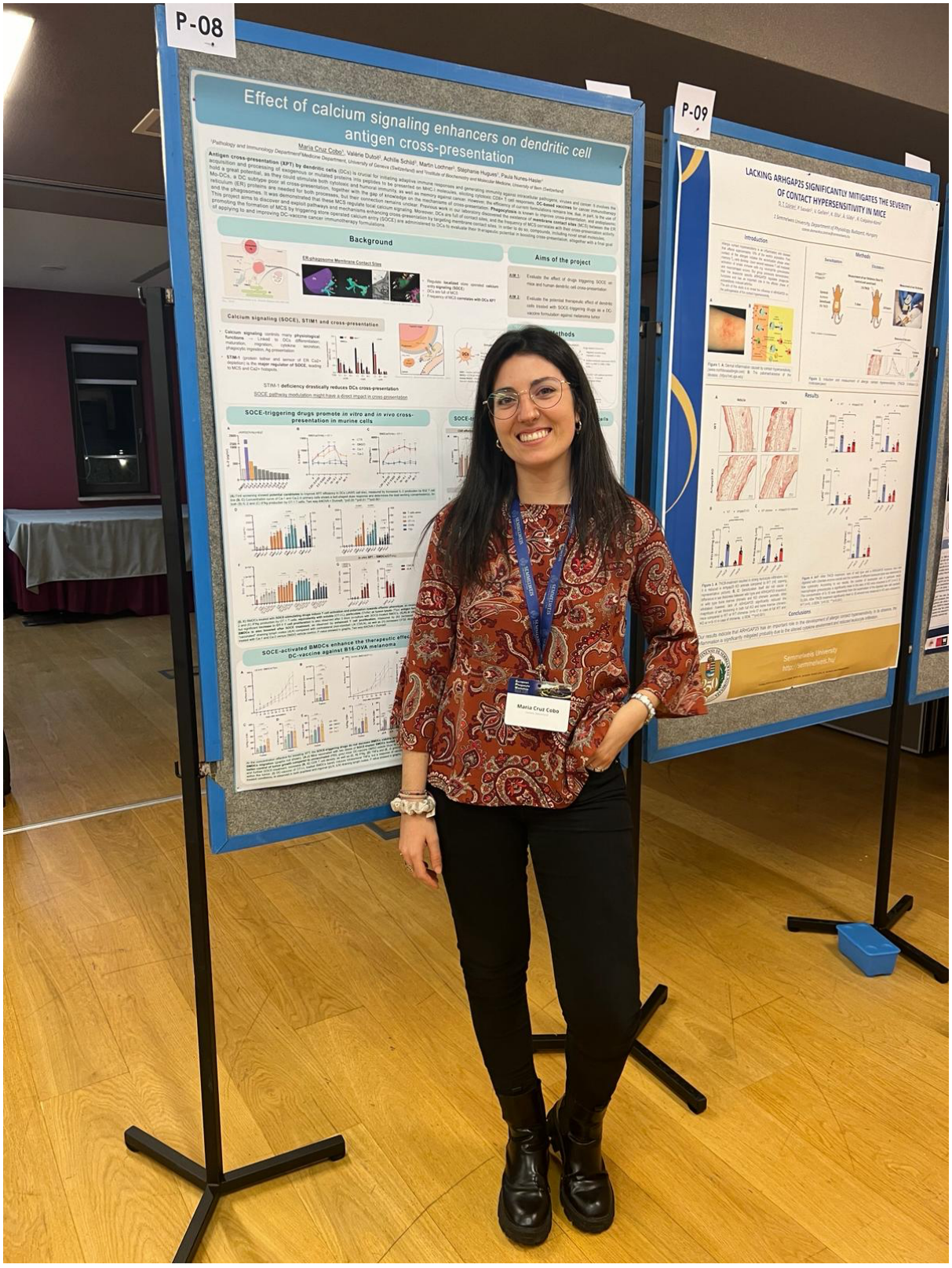
March 20 – 23, 2024

Visegrád, Hungary

Tamás Németh
scientific organizer

Balázs Enyedi
scientific organizer

Attila Mócsai
scientific organizer

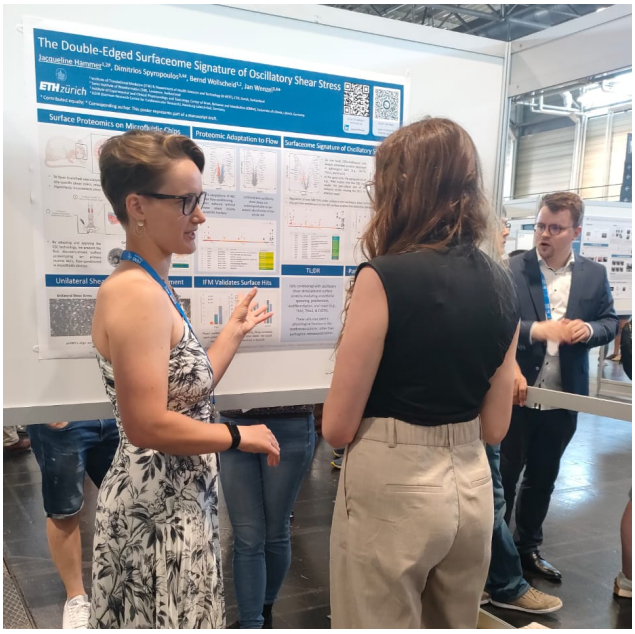

P-08
Effect of calcium signaling enhancers on dendritic cell antigen cross-presentation
Background
Aims of the project
Calcium signaling (SOCE), STIM1 and cross-presentation
SOCE-triggering drugs promote in vitro and in vivo cross-presentation in murine cells
P-09
LACKING ARHGAP25 SIGNIFICANTLY MITIGATES THE SEVERITY OF CONTACT HYPERSENSITIVITY IN MICE
Introduction
Methods
Results
Conclusions
Maria Cruz Cobo

Jacqueline Hammer (ETH Zurich, D-HEST)
Surface Proteoprofiling of Mechanosensing in Brain Endothelial Cells
Poster presentation at **FENS Forum 2024**
25 – 29 June 2024, Vienna (Austria)

First of all, I would like to thank Life Sciences Switzerland (LS2) and the Swiss Academy of Sciences (SCNAT) for giving me the opportunity to attend the FENS Forum 2024, held from June 25 to 29 in Vienna, Austria. The FENS Forum is Europe's largest neuroscience conference, covering a wide range of topics from basic to translational research. Lasting five days and encompassing a packed and diverse program, the conference has very high fees for registration and abstract submission. I am all the more glad to be receiving the financial support from LS2 and SCNAT so I could attend the conference without having to worry about covering these costs myself.

The conference program was packed with plenary lectures, symposia, and workshops. What renders the FENS Forum an extraordinary experience is that they did not shy away from additional features like a conference-specific app, AI summaries of all the thousands of posters, and a vivid frame program that included the opportunity to attend Jump the FENS, the conference party that prolonged networking well into the night.
The scientific program included talks on neural circuit function, neurodegenerative diseases, and the latest advances in neuroimaging. Particularly memorable for me was the opening plenary lecture on recent advances in using adenoviral vectors targeting and crossing the blood-brain barrier for gene therapy. This talk was held by Viviana Gradinaru from Caltech. Having worked in this direction before, I was familiar enough with previous efforts to appreciate the truly remarkable work she and her group achieved in moving the field forward.

My main motivation for attending the conference was to present a recent collaboration and soon-to-be shared first authorship. That is, I am a passionate neuroscientist who is determined to advance the state of the art by which OMICs technologies are applied to grant answers to neuroscientific questions. This incentive brought me to pursue my doctoral studies in the group of Bernd Wollscheid, who specializes in proteomic technologies that investigate the cell surface. Here, I have had the privilege of bridging the fields of neuroscience and proteomics in the context of a collaboration with Jan Wenzel's group from the University of Lübeck. This collab yielded compelling results that I was eager to share via a poster, titled "Surface Proteoprofiling of Mechanosensing in Brain Endothelial Cells". The feedback I received was invaluable for the quality of my manuscript writing. Having been out of touch with the field during long periods of my doctorate, I was very happy to get input from differently informed perspectives.



The FENS Forum also provided numerous networking opportunities through social events, lunches, and coffee breaks. The vibrant setting of Vienna, with its rich cultural history, added to the enriching experience that was attending the FENS Forum 2024. The knowledge gained, feedback received, and connections made contributed to my professional development. I am grateful to LS2 and SCNAT for making this possible. I highly recommend this conference to anyone in the field of neuroscience.

Léa Bernaleau
Department of Immunobiology, University of Lausanne
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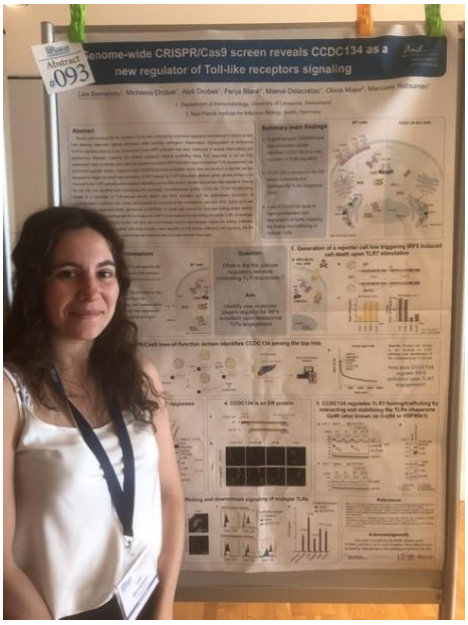
LS^2 Travel Grant Report

I would like to thank the Life Sciences Switzerland (LS^2) and the Swiss Academy of Sciences (SCNAT) for giving me the opportunity to attend and present my research work at the *19th International Conference on Innate Immunity*, held from the 6th to 11th of June 2024 in Loutraki, Greece.

This annual conference aims to gather immunologists from all around the world to discuss the latest progresses in innate immunity. Therefore, it was a perfect opportunity for me to present my current research project focused on the innate sensors called Toll-like receptors (TLRs), with a poster entitled “Genome-wide CRISPR/Cas9 screen reveals CCDC134 as a new regulator of Toll-like receptors signaling”. The 6-day conference was very well organized, with a limited attendance allowing to have one session at a time. It was an invaluable opportunity to attend all presentations and therefore gain insights into the latest discoveries and advancements both directly relevant to my project and on innate immunity in a broader sense. The scientific quality was excellent, and a large extent of the data presented were still unpublished results, which was very much appreciated and made the participation to this conference even more worthwhile. Amongst the many interesting talks, it was specially engaging to learn more about light sheet fluorescence microscopy and to see how researchers at the Udalova’s group are using it to study the different stages of neutrophil maturation. Furthermore, I was able to discuss in more detail with the speaker after his presentation of a cellular model that we are both currently using. I could also learn that another team was generating single cell RNA-sequencing (scRNA-seq) atlases of human and murine Tumor-Associated Dendritic Cells (TADC) and that these data would be available on a publicly accessible website, which could prove useful for future research projects. In addition to lectures and talks, there were numerous poster sessions, during which I had the chance to present my project twice, on the 4th and 5th day of the conference. These sessions were very interactive and perfect opportunities to exchange with colleagues with different expertise. I received much constructive feedback as well as new ideas that I intend to implement in my future research work.

Overall, it was an exceptionally motivating meeting, with both a scientific and social program that encouraged interaction with young researchers and potential new collaborators. It was an important networking opportunity, allowing me to talk about future career possibilities, which, being in the final year of my PhD, was an important aspect of attending this conference. Once again, I would like to thank LS^2 and SCNAT for their support, allowing me to participate to this conference that offered valuable scientific and professional interactions.



Ievgeniia Kocherova, Center of Experimental Rheumatology, University Hospital Zürich

8th Systemic Sclerosis World Congress
Prague, Czech Republic, March 14-16, 2024

I would like to thank Life Sciences Switzerland (LS2) and the Swiss Academy of Sciences (SCNAT) Tavel Grant for supporting my participation in the 8th Systemic Sclerosis World Congress, one of the most prestigious meetings for clinicians and researchers in the field of rheumatic and autoimmune diseases. This congress, held biennially, was hosted this year in Prague, Czech Republic. It offered a dynamic program that included hands-on workshops, lectures, oral presentations, and satellite sessions — creating a stimulating environment for participants dedicated to advancing research and treatment for scleroderma.

Our abstract, *"Unraveling cardiac fibrosis through multi-omics analysis: DYSF, MXRA5, and FOXF1 as promising targets,"* was selected for an oral presentation. It was an honour to share our results with the scientific community and patients at this highly renowned congress. Cardiac involvement, a frequent complication in systemic sclerosis, manifests as progressive myocardial fibrosis and ultimately leads to heart failure. Given the significance of this issue, our findings contribute to the understanding of rheumatic diseases by uncovering novel molecular players in the fibrogenic process, which sparked interest among researchers in the field.

Notably, the congress attracted researchers from various specialties, healthcare professionals, and patients from around the globe, enhancing its high scientific profile. This diversity fostered a highly interactive atmosphere in both the clinical and basic science sessions. The extensive patient-centred sessions were also well-received, complementing the medical aspects of the event.

Overall, attending the 8th Systemic Sclerosis World Congress was an inspiring experience, giving me the opportunity to present our findings in the context of the latest discoveries and trends in the field, while also exploring the beautiful city of Prague. I would like to extend my gratitude once again to LS2 and SCNAT for their generous support.

Conference Report: 4th International Conference on Engineered Living Materials

LS2 Travel Grant Recipient: Roberto Avendaño

Conference Dates: September 18-20, 2024, Saarbrücken, Germany

Introduction: This conference brought together experts in synthetic biology and materials science, providing me the option of either presenting my current research or expanding professional connections. During this conference, I presented my poster entitled "Self-patterning engineered living materials based on *E. coli* curli nanofibers". The research focuses on the design of engineered living materials by using *E. coli* biofilms; I develop the modification of their spatial patterns through synthetic gene regulatory networks. This research shows how to control the production of variants of curli fibers to produce biofilms with dynamic features for applications in biocatalysis and bioremediation.

I had very interesting discussions with several well-known researchers. For example, Neel Joshi was able to speak about my poster for about 30 minutes and thanked me for the novelty of my approach. He invited me to his upcoming talk at EPFL, giving me extra insight into his latest work.

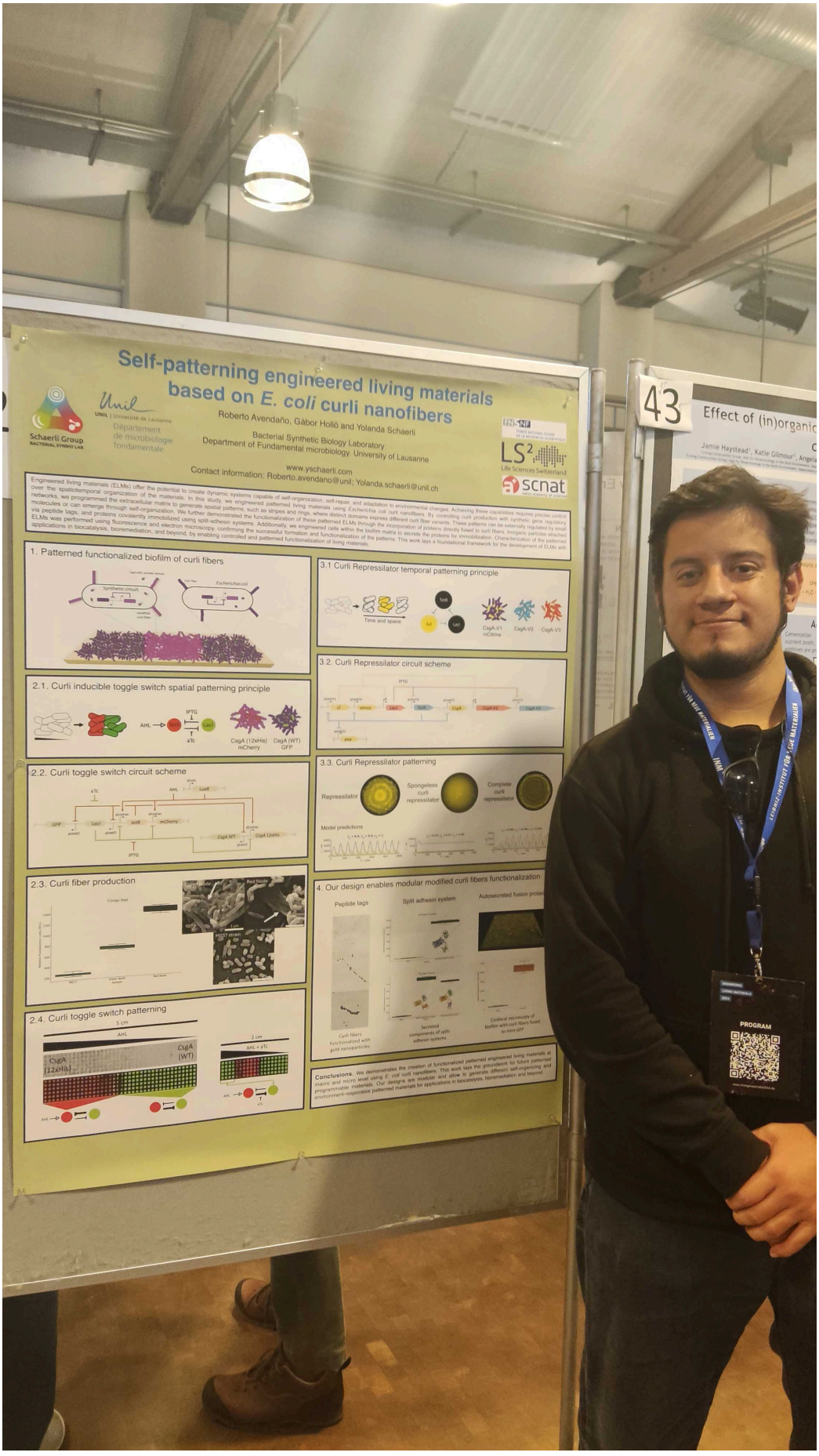
I also took feedback from Zhuojun Dai, the principal investigator of the key paper that I recently presented in a journal club, and Anton Kan from ETH. They provided important suggestions regarding how limitations of recombinant CsgA may be overcome.

I had an opportunity to meet Tom Ellis, who expressed his admiration for my work after a discussion with my supervisor, Yolanda Schaerli. These interactions were of extreme value in getting critical feedback touching on my research, especially in the direction of finishing my PhD and publication.

I also discussed the common challenges in biofilm engineering with Anton Kan, a researcher at ETH. We deliberated on strategies of using the limitations of the existing methods of recombinant production of curli, one of the most important fields in the development of functionalised living materials.

The conference has provided the platform for the presentation of my research work, but it also gave me an opportunity to lay the foundation for future collaborations. To that aspect, for example, the invitation by Neel Joshi to a talk at EPFL and further interactions with researchers such as Zhuojun Dai have opened avenues for probable postdoctoral collaboration.

I conclude that this conference was an important milestone in my PhD life. It was a wonderful opportunity to represent my work, receive expert feedback on it, and explore new avenues of research. I'm very grateful to the LS2 Travel Grant Committee for this enriching experience. Enclosed is a photo of myself presenting my poster at the conference.


Self-patterning engineered living materials based on E. coli curli nanofibers
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Schaerli Group
Unil
Université de Lausanne
Département de microbiologie fondamentale
LS2
Life Sciences Switzerland
scnat
1. Patterned functionalized biofilm of curli fibers
2.1. Curli inducible toggle switch spatial patterning principle
2.2. Curli toggle switch circuit scheme
2.3. Curli fiber production
2.4. Curli toggle switch patterning
3.1 Curli Repressilator temporal patterning principle
3.2. Curli Repressilator circuit scheme
3.3. Curli Repressilator patterning
4. Our design enables modular modified curli fibers functionalization
Peptide tags
Split adhesin system
Conclusions
43
Effect of (in)organic
PROGRAM

Travel Grant Report

Conference Name: Biomolecular Horizons 2024
Location: Melbourne Convention & Exhibition Centre, Melbourne, Australia
Dates: September 22-26, 2024

Overview

I was honored to attend Biomolecular Horizons 2024, which brought together three prestigious congresses: the 26th Congress of the International Union of Biochemistry and Molecular Biology (IUBMB), the 17th Congress of the Federation of Asian & Oceanian Biochemists & Molecular Biologists (FAOBMB), and the 22nd ComBio Conference. This unique event provided a significant platform for scientists at all stages of their careers, from Nobel Laureates to emerging researchers.

Poster Presentation

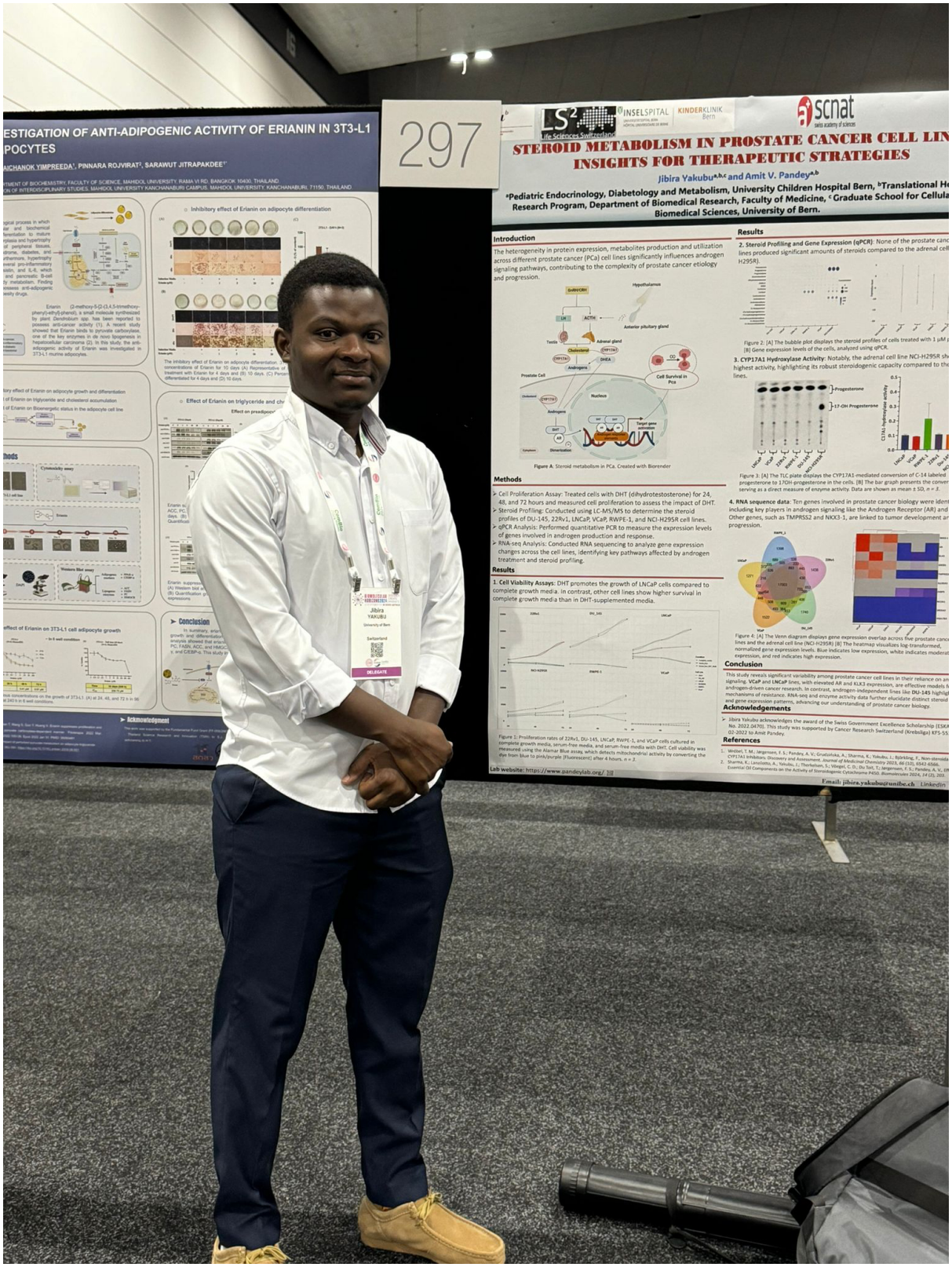
During the conference, I presented my poster titled **"Steroid Metabolism in Prostate Cancer Cell Lines: Insights for Therapeutic Strategies."** This work focuses on the critical role of steroid metabolism in prostate cancer progression and explores potential therapeutic interventions. Engaging with fellow attendees allowed me to receive valuable feedback and insights, further enriching my research.

Key Takeaways

1. **Networking:** I had the opportunity to connect with leading experts and fellow researchers, fostering collaborations that could be beneficial for my future work.
2. **Latest Research:** The conference featured cutting-edge research presentations that inspired me to explore new methodologies and ideas for my own projects.
3. **Workshops:** Participating in workshops allowed me to gain hands-on experience with new technologies and techniques relevant to my field.

Conclusion

Attending Biomolecular Horizons 2024 was an invaluable experience that significantly contributed to my professional development. I extend my gratitude to the LS2 and SCNAT for the travel grant, which made my participation possible. I look forward to applying the insights gained from this experience to my future research endeavors.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ESTIGATION OF ANTI-ADIPOGENIC ACTIVITY OF ERIANIN IN 3T3-L1 POCYTES
AICHANOK YIMPREEDA, PINNARA ROJVIRAT, SARAWUT JITRAPAKDEE
Inhibitory effect of Erianin on adipocyte differentiation
Conclusion
Acknowledgment
Life Sciences Switzerland
INSELSPITAL
KINDERKLINIK Bern
scnat
STEROID METABOLISM IN PROSTATE CANCER CELL LIN
INSIGHTS FOR THERAPEUTIC STRATEGIES
Jibira Yakubu and Amit V. Pandey
Pediatric Endocrinology, Diabetology and Metabolism, University Children Hospital Bern,
Research Program, Department of Biomedical Research, Faculty of Medicine,
Biomedical Sciences, University of Bern.
Introduction
The heterogeneity in protein expression, metabolites production and utilization across different prostate cancer (PCa) cell lines significantly influences androgen signaling pathways, contributing to the complexity of prostate cancer etiology and progression.
Hypothalamus
Anterior pituitary gland
Adrenal gland
Prostate Cell
Nucleus
Cell Survival in Pca
Figure A. Steroid metabolism in PCa. Created with Biorender
Methods
Cell Proliferation Assay: Treated cells with DHT (dihydrotestosterone) for 24, 48, and 72 hours and measured cell proliferation to assess the impact of DHT.
Steroid Profiling: Conducted using LC-MS/MS to determine the steroid profiles of DU-145, 22Rv1, LNCaP, VCaP, RWPE-1, and NCI-H295R cell lines.
qPCR Analysis: Performed quantitative PCR to measure the expression levels of genes involved in androgen production and response.
RNA-seq Analysis: Conducted RNA sequencing to analyze gene expression changes across the cell lines, identifying key pathways affected by androgen treatment and steroid profiling.
Results
1. Cell Viability Assays: DHT promotes the growth of LNCaP cells compared to complete growth media. In contrast, other cell lines show higher survival in complete growth media than in DHT-supplemented media.
Figure 1: Proliferation rates of 22Rv1, DU-145, LNCaP, RWPE-1, and VCaP cells cultured in complete growth media, serum-free media, and serum-free media with DHT. Cell viability was measured using the Alamar Blue assay, which detects mitochondrial activity by converting the dye from blue to pink/purple (fluorescent) after 4 hours. n = 2.
Results
2. Steroid Profiling and Gene Expression (qPCR): None of the prostate canc lines produced significant amounts of steroids compared to the adrenal cell H295R).
Figure 2: [A] The bubble plot displays the steroid profiles of cells treated with 1 µM [B] Gene expression levels of the cells, analyzed using qPCR.
3. CYP17A1 Hydroxylase Activity: Notably, the adrenal cell line NCI-H295R sh highest activity, highlighting its robust steroidogenic capacity compared to th lines.
Progesterone
17-OH Progesterone
Figure 3: [A] The TLC plate displays the CYP17A1-mediated conversion of C-14 labeled progesterone to 17OH-progesterone in the cells. [B] The bar graph presents the conver serving as a direct measure of enzyme activity. Data are shown as mean ± SD, n = 3.
4. RNA sequence data: Ten genes involved in prostate cancer biology were iden including key players in androgen signaling like the Androgen Receptor (AR) and Other genes, such as TMPRSS2 and NKX3-1, are linked to tumor development an progression.
Figure 4: [A] The Venn diagram displays gene expression overlap across five prostate canc lines and the adrenal cell line (NCI-H295R) [B] The heatmap visualizes log-transformed, normalized gene expression levels. Blue indicates low expression, white indicates moderat expression, and red indicates high expression.
Conclusion
This study reveals significant variability among prostate cancer cell lines in their reliance on an signaling. VCaP and LNCaP lines, with elevated AR and KLK3 expression, are effective models f androgen-driven cancer research. In contrast, androgen-independent lines like DU-145 highlig mechanisms of resistance. RNA-seq and enzyme activity data further elucidate distinct steroid and gene expression patterns, advancing our understanding of prostate cancer biology.
Acknowledgements
Jibira Yakubu acknowledges the award of the Swiss Government Excellence Scholarship (ESKA No. 2022.0470). This study was supported by Cancer Research Switzerland (Krebsliga) KFS-55 07-2022 to Amit Pandey.
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DELEGATE
Jibira
YAKUBU
University of Bern
Switzerland

Melanie Brunner (University of Fribourg)
HUPO 2024, 23rd Human Proteome Organization World Congress

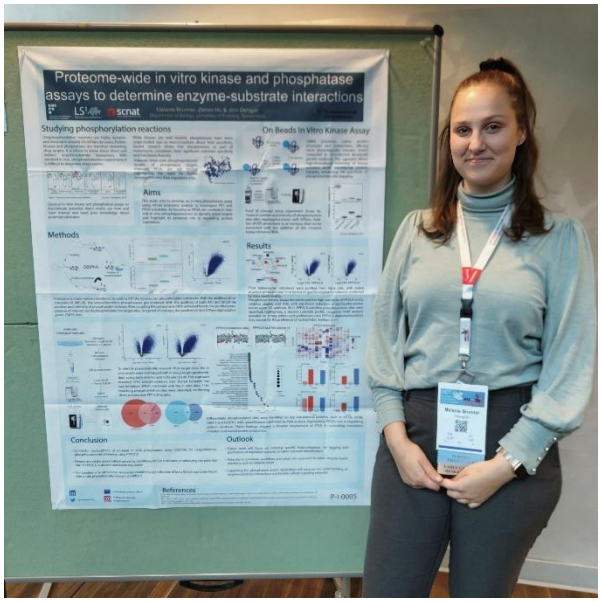
From October 20th to 24th, 2024, I attended the HUPO World Congress in Dresden, Germany, an event that brought together global leaders in proteomics to share insights and advancements in the field. Thanks to the travel grant from the Life Sciences Switzerland (LS2) and Swiss Academy of Sciences (SCNAT) I was able to participate in this prestigious conference.

During the congress, I presented a poster titled "Proteome-wide in vitro kinase and phosphatase assays to determine enzyme-substrate interactions". My research focuses on understanding enzyme-substrate interactions by utilizing comprehensive in vitro assays that target kinases and phosphatases across the proteome. This work contributes to the broader goal of identifying regulatory pathways and understanding post-translational modifications that control protein function, which are critical in many diseases.

The conference provided an invaluable opportunity to engage with pioneering proteomics research, focusing on cutting-edge methods in mass spectrometry, quantitative proteomics, and data analysis. Notably, presentations on advanced methods for protein-protein interaction mapping, single-cell proteomics, and structural proteomics offered fresh insights that I plan to integrate into my own research. Emerging technologies, such as new mass spectrometers with improved sensitivity and the application of artificial intelligence in proteome data analysis, were some of the key trends highlighted at the congress.

The event also fostered networking with researchers and potential collaborators from both academia and industry. I had the chance to engage in thought-provoking discussions on novel methodologies for studying post-translational modifications and protein interactions, which will undoubtedly enhance my future work. In addition, the workshops and roundtable sessions provided a platform to exchange knowledge and ideas on the latest bioinformatics tools for large-scale proteomic data analysis, enriching my skill set and offering new approaches for analyzing complex datasets.

In summary, attending the HUPO World Congress 2024 was an incredibly enriching experience. It allowed me to present my research, broaden my understanding of the latest developments in proteomics, and establish valuable connections with experts in the field. The knowledge and skills I gained will be instrumental in advancing my research and contributing to the broader scientific community.



Sourabh Monnappa, EPFL, Lausanne

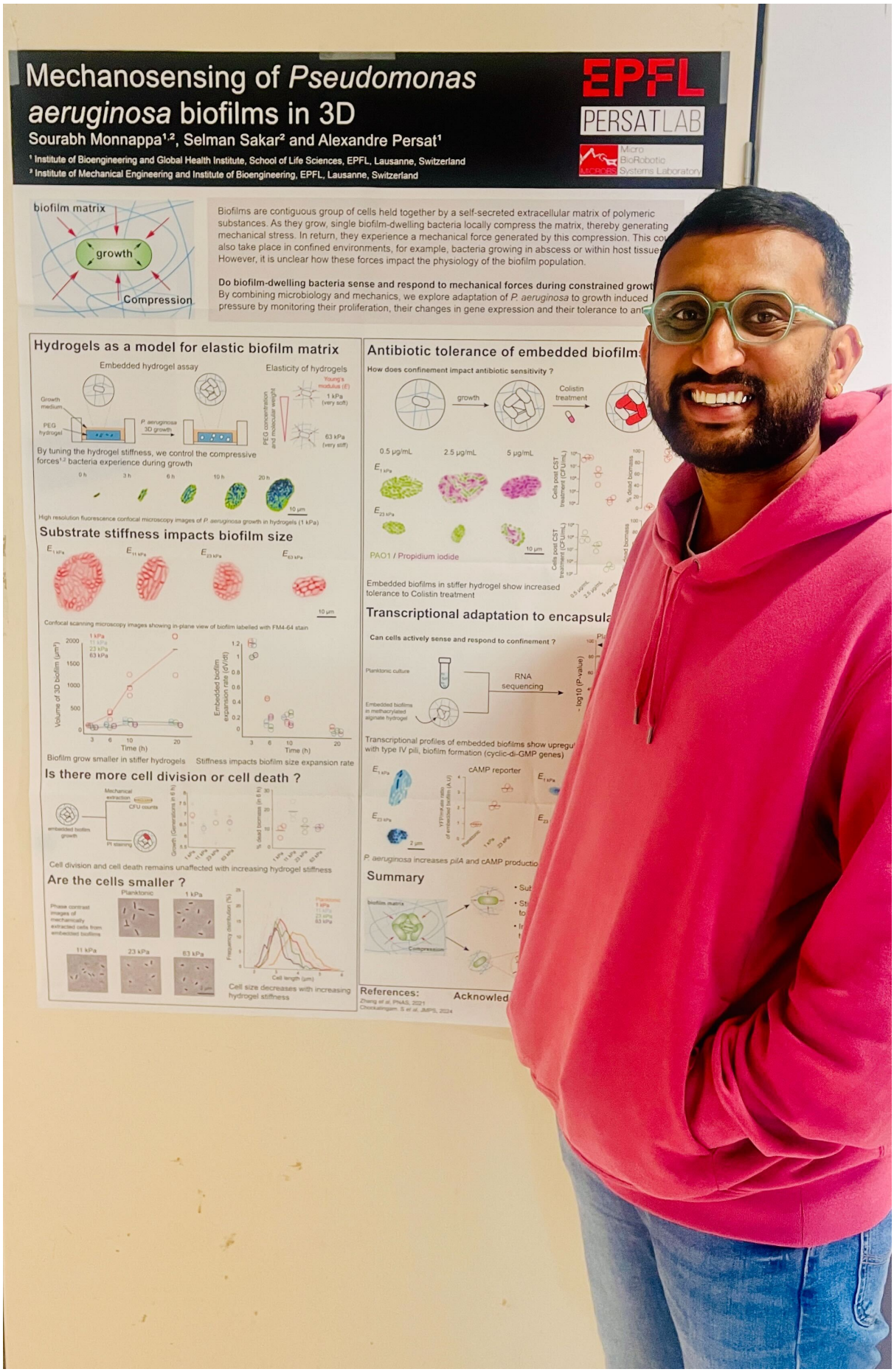
EMBO BACNET 2024, Sant Feliu du Guixols, Spain

I am sincerely grateful to Life Sciences Switzerland (LS2) and the Swiss Academy of Sciences (SCNAT) for their support, which enabled me to attend the EMBO BACNET Workshop on Bacterial Networks held in Sant Feliu de Guixols, Spain, from September 15–20, 2024. BACNET stands out as one of the best microbiology conferences I've attended so far. Set in this stunning location, where it has been held for years, the workshop brought together around 160 attendees. The setup and surroundings created an inspiring and unforgettable experience.

With a smaller crowd, I was able to attend every session, immersing myself in new concepts. The strong focus on interdisciplinarity highlighted the vast potential for addressing fundamental questions as well as developing practical solutions in microbiology. Beyond my PI's presentation (Prof. Alexandre Persat), I particularly enjoyed talks by Jordi van Gestel on predator-prey interactions, Bonnie Bassler's new mechanistic insights into quorum sensing, Silvia Bulgharesi on multicellularity within oral microbiomes, and Donato Giovanelli's exploration of trace elements role in living systems around us. Adding to this experience were the informal discussions during tea breaks, engaging "meet the speaker" sessions over lunch, and dinners with stunning views, all of which made the experience truly memorable.

A standout feature of the conference was the 1-minute flash talk for each poster, designed to pitch our work to the entire audience and draw interest for the poster sessions. This format was both intense and entertaining. I presented my PhD project, "Mechanosensing of *Pseudomonas aeruginosa* biofilms in 3D," during a highly interactive 3-hour poster session, which provided invaluable feedback and sparked thought-provoking questions. Despite leaving me with a sore throat, the engaging discussions were well worth it. Additionally, the poster sessions served as excellent networking opportunities for exchanging ideas.

The conference concluded with a lively party featuring a professional DJ, offering a perfect end to an inspiring week. Evening sessions ran until 10:30 p.m., often followed by informal gatherings that allowed for meaningful personal and professional connections. This experience was both exciting and transformative, helping clarify my career path as I approach graduation. I am deeply thankful to LS2 and SCNAT for their generous support in making this opportunity possible.


Mechanosensing of Pseudomonas aeruginosa biofilms in 3D
Sourabh Monnappa[1,2], Selman Sakar[2] and Alexandre Persat[1]
[1] Institute of Bioengineering and Global Health Institute, School of Life Sciences, EPFL, Lausanne, Switzerland
[2] Institute of Mechanical Engineering and Institute of Bioengineering, EPFL, Lausanne, Switzerland
EPFL
PERSATLAB
Micro BioRobotic Systems Laboratory
biofilm matrix
growth
Compression
Biofilms are contiguous group of cells held together by a self-secreted extracellular matrix of polymeric substances. As they grow, single biofilm-dwelling bacteria locally compress the matrix, thereby generating mechanical stress. In return, they experience a mechanical force generated by this compression. This co also take place in confined environments, for example, bacteria growing in abscess or within host tissue However, it is unclear how these forces impact the physiology of the biofilm population.
Do biofilm-dwelling bacteria sense and respond to mechanical forces during constrained growt
By combining microbiology and mechanics, we explore adaptation of P. aeruginosa to growth induced pressure by monitoring their proliferation, their changes in gene expression and their tolerance to ant
Hydrogels as a model for elastic biofilm matrix
Embedded hydrogel assay
Elasticity of hydrogels
Growth medium
PEG hydrogel
P. aeruginosa 3D growth
Young's modulus (E)
1 kPa (very soft)
63 kPa (very stiff)
PEG concentration and molecular weight
By tuning the hydrogel stiffness, we control the compressive forces[1,2] bacteria experience during growth
0 h
3 h
6 h
10 h
20 h
10 µm
High resolution fluorescence confocal microscopy images of P. aeruginosa growth in hydrogels (1 kPa)
Substrate stiffness impacts biofilm size
Confocal scanning microscopy images showing in-plane view of biofilm labelled with FM4-64 stain
Volume of 3D biofilm (µm³)
Time (h)
Biofilm grow smaller in stiffer hydrogels
Embedded biofilm expansion rate (dV/dt)
Stiffness impacts biofilm size expansion rate
Is there more cell division or cell death ?
Mechanical extraction
CFU counts
embedded biofilm growth
PI staining
Growth (Generations in 6 h)
% dead biomass (in 6 h)
Cell division and cell death remains unaffected with increasing hydrogel stiffness
Are the cells smaller ?
Planktonic
1 kPa
11 kPa
23 kPa
63 kPa
Phase contrast images of mechanically extracted cells from embedded biofilms
Frequency distribution (%)
Cell length (µm)
Cell size decreases with increasing hydrogel stiffness
Antibiotic tolerance of embedded biofilms
How does confinement impact antibiotic sensitivity ?
growth
Colistin treatment
0.5 µg/mL
2.5 µg/mL
5 µg/mL
Cells post CST treatment (CFU/mL)
% dead biomass
PAO1 / Propidium iodide
Embedded biofilms in stiffer hydrogel show increased tolerance to Colistin treatment
Transcriptional adaptation to encapsula
Can cells actively sense and respond to confinement ?
Planktonic culture
Embedded biofilms in methacrylated alginate hydrogel
RNA sequencing
- log10 (P-value)
Transcriptional profiles of embedded biofilms show upregu with type IV pili, biofilm formation (cyclic-di-GMP genes)
cAMP reporter
YFP/mKate ratio of activated Vfr (A.U)
P. aeruginosa increases pilA and cAMP productio
Summary
biofilm matrix
Compression
References:
Acknowled
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LS2 Travel grant report

HUPO World Congress 2024, Dresden Germany

Alexandre Leytens, University of Fribourg

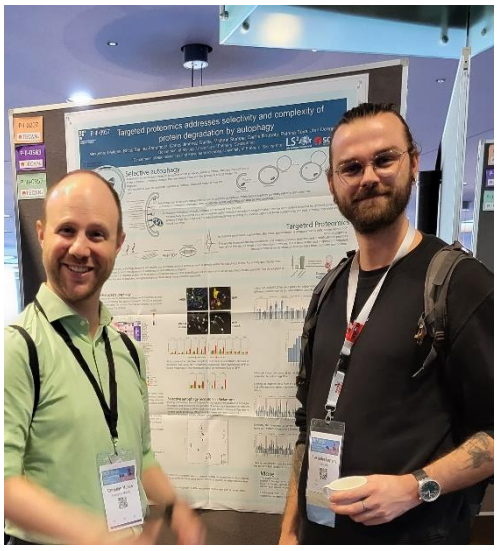
Thanks to the travel grant from LS2 and SCNAT, I attended the Human Proteome Organization (HuPO) world congress in Dresden in October 2024. This congress gathered over 1800 participants and focused on the latest developments and highlights in the application of proteomics techniques. Although it is organized by the Human proteome project, the congress focuses on proteomics across multiple organisms.

To briefly summarize proteomics, it is a field focusing on the large-scale study of proteins. This usually consists of identifying proteins and quantifying them in very diverse biological samples, ranging from simple cell lysates generated in a lab to patient-derived clinical samples. Working with proteins is challenging due to their incredible diversity, and unlike DNA or RNA, it is not possible to amplify proteins. Partly because of these inherent difficulties, proteomics is a very active and technical field, and every year, new machines, techniques and software are released to push proteomics forwards. This congress was the perfect occasion to learn about all these upcoming developments.

This is a fast-evolving field, and a lot of techniques have completely changed since the beginning of my PhD in the past few years. This congress highlighted new trends in proteomics, such as increased sensitivity to allow working with very low amounts of sample. Proteomics studies on single-cells went from a simple proof of concept to actual usable methods that deliver biological insights within the last few years with the development of the newest machines and protocols. A lot of sessions were concerned with bioinformatics, with new ways of analyzing data and make its (re-) use easier which is becoming more and more important as proteomic techniques now allow very large-scale studies with several hundreds or even thousands of samples.

Finally, a session that I found especially interesting was on structural proteomics. Although completely separated from my personal research interests, I enjoyed seeing all the brilliant ideas researchers came up with to obtain proteome-wide structural insights, from limited proteolysis approaches to cross-linking or exploiting thermal stability, I was amazed by the utility of these techniques.

Next to these talks, I had the opportunity to present my own poster titled “Targeted Proteomics addresses selectivity and complexity of protein degradation by autophagy” showing my work at the intersection of proteomics and autophagy. I received great feedback from prominent experts (proof on the picture 😊) in the field, which was great!



I used this opportunity to network and meet a lot of researchers not only at my own poster, but throughout all the events organized around the conference. I met up with many friends and colleagues from Switzerland and around the globe. Overall, this was a great opportunity, and I enjoyed it very much. Many thanks to LS2 and SCNAT for the grant!

Name: Luca Fusar Bassini
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Conference: iSCMS, Copenhagen, 26-28.10.2024 (https://singlecellms.org/)

The iSCMS conference spanned two days and dived into cutting-edge advancements in single-cell proteomics, spatial metabolomics, and cellular imaging, attracting renowned researchers and innovators. On Sunday, Erwin Schoof kicked off with a welcome address, followed by an opening keynote from Neil Kelleher, exploring high-resolution top-down proteomics in brain cells. The morning sessions highlighted single-cell proteomics, spatial visual proteomics for cancer research, and low-stress single-cell isolation by Jonathan Whitchurch. The next session brought insights into targeted multimodal analysis for lung metabolism and innovative single-cell metabolomics by Thomas Hankemeier. Afternoon sessions continued with themes on metabolic decoding, statistical design in single-cell mass spectrometry by Olga Vitek, and single-cell proteomics pipelines. Kathryn Lilley concluded the day with an exciting keynote on studying in subcellular localization mechanisms beyond protein expression by cellular fractionation.
Monday opened with Karl Mechtler's keynote, probing the depth of single-cell proteomics. Key discussions by Jesper Olsen and Erwin Schoof revealed new insights into protein turnover and melanoma's resistance mechanisms. Later, Carsten Hopf and Fabian Coscia delve into MALDI imaging and cancer tissue proteomics, while Jason Derks presented on single-nucleus proteomics. Afternoon themes shifted to tissue-level spatial multiomics, digital microfluidics, and metabolic profiling, with Theodore Alexandrov.

During the conference, I presented my poster on our pioneering work developing a 3D lipidomic atlas of the adult mouse brain, aiming to bridge the spatial complexity of lipid distribution with functional brain architecture. The poster overviewed our use of Matrix-Assisted Laser Desorption Ionization Mass Spectrometry Imaging (MALDI-MSI) to analyze hundreds of lipids across brain sections from multiple mice. By mapping lipids at a micrometric scale, we offered an unprecedented spatial description of lipid metabolism.

Beyond presenting my work, the conference provided invaluable networking opportunities. A highlight was meeting Niels Skotte at my poster, a Huntington's PI interested in spatial lipidomics, with a background in antisense oligonucleotides, which closely aligns with my master's thesis topic. Our conversation sparked ideas for possible collaborations on lipid mapping in neurological disorders. I also connected with a postdoc from Nikolai Slavov's lab, who, although lacking in background, showed genuine curiosity about our dataset's potential for spatial lipidomics + proteomics, emphasizing the broadening appeal of spatial lipidomics in various biological fields. Further notable interactions included Bogdan Budnik, a Boston-based PI interested in our dataset. In fact, throughout the event, I noticed a strong engineering slant, with sessions heavily oriented toward technical methods rather than deep biological or computational analysis. This approach provided a refreshing perspective that broadened my view of a computationalist. I've also participated in and co-organized a pre-event hackathon the day before the conference, an occasion that made it easier to connect with fellow PhD students from other labs and sparked a good exchange of tools and ideas.

Over dinner, Manuel Liebeke expressed appreciation for the project and our methods. The general sentiment was one of intrigue and acknowledgment, a solid affirmation of the work we're pioneering in lipidomics. Adding to my contributions, I was honored to introduce on stage the event I am organizing with our lab, The Single-Cell and Spatial Metabolomics Online Day. This event, which I founded, is a first-of-its-kind virtual conference designed to showcase key advancements in metabolomics, both in single-cell and spatial dimensions, over the past year. The program will spotlight major methodological breakthroughs, including renowned experts like Jonathan Sweedler, Peter Nemes, Theodore Alexandrov, Manuel Liebeke, and Melanie Bailey to share their insights. In addition, emerging researchers will present speed talks, with interactive Q&A sessions on Zoom, enabling an accessible and engaging format. Community-building efforts will be enhanced by a dedicated Discord server, and all talks will be open-access on YouTube.

Overall, the conference was both affirming and enlightening, marking meaningful steps forward in our research and establishing new professional connections. The positive reception of our lipid atlas underscored its potential impact on the field, while the conference's engineering-focused discussions broadened my perspective on integrating technical innovations with biological analysis. I look forward to applying these insights to our work and continuing to build momentum for the Single-Cell and Spatial Metabolomics Online Day.

Irida Papapostolou (Universität Bern)
DPG conference
18th - 21st of September 2024, Vienna

The DPG annual conference is about the physiology of ion channels and their role in the development of diseases. Once per year scientists from laboratories in Germany, Austria and Switzerland meet and present their work at this conference. Attendees of different scientific background have the chance to meet and network with each other. Additionally, after every oral or poster presentation there are discussions which lead to the exchange of ideas and concepts and consequently to the development of projects. All in all, because of the positive impact this conference has on the scientific development of the participants, it was very important for me to attend.

Unfortunately, due to severely bad weather conditions, all connecting trains from Switzerland to Vienna were cancelled and I had to travel by plane. The expenses shot up and made it questionable whether I should participate at the DPG or not. But the LS2 travel grant certainly helped my laboratory to cover the travel costs.

It gave me the chance to attend and present the results of my PhD project in a poster. In my project, I am investigating the role of the TRPM4 ion channel in cancer hallmark function in 2D and 3D colorectal cancer models. By presenting to the rest of the conference participants, I received valuable input that will help me develop the project further.

I am extremely grateful for the financial support from Life Sciences Switzerland (LS2) and the Swiss Academy of Sciences (SCNAT), as they were very helpful in covering the travel expenses for such an important conference.

LS² Travel Grant Report – Khalid Ibrahim, LBEN and LMNN, EPFL – CBIAS 2024

khalid.ibrahim@epfl.ch

I am extremely grateful for the support of Life Sciences Switzerland (LS²) and the Swiss Academy of Sciences (SCNAT), who have awarded me a travel grant to allow me to attend and present at the Crick BioImage Analysis Symposium (CBIAS) 2024, held at the Francis Crick Institute in London. This symposium brought together leading experts, researchers, and industry professionals to discuss the latest advancements in bioimage analysis, machine learning, and microscopy.

At the symposium, I had the opportunity to give an oral presentation titled "*Intelligent and Self-Driving Microscopy of Protein Aggregation*." In my talk, I introduced novel methods that integrate artificial intelligence with automated microscopy to detect the onset of protein aggregation and study the kinetics and biomechanics of this fleeting process. The presentation was well received, and I had engaging discussions with experts who provided valuable feedback on my research. I also had the opportunity to connect with researchers working on related topics, opening potential avenues for future collaboration.

The conference featured an impressive lineup of talks and discussions covering a wide range of topics in bioimage analysis, artificial intelligence applications, and novel microscopy techniques. There were many notable talks from speakers like Richard Marsh, Laura Wiggins, Rolf Harkes, Assaf Zaritsky, Christophe Leterrier, Guillaume Jacquemet, and Sophia Maedler. I had lots of fruitful discussions with the speakers and other attendees during breaks and poster sessions.

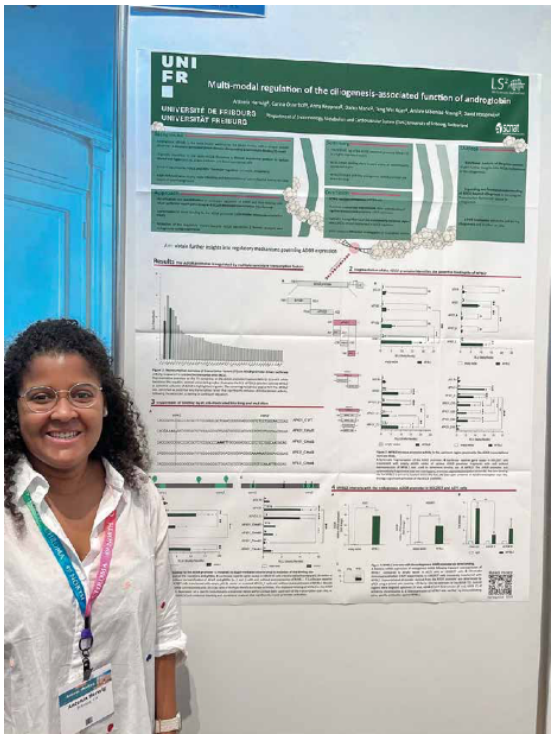
Attending the Crick BioImage Analysis Symposium 2024 was an enriching experience. I was able to deepen my understanding of cutting-edge developments in bioimage analysis and gain insights into how AI-driven microscopy is shaping the future of biomedical research. The discussions and networking opportunities were invaluable, as they provided inspiration for refining my methodologies and incorporating new analytical approaches into my research.

Moreover, the event facilitated interactions with fellow scientists from diverse backgrounds, which led to thought-provoking conversations on the challenges and opportunities in the field. I am particularly excited about potential collaborations that emerged from this meeting, which could lead to interdisciplinary projects in the near future.

I would like to sincerely thank LS² and SCNAT for their generous support, which enabled me to attend this prestigious symposium and share my research with an international audience. I look forward to applying the knowledge and connections gained from this event to further my work in bioimage analysis and intelligent microscopy.

Antonia Louise Herwig (University of Fribourg)

Conference Report: 103rd annual meeting of the German physiology society, Austrian physiology society and life sciences Switzerland (LS^2) physiology



I'm grateful to the LS2 Travel Grant for making it possible for me to attend the 103rd Annual Meeting of the German Physiology Society, Austrian Physiology Society, and Life Sciences Switzerland (LS2) Physiology, held from September 19 to 21, 2024, in the beautiful city of Vienna, Austria. It was an amazing opportunity to present my research and connect with the international scientific community in such an inspiring setting.

I had the opportunity to present the first part of my PhD work, where I focused on the transcriptional regulation and functional domains of androglobin (ADGB), a conserved protein involved in ciliogenesis during the „Hypoxia and Blood“ poster session. During that session, I received valuable feedback on my research in particular on its transcriptional regulation and control by transcription factors like MYBL2, which gave me new ideas and directions for my research. It also offered the opportunity to discuss my work with fellow PhD students and experts in related areas, which helped me see how my research connects with broader physiological processes, revealing intersections between my research and other areas like hypoxia response, cellular signaling and cell cycle regulation.

Beyond my own presentation, I attended sessions on a range of topics, including gene expression, cellular signaling, and the roles of hemoglobin and nitric oxide in cardiovascular or renal physiology. I particularly enjoyed attending the Oxygen and Blood session, which focused on the hypoxia response in immune cells and oxygen-binding proteins. Although hypoxia is not directly related to my main research area, it provided an interesting perspective on how cells adapt to low-oxygen conditions. Beyond this, the sessions on gene regulation, cellular signaling, and non-canonical roles of hemoglobin and nitric oxide in physiological processes was especially insightful. These sessions offered new interdisciplinary ideas and methods, which I’m excited to explore and hope to apply to my own research.

Overall, the meeting provided an excellent platform for professional growth, networking, and exposure to cutting-edge research. I am thankful to the LS2 for enabling me to participate in this event, which will have a lasting impact on my academic development.