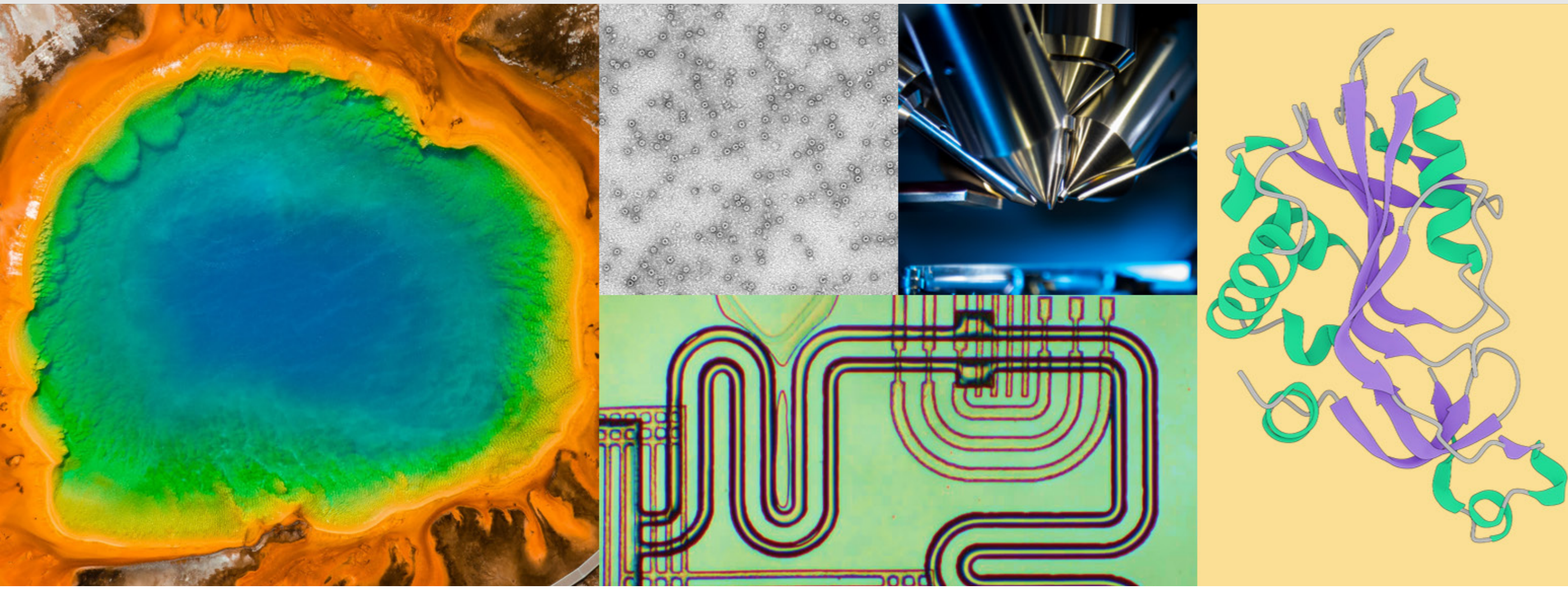
PROHITS

Prokaryote proteomics at high temperature for single cells



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PROHITS

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This issue of the newsletter has been edited by Sunu Lama (DC7) and Onyeka Francis Offor (DC9).

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the European Union

The University of Debrecen has received the funding 2020-2.1.1-ED-2023-00269 from the Hungarian National Research, Development and Innovation Fund to cover the participation of DC10 in PROHITS.

PROHITS at a glance

The project in a nutshell

PROHITS is a Marie Skłodowska-Curie Doctoral Network (MSCA-DN) project with the overall aim of resolving the proteome of prokaryotes at single-cell level and at a range of temperatures. This will be achieved by integrating experimental and computational approaches, and will improve our understanding of thermophile biology to optimally design cell factories and the related industrial processes.

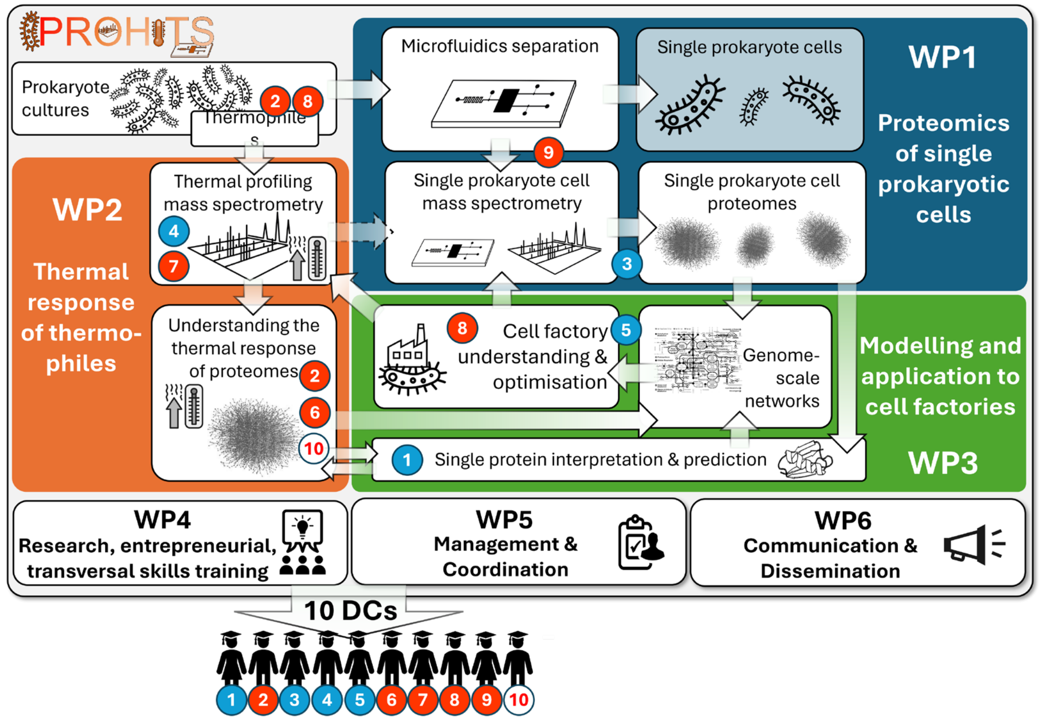
The PROHITS DN will advance 1) microfluidics to separate single prokaryotic cells, 2) mass spectrometry (MS) and its associated bioinformatics to handle single prokaryotic cells, and 3) MS-based thermal proteome profiling to study the thermal response of the proteome of thermophiles. We will use the information generated to 4) understand the in vivo stability of proteins, and 5) create genome-scale models of thermophiles to 6) optimize them as cell factories. Two main technological developments are thus expected:

- Instrumentation to determine the proteome of single prokaryotic cells and its response to temperature changes.
- Improved cell factory modelling by including proteome and thermal response information, so guiding metabolic engineering approaches to optimize environmentally sustainable industrial processes.

PROHITS represents a platform to train ten doctoral candidates (DCs) with translational and interdisciplinary, as well as transversal and entrepreneurial skills , resulting in:

- Excellent understanding of both experiment and computation, and of the challenges and opportunities at the interface between these.
- The ability to solve challenges in the determination, (biological) interpretation, and (industrial) application of thermophilic proteomes, along with broader method applicability to all prokaryotes.
- Engagement with the societal impact of their research, and awareness of innovation opportunities.

The Network is organised into six Work Packages as follows:



For more information, visit https://prohits.eu.

Consortium

PROHITS brings together 7+1 beneficiary institutions from six different European countries. Four academic organisations (VUB, VIB, UiB, UniVie, CNRS and UD) and two companies (NovoArc GmbH and Cellenion SASU) join forces with the support of two partner universities (Universiteit Gent and Université de Strasbourg) and a partner company (Bruker Daltonics GmbH& Co. KG) to build up a highly interdisciplinary network to tackle the ambitious goals of the project.

Partner institutions

Vrije Universiteit Brussel (VUB)
Prof. Dr. Wim Vranken
Prof. Dr. Eveline Peeters

Universitetet i Bergen (UiB)
Prof. Dr. Harald Barsnes

Centre National de la Recherche Scientifique (CNRS)
and Université de Strasbourg (UNISTRA)
Dr. Christine Carapito

Cellenion SASU
Dr. Anjali Seth

Bruker Daltonics GmbH& Co. KG
Mr. Pierre-Olivier Schmit

Vlaams Instituut voor Biotechnologie (VIB)
and Universiteit Gent (UGent)
Prof. Dr. Lennart Martens

Universität Wien (UniVie)
Prof. Dr. Jürgen Zanghellini

NovoArc GmbH
Dr. Julian Quehenberger

Debreceni Egyetem (UD)
Prof. Dr. Éva Csősz

Meet the supervisors

CELLENION
A BICO COMPANY

Dr. Anjali Seth

Anjali Seth is currently the head of Single Cell Proteomics in Cellenion, Lyon. She graduated with a Master's in Inorganic and Physical Chemistry from Ecole Normale Supérieure de Paris in 2010. She then obtained a PhD from Pierre and Marie Curie University for her research on magnetic nanoparticles for targeted drug delivery in collaboration with the pharmaceutical company Servier. Next, she underwent a two-year postdoctoral project in Oxford where she used magnetic particles and ultrasound for cancer theranostics. Thereafter, she went back to France, at the Ecole Centrale de Lyon, to work on the creation of cell aggregates by electrophoresis in microfluidic chips. In 2019 she joined Cellenion, a company specialized in the fields of single-cell isolation, to develop and lead the single cell proteomics R&D department.

1. Describe your background, your research, your goals and contributions to the field
My work began with developing magnetic nanoparticles for targeted drug delivery during my PhD, followed by two postdoctoral projects in cancer applications and cell aggregates in microfluidics system. Since joining Cellenion in 2019, I've been building and leading the single-cell proteomics R&D team. Over the last 6 years, I've helped advance single-cell proteomics by mass spectrometry into a reliable and insightful tool for studying cellular biology.

2. Present your company
As the head of single cell proteomics at Cellenion, my job is to develop new strategies for single cell proteomics sample preparation. My role is very varied, from being in the lab, at the bench doing sample preparation, testing new software on our instrument to presenting key results during research conferences. I also lead the engineering group, making sure that the requests/needs coming from the research community can be translated into meaningful new functionalities for our instrument. Thanks to my position in between research, engineering and business development, I could forge strong relationships with key opinion leaders in the proteomics field, and win-win collaborations with key stakeholders from the mass spectrometry industry (ThermoFisher Scientific, Bruker, Evosep).

3. What inspired you to pursue a career based on research?
From my first internship up to this day, I've always liked to be in the lab, trying to crack the problem and make things work. My research has always been very application driven and I guess that why I've always been on the engineering side of things. I love to build stuff and to imagine new solutions, way to make things work. I also love the science behind what we do and being able to translate some request and ideas from the scientific community into concrete solutions feels very rewarding.

4. What has been a significant moment in your research path?
Encounters with new and special people have always been one of the main drivers for what I do. Meeting and collaborating with various members of the proteomics community has been a tremendous pleasure, a great learning experience and, more importantly, a lot of fun. Seeing the instruments, protocols and workflows that I've, together with my team, imagined, designed, tested and pushed to the market becoming the world leading solution for single cell proteomics sample preparation has been a great satisfaction.

5. What outlines a good supervising and/or management strategy in your eyes and how do you implement it in your company?
I always had a strong focus on innovation. Working in a small tech company allowed me to explore multiple ideas and always try to think outside of the box. I encourage my students to do the same; to be very creative and to trust they can be the leaders on their research. I like to see young researchers becoming more and more independent, developing their skills to become tomorrow's leaders.

6. What does PROHITS mean to you?
PROHITS has been a really nice adventure so far. The group of PIs interacts really in a positive way to one another and the project has been a real pleasure so far. Everybody comes from very diverse background, and this had been a strength since the beginning. People are open to new ideas and concepts, and all opinions are valued. The team of PhD students seems to be getting along really nicely as well, allowing them to make the most out of the EU project and its strong focus on collaboration.

7. What is your and your team's contribution to PROHITS?
In the PROHIT project, our role is to develop new sample preparation strategies for single prokaryotic cell. The goal of Francis (the PhD student working with me) is to evaluate several workflows to prepare single thermophiles before their proteome can be analysed using mass spectrometry. This includes cell isolation, cell lysis, protein digestion and a clever strategy to transfer peptides to the LC system.

8. Which milestones do you think are the most important?
Demonstrating that we can achieve one single procaryotic cell (of about 1 micron in diameter) isolation was the first milestone of the project. The following ones will be more focusing on the feasibility and outcomes of the proteomics analyses. We need to build a strong understanding of which proteins; one could identify and quantify for such small samples.

9. What challenges might we expect in PROHITS?
The first challenge was analytical. We didn't even know if the current mass spectrometers used for single mammalian cells proteomics analyses would be sensitive enough to detect signal coming from a single prokaryotic cell. Now that this has been proven to be feasible, we'll need to focus on how these finding can be interpreted and used in a broader context. With prokaryotic organism, we don't know yet what to expect in term of single cell proteomics. Analysing these species at the single cell level might open a whole world of possibilities or we might realise that bacteria/archaea are so highly cooperative organisms that behave more as a swarm and are more insightful as a whole group.

10. What impact do you think PROHITS will have? Both within science but also societal?
Within science, PROHITS will give us an insight on what we are able to achieve as of today and will probably highlight what the next frontiers in proteomics will be. Throughout the project, we'll be pushing the boundaries of what we are able to achieve today, in term of technology, analytics, etc. The impact on the society will hopefully be to prove that a production of different chemical compounds using a greener approach is feasible and ready to be adopted more routinely..

About - Cellenion SASU

Cellenion offers solutions and technologies for controlled cell dispensing with applications in the fields of single cell and single cellular aggregates isolation. Our systems allow high throughput, image-based automated dispensing of single cells and/or cell aggregates onto any substrates of choice. Together with a range of dedicated consumables, the solutions enable miniaturization of sample preparation protocols on the same instrument before downstream analysis. With no dead volumes and outstanding recovery rates, Cellenion's platforms offer unique capacities for applications including single-cell omics, rare cells, cell line development, drug screening and 3D model development. Cellenion operates from Lyon, France. The company is a subsidiary of SCIENION GmbH, and its products are sold by SCIENION worldwide.

Meet the supervisors

Dr. Christine Carapito

Chrisitne Carapito is currently a researcher director at CNRS, a French public research organization and University of Strasbourg. She hold a PhD in an analytical chemistry from the University of Strasbourg (Hubert Curien Multidisciplinary Institute) and after completing her PhD, Christine enriched her expertise as a postdoctoral fellow at the Institute of Molecular Systems Biology at the Swiss Federal Institute of Technology Zurich (ETH Zurich). Recruited in October 2010 as a CNRS research fellow in analytical chemistry and having been authorised to supervise research since 2017, Christine continued to work at the intersection of disciplines: development of mass spectrometry and bioinformatics methodologies for the analysis of proteomes and their integration with other –omics images in various complex biological matrices including human, bacteria and plants. In 2018, she has also been awarded the CNRS bronze medal for her research on proteins at the BNU (National and University Library of Strasbourg). Her team now is dedicated on the development of highly sensitive liquid chromatography coupled with mass spectrometry methods for the deeper functional proteomics analysis.

1. Describe your background, your company, your goals, and contributions to the field.
I have been happily immersed in the development of mass spectrometry–based analytical methods for the past 12 years. I fell into the mass spectrometry “cauldron” during my Master’s internship and never felt like climbing back out. Mass spectrometry is an incredible tool that keeps surprising us with its ever-expanding possibilities! Ten years ago, analyzing the proteome of a single cell sounded like science fiction; today, it’s just a (very cool) reality. I keep repeating that we have been living through the most exciting time ever for proteomic analysis over the past two years. I love analytics and its challenges, and I particularly enjoy assembling all ingredients needed to tackle them. My research focuses on the development of increasingly sensitive liquid-chromatography (LC) coupled to MS methods for deeper proteome characterization, while always keeping in mind the critical importance of quantification, without which the resulting conclusions would be highly incomplete.

2. Present your research group.
I am a research director at CNRS, a French public research organization, and University of Strasbourg, where I co-lead a team of around forty people. Together, we develop mass spectrometry–based methods to characterize proteins, protein complexes, and highly complex proteomes. Our work spans both functional and structural proteomics. What unites us is a shared taste for precise and rigorous analytics. We share and fight for instrument time, we enjoy digging into what really goes on inside these incredible machines that are mass spectrometers. To achieve this, we work to bring together people with diverse backgrounds and skill sets, ranging from physics and analytical chemistry to biology and bioinformatics, an interdisciplinary environment required to succeed in our field.

3. What inspired you to pursue a career based on research?
I was first drawn to MS-based proteomics during a Master’s courses, when it was presented as a technology aiming at generating a large set of small building blocks (peptides) to be assembled in order to reconstruct an understandable image of the living system under study (proteins interacting with each other to run the machineries of life). I have always enjoyed analyzing things and considering every possible outcome or alternatives for a given question or problem. I have been very fortunate throughout my career to meet people who share my passion for analytics. In my view, one of the greatest advantages of being an academic researcher is our freedom to choose whom we collaborate with. Being daily surrounded by people who share a common passion and goal is undoubtedly the most motivating aspect of our job and a good recipe for fulfilment at work.

4. What has been a significant moment in your research path?
My favourite moments in my professional career are those when I sit on the examination committee and listen to my students defend their PhD theses. These moments are very precious, as they allow me to witness the many progresses made, the evolution of young researchers after three to four years of hard work, their accumulation of knowledge and skills, their growing confidence, and their pride. Participating in the training of the next generation of MS experts, seeing young researchers continue with commitment and passion, is the greatest satisfaction of my work as an academic researcher, and it represents both my proudest achievement and my strongest motivation to keep going.

5. What outlines a good supervising and/or management strategy in your eyes, and how do you implement it in your research group?
Supervising means to me, leading by example in terms of integrity, commitment, and reliability; trying to act as a guide without restricting personal initiatives and ideas; listening to everyone’s ideas and providing clear arguments when one or the other cannot be implemented; encouraging autonomy and allowing people to develop their sense of responsibility. My daily concern is to contribute to creating a safe environment prone to open exchanges and close collaborations between people in a positive atmosphere of mutual stimulation rather than competition. I believe that a positive working environment is key to fostering the self-confidence we so greatly need in order to absorb criticism and respond constructively to the constant evaluation processes we are exposed to in our job.

6. What does PROHITS mean to you?
PROHITS was born from a shared desire to create and collaborate on a project together with scientific friends with diverse backgrounds. We built and shaped the project as a team considering and valuing everyone’s ideas and it is this collective effort that has made us a close-knit and highly motivated group today. This dynamics started among the projects’ PIs and I am very happy to see that the same collaborative spirit has taken root among PROHITS DCs as well.

7. What is your and your team’s contribution to PROHITS?
In the project, my team plays a central role, as the consortium relies on us to generate valuable and informative mass spectrometry data from the biological samples prepared by the biologists and microbiologists on the one hand and to feed the algorithms and software developments by the bioinformatics on the other hand. With Dinu, we are developing thermal proteome profiling strategies highly relevant for the study of the specificities of thermophilic organisms’ proteomes. And with Sunu, Francis and Anjali, the major analytical challenge we committed ourselves to is to succeed in single cell proteome analysis of the thermophiles of interest selected by the consortium. Achieving

About - LSMBO

The BioOrganic Mass Spectrometry laboratory (LSMBO) belongs to the Institut Pluriscipliniare Hubert Curien (IPHC) of the University of Strasbourg. The LSMBO is hosting an IBiSA-certified proteomic platform (Strasbourg Grand Est Proteomic Platform) and is the Strasbourg node of the French Proteomic Infrastructure (ProFI). The LSMBO is a 30 year-experienced team in the structural study of peptides and proteins by mass spectrometry. The laboratory is renowned for developing new methods in proteomic analysis, bioinformatics and structural mass spectrometry for the analysis of protein/protein interactions in large complexes. Besides that, long term collaborations with several pharmaceutical companies cover topics such as full characterization of natural and/or recombinant proteins used in human therapy, toxicoproteomics, protein/drug interaction.

The LSMBO team develops innovative methodologies in chromatography, mass spectrometry (MS) and bioinformatics for :

- Functional proteomic analysis for the identification and quantification of thousands of proteins in complex biological matrices (sample preparation, targeted (PRM) and global (DIA) quantitative LC-MS/MS analysis, statistical analysis and integration of multi-omics data).
- Structural proteomic analysis for the characterization of either proteins alone or in complexes. The combination of native MS, mass photometry, ion mobility, H/D exchange and chemical cross-linking approaches followed by MS is applied to integrative structural biology projects.
- Characterization of therapeutic proteins (monoclonal antibodies).
- Interpretation of functional (Proline) and structural proteomic data.

The LSMBO hosts the Strasbourg Grand Est proteomics platform (PSGE) and is the Strasbourg node of the national Proteomics Infrastructure ProFI. The LSMBO is a partner of two TIT programs of the University of Strasbourg, IMS and TransplantexNG.

Meet the supervisors

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this later objective would allow us to contribute pushing the limits of proteomics a step further. From the very beginning of the project, we have put pressure on ourselves and have been deeply committed to start generating valuable data as soon as possible. Now that the data are flowing in, we can relax a bit. ;-)

8. Which milestones do you think are the most important?
During early discussions on how to shape the PROHITS project, I brought up the idea of performing single-cell analysis on the prokaryotes of interest for the consortium, likely because I was feeling a bit euphoric after we had successfully implemented single-cell analysis on mammalian cells in the lab. However, I would not have embarked on this adventure if Anjali had not agreed to join us. I believe that it is our close collaboration and the close interactions between Francis (DC9) and Sunu (DC6) that give us best chances to achieve this ambitious analytical goal.

9. What challenges might we expect in PROHITS?
The analytical challenges of the PROHITS project are numerous, and we have set the bar high. Nevertheless, I am convinced that we are a unique and ideal consortium to tackle those challenges. Indeed, within our group, all the necessary ingredients are gathered to meet our ambitious goals: microbiologists, protein biochemists, instrumentalists, and bioinformaticians. We are doing everything possible to push our methods to their limits in terms of sensitivity and quantification accuracy. The results obtained so far both on thermal proteome profiling and the preliminary results achieved on single prokaryotic cells proteome analysis are very promising and encouraging.

10. What impact do you think PROHITS will have? Both within science and society?
If we succeed in the analytical challenges we have set for the PROHITS project, we will have contributed to push the limits of proteomics a step further. We will have contributed to train experts of tomorrow in cutting-edge proteomics and "deliver" to the society highly skilled young researchers with a strong collaborative spirit who will, tomorrow, participate in shaping our research field.

DCs ready for their team building activity during Workshop 2

Project progress

Meetings

Supervisory Board meetings
The Supervisory Board met online in October 2025 in preparation for Workshop 2. The SB meets twice per year to discuss all high-level project matters, and has Caroline Jachmann (DC3) as DC representative.

Subcommittee meetings
The research subcommittee meets online once per month to regularly discuss key scientific topics. It involves all supervisors and DCs, with Alexandre Bouillon (DC1) acting as DC representative.
The data management, and training and dissemination subcommittees meet online, typically every 2-3 months. They count with the involvement of Kenneth Valerio Aguilar (CD4) and Josephine Boel Andresen (DC2) as DC representatives, respectively.

Reporting (July 2025 - January 2026)

Deliverables

D1.5 Evidence of isolated single prokaryote cells by microfluidics resulting in preliminary MS data
D3.1 A pipeline to collect and predict single protein characteristics for thermophiles
D4.2 First ESR research, network-wide trainings and PCDP progress reports
D2.5 Culture and transfer protocol for a medium-temperature (~55 degrees) prokaryote resulting in thermal proteome profiling data
D6.4 First Public engagement activities report

Milestones

M1 First single prokaryote cells successfully isolated
M5 First 5 thermophile cultures optimised
M6 Optimized sample preparation protocol for efficient digestion of thermophilic prokaryotes
M7 Optimized fragmentation pattern and MS instrument settings
M14 All DCs presented poster at conference

Secondments (July 2025 - January 2026)

Completed:

DC4 Kenneth Valerio at **VIB/UGent, Belgium**	July 2025	Duration: 1 month
DC2 Josephine Boel Andresen at **Cellenion, France**	September 2025	Duration: 2 weeks

Ongoing:

DC1 Alexandre Bouillon at **UniVie, Austria**	Dec 2025 - Feb 2026	Duration: 3 months
DC10 Mansi Jain at **CNRS, France**	January 2026	Duration: 1 month

Project progress

Workshop 2 - Project assessment and DC direction. MS in-depth

Workshop 2 took place on 24th-28th November 2025 in Debrecen (Hungary), with UD acting as host. After having their progress presentations and a meeting of the Supervisory Board online, the DCs dove into a week full of training sessions, including:

- **Biostatistics,** led by Prof. Zoltán Varga and Dr. Eniko Nizsaloczki (UD)
- **Article writing,** led by Dr. Iván Uray (UD)
- **Proteomics data analysis,** led by Prof. Lennart Martens (VIB)
- **Microfluidics,** led by Dr. Anjali Seth (Cellenion)
- **Thermophile biology,** led by Prof. Eveline Peeters (VUB)
- **Workshop: What makes a good presentation?,** led by Prof. Éva Csősz (UD)
- **Project management,** led by Dr. Eszter Tóth (UD)
- **Time management,** led by Nóra Kovács (UD)

The Consortium will meet again in Vienna in September 2025 for Workshop 3. The event will be hosted by UniVie and will have a focus on cell factories and GEMs.

Group picture of DCs with Prof. Éva Csősz

Group picture of DCs during one of the training sessions

Contributions at scientific meetings

Bouillon, A., Vranken, W. Do you speak protein? Understanding and Predicting Protein Thermal Stability. Poster presented at the Bioinformatics in Bergen 2025 Conference, 2-3th June 2025 (Norway). https://doi.org/10.5281/zenodo.15830553

Andresen, J.B., Peeters., E. Thermophilic proteomics - Turning on the heat for a new generation of microbial cell factories. Poster presented at the Belgian Society for Microbiology's Annual Symposium 2025, 21st February 2025, Brussels (Belgium). https://doi.org/10.5281/zenodo.15055847

Andresen, J.B., Jain, M., Peeters, E. Turning up the heat in temperature-responsive gene regulation of a thermophilic cyanobacterium. Poster presented at the 15th Workshop on Cyanobacteria, 4-7th June 2025 (USA). https://doi.org/10.5281/zenodo.15797315

Andresen, J.B., Jain, M., Csosz, E., Ciobanu, D.Z., Carapito, C., Aguilar, K.V., Barsnes, H., Peeters, E. TLean, green, heat-combating machine: a proteomics-based investigation. Poster presented at the Thermophiles 2025 Conference, 7th-11th September 2025 (Germany). https://doi.org/10.5281/zenodo.17242994

Jachmann, C., Martens, L. ProteoBench: a community-curated platform for comparison of proteomics data analysis workflows. Oral presentations at BePac 2024, 5th-6th December 2024 (Belgium) and HUPO-PSI Spring Meeting 2025 31st March-3rd April 2025 (Germany).

Jachmann, C., Martens, L. Fantastic PTMs and how (not?) to find them using msqrob2PTM. Short oral presentation at the EuPA 2025 Conference, 16th-20th June 2025 (France).

Aguilar, K.V., Barsnes, H. Cracking the Heat Code: Proteomic Adaptation in Thermophilic Microbes. Poster presented at the Bioinformatics in Bergen 2025 Conference, 2nd-3rd June 2025 (Norway). https://doi.org/10.5281/zenodo.15829399

Rimón, M.J., Zehetner, L., **Zanghellini, J.** From genome to metabolism: Pan genome-scale metabolic model reconstruction of the extremophile genus *Sulfolobus*. Poster presented during the Panel B PhD retreat of the Vienna Doctoral School in Chemistry (DoSChem) of University of Vienna, 2nd April 2025 (Austria), at the Metabolic Pathway Analysis (MPA) Conference, 29th July-1st August 2025 (Austria), and at the Thermophiles 2025 Conference, 7th-11th September 2025 (Germany). https://doi.org/10.5281/zenodo.16993560

Ciobanu, D.Z., Andresen, J.B., Jachmann, C., Aguilar, K.V., Baes, R., Peeters, E., Martens, L., Barsnes, H., Carapito, C. Thermal Proteome Profiling as a powerful approach to investigate the proteome stability of thermophiles. Poster presented at the Thermophiles 2025 Conference, 7th-11th September 2025 (Germany). https://doi.org/10.5281/zenodo.17242831

Lama, S., Offor, O.F., Anjali, S., Carapito, C. Towards single cell proteomics of thermophilic prokaryotes. Poster presented at 6th European Symposium on Single Cell Proteomics, 26-27th August 2025 (Austria). https://doi.org/10.5281/zenodo.16982548

Carvalho, A. C., Peeters, E., Zanghellini, J., Quehenberger, J. Towards a novel tetraether lipid producer *Haloferax volcanii*. Poster presented during the Panel B PhD retreat of the Vienna Doctoral School in Chemistry (DoSChem) of University of Vienna, 2nd April 2025 (Austria), and the Thermophiles 2025 Conference, 7th-11th September 2025 (Germany). https://doi.org/10.5281/zenodo.17243082

Jain, M., Carvalho, A., Quehenberger, J., Andresen, J. B., Peeters, E., Csosz, E. Assessment and Comparison of Sample Preparation Strategies for High Yield Proteomics Analysis of Thermophilic Prokaryotes. Poster presented at the Hungarian Molecular Life Sciences 2025 Conference, 28-30th March 2025 (Hungary). https://doi.org/10.5281/zenodo.15118730

Jain, M., Carvalho, A., Quehenberger, J., Andresen, J. B., Peeters, E., Csosz, E. Evaluation of Different Sample Preparation Strategies to Identify the Best Approach for High-Yield Bottom-Up Proteomics Analysis of Thermophilic Prokaryotes. Poster presented at the European Proteomics Association 2025 Conference, 16-20th June 2025 (France). https://doi.org/10.5281/zenodo.15753948

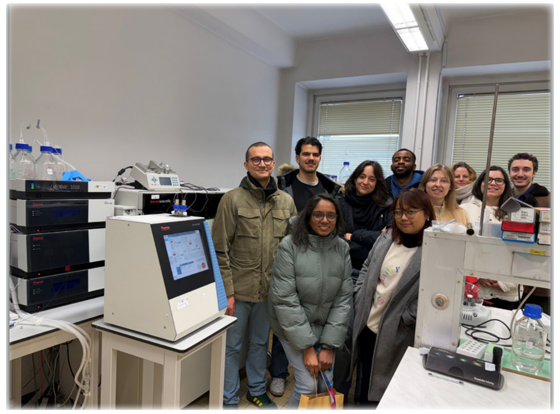
Jain, M., Carvalho, A., Quehenberger, J., Andresen, J. B., Peeters, E., Csosz, E. Phosphoproteomic Analysis Of Thermophilic Prokaryotes: Expanding The Phosphorylation Landscape In Extreme Environments. Poster presented at the Central and Eastern European Proteomic Conference (CEEPC) 2025, 14th-17th October 2025 (Hungary). https://doi.org/10.5281/zenodo.17398872

Project progress

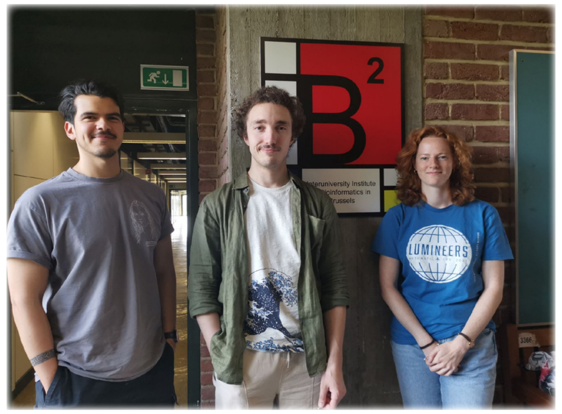
News

- Josephine Boel Andresen (DC2) and Dinu Zinovie Ciobanu (DC2) published an introductory article in the 43rd issue of the Marie Curie Alumni Association newsletter.
- Alexandre Bouillon (DC1) and Josephine Boel Andresen (DC2) participated in the I Love Science Festival in Brussels on 12-13th October 2025. During the festival, they had a booth where kids were offered a hands-on wet lab protein booth called "Protein to the extreme!".
- Mansi Jain (DC10) led an educational workshop and a laboratory open visit at UD during the European Researchers' Night 2025.
- Alexandre Bouillon (DC1) participated in the Wise Night: Meet Today's Curie event during the European Researchers' Night 2025 in Brussels.


Josie and Alexandre in their booth at ILSF 2025


DCs with MS equipment at UD during Workshop 2

Mansi during the European Researchers' Night


Kenneth, Alexandre and Caro at Bio2Byte

DCs at the Thermophiles 2025 Conference

Journal club

The fellows meet online every 2-3 months to discuss about articles relevant to the project.

1st Journal club session:

Date: 17 December 2024
Article: Transcriptional and translational dynamics underlying heat shock response in the thermophilic crenarchaeon *Sulfolobus acidocaldarius*
DOI: https://doi.org/10.1128/mbio.03593-22
Chair: Josephine Boel Andresen (DC2)

2nd Journal club session:

Date: 18 February 2025
Article: Toward Single Bacterium Proteomics
DOI: https://doi.org/10.1021/jasms.3c00242
Chair: Onyeka Francis Offor (DC9)

3rd Journal club session:

Date: 15 April 2025
Article: Meltome atlas—thermal proteome stability across the tree of life
DOI: https://doi.org/10.1038/s41592-020-0801-4
Chair: Alexandre Bouillon (DC1)

4th Journal club session:

Date: 1 July 2025
Article: Oxidative Stickland reactions in an obligate aerobic organism – amino acid catabolism in the Crenarchaeon *Sulfolobus solfataricus*
DOI: https://doi.org/10.1111/febs.14105
Chair: Ana Carvalho (DC8)

5th Journal club session:

Date: 15 December 2025
Article: Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins
DOI: https://doi.org/10.1074/mcp.TIR119.001481
Chair: Kenneth Valerio Aguilar (DC4)

Project videos

Introduction to PROHITS by Prof. Wim Vranken	https://youtu.be/nBrxb17nXN0
Meet DC1, Alexandre Bouillon	https://youtu.be/5gzy21yvb9w
Meet DC2, Josephine Boel Andresen	https://youtu.be/c2qbaiP32-M
Meet DC3, Caroline Jachmann	https://youtu.be/Y5WZBl6V32Q
Meet DC4, Kenneth Valerio Aguilar	https://youtu.be/BedNwMva-NM
Meet DC5, María José Rimón	https://youtu.be/KBl4goRsH1s

Stay tuned!

LinkedIn
https://tinyurl.com/4cayu96f

Bluesky
https://tinyurl.com/535s4s9f

YouTube
https://tinyurl.com/ytp5ueuj

PROHITS newsletter
https://tinyurl.com/3wesyhv3

Instagram
https://tinyurl.com/2a6vssjc

X/Twitter
https://tinyurl.com/yc2538zz

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