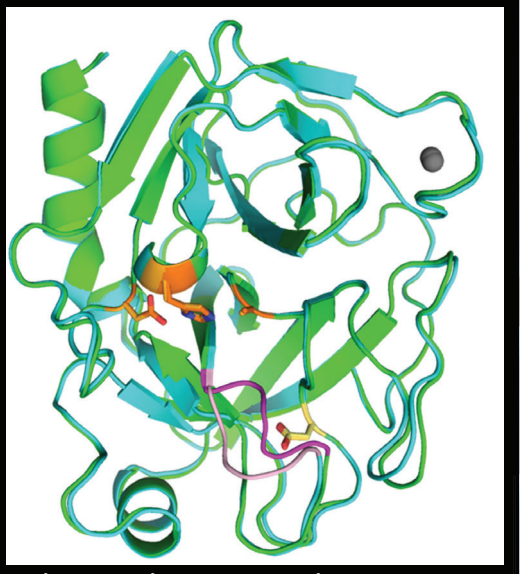
IN THIS ISSUE:



May 2026



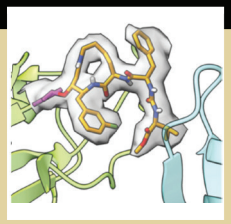
Coban et al., Science Advances, 2026

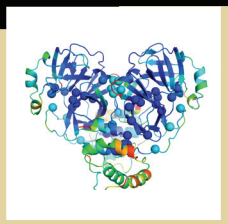
INTERNATIONAL PROTEOLYSIS SOCIETY

# QUICKCUTS


Edited by:
Olivier Julien
Laura Edgington-Mitchell







THE PREMIER RESOURCE
FOR ALL YOUR IMPORTANT PROTEASE NEWS

## A Message From the President:

Dear Protease Friends,

I am delighted to share the first issue of QuickCuts during my tenure as IPS President. I have now handed over the editor's role to our incoming Vice President, Olivier Julien, known to most as OJ. My sincere thanks to OJ for preparing this issue, and to all of you for your contributions.

First, I'd like to extend an enormous thank you to Ana Paula Lima and Maria Luiza Vilela Oliva for hosting the 13th General Meeting of the IPS in Búzios, Brazil. It was a vibrant meeting in a stunning location, with truly phenomenal scientific exchange, and a real pleasure to reconnect in person with so many of you. I would also like to acknowledge Priscilla A. L. Smeltzer, Vanderley Fraga, and Nathalia Rodrigues, whose tireless efforts ensured the meeting ran seamlessly. Thank you to all who generously volunteered their time to lead IPS Workshops: Antoine Dufour, Anthony O'Donoghue, OJ, Galia Blum, Kostas Kalogeropoulos, Christian Sommerhoff, Fernanda dos Reis Rocho and Guy Salvesen. Training remains a core priority for the IPS, and we are deeply grateful for your ongoing contributions.

My warmest congratulations go to Bob Lazarus and Luiz Juliano on receiving Lifetime Achievement Awards. I also congratulate Daniele

## IPS COUNCIL

Ferrari and Wayne Monteiro, recipients of the Henner Graeff Awards for best oral presentations. Congratulations as well to the 19 travel award recipients and the 12 poster award winners, who are highlighted later in this issue. I was incredibly honoured to receive the Young Investigator Award, now renamed in memory of Ulrich auf dem Keller, who established this award during his presidency. This was the first IPS meeting without Ulrich. While his absence was deeply felt, his legacy was evident in the outstanding work of his trainees and collaborators, and in the spirit of the meeting itself.

I extend my sincere thanks to the outgoing IPS Council members: Ruth Geiss-Friedlander (President, now ex officio), Catherine Moali (Secretary), Eiichiro Nishi (Treasurer), Kyoko Shirakabe, Jeanne Hardy, and Antoine Dufour. Under Ruth's leadership, the society strengthened its webinar program, improved transparency of award processes, and refreshed its digital presence. Special thanks to OJ and Jeanne for their excellent work on the website, and to Christian Sommerhoff for his long-standing service as webmaster from 2006-2023.

I am delighted to welcome our incoming Council members: OJ (Vice President), Lakshmi Wijeyewickrema (Secretary), Irina Bezsonova (Treasurer), Kostas Kalogeropoulos, Charaf Benarafa, and Endo Satoshi. Together with Marcin Drag, Kostas will lead an exciting program of webinars and workshops this year. Henry Maun continues as Industry Liaison, and Ana Paula Lima has taken on the newly established role of Executive Director of Awards, overseeing nominations and selection across all major IPS awards. As a society, we will continue to prioritise training, transparency, and opportunities for our early-career community, and I look forward to building on this momentum together.

We are thrilled to announce that the 14th General Meeting will be held in Freiburg, Germany, from 26 September to 1 October 2027. Thomas Reinheckel and Ruth Geiss-Friedlander, together with the Scientific Board, are already preparing what promises to be an outstanding meeting. Hosted at Europa Park, it is sure to be a wild ride, both scientifically and on the roller coasters during free time! More details will be forthcoming, but for now, please save the date for this exciting event.

I encourage you to ensure that your membership is up to date, even if you were unable to attend the recent meeting. Membership dues are the society's primary source of income and enable initiatives such as our extensive travel award program. Your support helps makes these opportunities possible. https://www.protease.org/membership We also encourage submissions from our members for the upcoming issues of QuickCuts. We would love to highlight more of your papers and protease-related news items, so please send them through!

*See you in Freiburg in 2027!*

Finally, I look forward to seeing many of you at the upcoming Gordon Research Conference on Proteolytic Enzymes and their Inhibitors in Italy. Galia, Lakshmi, and Anthony have assembled a stellar program, and it promises to be a wonderful opportunity to connect with science and colleagues against the backdrop of beautiful Tuscany and the lingering scent of jasmine. I hope to see many of you there.

Laura Edgington-Mitchell, IPS President
Email: Laura.EdgingtonMitchell@unimelb.edu.au

# IPS 2025 Meeting Report

## 13th General Meeting of the International Proteolysis Society
## Búzios, Rio de Janeiro – Brazil
## October 26-30, 2025


Ana Paula Lima, Antoine Dufour and Ruth Geiss-Friedlander, IPS 2025

**Many thanks to the organisers!!!**

**Ana Paula Lima – Universidade Federal do Rio de Janeiro**

**Maria Luiza Oliva – Universidade Federal de São Paulo**

# IPS 2025 Meeting Report

The 13th General Meeting of the International Proteolysis Society (IPS) was held from October 26 - 30, 2025, at the Hotel Atlântico Búzios in the stunning coastal town of Búzios, Rio de Janeiro, Brazil. Celebrating the 25th anniversary of the IPS, this landmark event brought together a truly global community of protease researchers, clinicians, industry representatives, and trainees for an intensive and inspiring week of scientific discovery, professional development, and international collaboration. Set against Brazil's Atlantic coast, IPS Brazil 2025 provided a strong platform for scientific exchange, professional networking, and discussion of future directions in proteolysis research.

Prior to the main conference, IPS Brazil 2025 featured a two-day pre-meeting training course held on October 23–24 at the renowned Instituto Oswaldo Cruz (FIOCRUZ) in Rio de Janeiro. Continuing IPS's longstanding commitment to fostering the next generation of scientists, these workshops provided intensive hands-on and theoretical training opportunities for young investigators in cutting-edge proteolysis methodologies. (see page 8-9)

The main IPS Meeting officially opened on October 26th with registration, networking events, and a celebratory opening ceremony honoring the society's legacy from 1999–2025. Jeanne Hardy chaired a wonderful panel session to honor the society's legacy and future. Christopher Overall chaired the opening scientific program, followed by a powerful inaugural lecture by Charles Craik (University of California, San Francisco), who presented on the future of conditionally activated therapeutics. This opening session appropriately set the tone for a conference deeply focused on both mechanistic understanding and translational applications of proteolysis.

Over the following five days, the meeting featured a broad and comprehensive scientific agenda, including plenary lectures from Michael Glickman, Irit Sagi, and Matthew Bogyo, as well as a diverse range of thematic sessions addressing neurobiology and aging, therapeutic targeting of proteolysis, structural biology, cancer, cellular homeostasis, immunity, cardiovascular biology, host-pathogen interactions, post-translational modifications, and targeted protein degradation. Particularly notable was the dedicated special symposium on pharmacological inhibition of Cathepsin C (DPP1) in neutrophil-mediated diseases, reflecting the conference's ability to bridge basic science with clinical and pharmaceutical development.

The scientific program showcased the full breadth of contemporary proteolysis research, spanning molecular enzymology, degradomics, structural biology, therapeutic innovation, infectious disease, proteostasis, and systems-level protease analysis. Contributions from academia, biotechnology, and pharmaceutical industries underscored IPS's increasingly translational and interdisciplinary nature. The inclusion of emerging technologies, protease-selective inhibitors, activity-based probes, and targeted protein degradation strategies highlighted the field's continued expansion into highly innovative biomedical frontiers.

Poster sessions and trainee presentations remained a cornerstone of the meeting, offering early-career scientists valuable opportunities to present research, receive feedback, and build international collaborations. The conference culminated in major IPS award presentations.

Beyond the scientific sessions, IPS Brazil 2025 embraced the rich social and cultural environment of Brazil through welcome receptions, networking events, optional boat tours, and a banquet dinner, fostering personal connections and collaborative spirit among attendees. These activities reinforced the society's emphasis not only on scientific rigor but also on global community and friendship.

As the conference closed with reflections on IPS's future beyond its 25th anniversary, participants left Búzios energized by new ideas, strengthened collaborations, and a renewed commitment to advancing protease science worldwide. IPS Brazil 2025 was a fitting celebration of the society's achievements while simultaneously setting an ambitious course for the next generation of proteolysis research.

We extend our deepest appreciation to the Brazilian organizers, workshop coordinators, IPS leadership, scientific committee, speakers, sponsors, and volunteers whose dedication made this anniversary meeting an extraordinary success. Through scientific excellence, educational commitment, and international collaboration, the 13th IPS General Meeting in Brazil exemplified the enduring strength and future promise of the International Proteolysis Society.

**- Daniel Sojka, Biology Centre, Czech Academy of Sciences, Czech Republic**

# IPS 2025 Meeting Report


**IPS Members and Award Winners**
Buzios, 2025

# IPS 2025 Meeting Report


# IPS 2025 Meeting Report

# IPS 2025 Workshop Report

## Hands-on Practical Enzyme Kinetics Workshop

The workshops were held on the beautiful campus of the Oswaldo Cruz Foundation (FIOCRUZ). After hearing about the origin of the institute founded by Oswaldo Cruz, a noted physician and epidemiologist and its storied 125-year history in research and development in biological sciences, each workshop went with their tutors to different locations.

Tutors for the Kinetics workshop were Christian Sommerhoff, Fernanda dos reis Rocho and Guy Salvesen. The tutors welcomed the participation of a diverse set of 20 participants from around the world with expertise ranging from undergraduate to principal investigator. The first day focused primarily on theory and a little bit of preparation of materials.

We asked why we need to understand and measure enzyme kinetics. The answers are varied. From "I need it to get my paper published in a good journal", to "it helps me understand which proteases are primarily targeting which substrates", to "which inhibitor should I use under which conditions to block my favorite enzyme". Enzyme kinetics is a pretty dry topic for most people. And it needs to be livened up and more readily comprehended by hands on experience in the laboratory.

Christian started off the first day with a presentation guiding participants through the intricacies of enzyme kinetics. They learned about substrate/enzyme/inhibitor interactions and the impacts that different types of inhibitors play on the capacity of enzymes to cleave peptide substrates. Fernanda showed how to determine kinetic constants for protein substrates and Guy added some practical suggestions to guide the group toward the next part of the day, wet lab investigations generously provided in the laboratory of Professor Eduardo Caio Torres dos Santos. After learning about the difference between equilibria and rates, groups were assigned based on their interest in steady state kinetics or transient pre steady state kinetics using reagents prepared by Fabiana, Prof Caio's laboratory manager and under the watchful eyes of the tutors each group set up their experiments.

***- Guy Salvesen,***
***Professor Emeritus,***
***Sanford Burnham Prebys***

# IPS 2025 Workshop Report

## TAILS Proteomics Substrate Discovery: Data Analysis

The IPS organized a series of hands-on workshops for researchers seeking an introduction to modern techniques for protease characterization, spanning from fundamental biology to state-of-the-art experimental and analytical approaches.

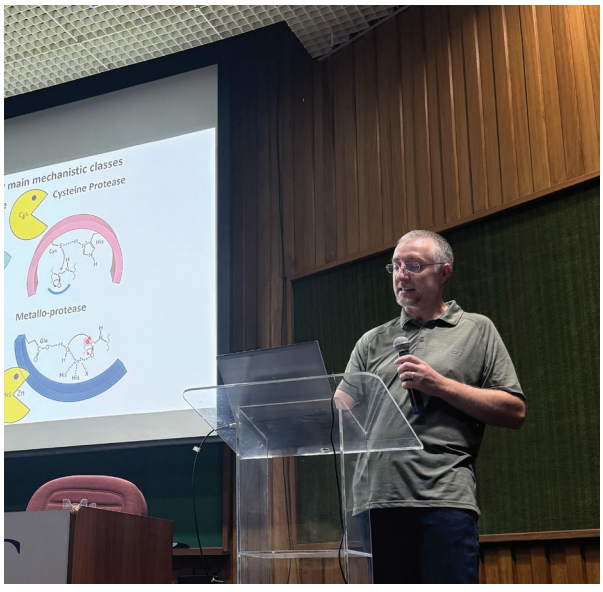
Day 1 focused on foundations. The program opened with an introduction to proteases, their regulation, specificity, and roles in health and disease, followed by an overview of protease inhibitors and activity assays. This was followed by an introduction to mass spectrometry–based proteomics, covering LC–MS principles, instrumentation, data acquisition, identification, and quantification. The afternoon moved into degradomics, presenting enrichment strategies and major workflows (TAILS, subtiligase, PICS), with emphasis on experimental design across in vitro, in vivo, and clinical settings.

Day 2 began jointly with degradomics data analysis, including the use of MEROPS and TopFIND, annotation of cleavage events, generation and interpretation of IceLogos, and approaches for normalization, statistics, visualization, and validation. The workshops then split. Workshop 2 explored protease imaging and applications, including activity-based probes, gel-based profiling, and emerging diagnostic and therapeutic concepts. Workshop 3 focused on emerging technologies (single-cell and spatial proteomics, AI in proteomics) and concluded with degradomics searches and data exploration with FragPipe and CLIPPER 2.0.

The program was delivered by Anthony O'Donoghue (protease biology and specificity), Antoine Dufour (degradomics and protease systems biology), Olivier Julien and Konstantinos Kalogeropoulos (proteomics, degradomics and data analysis), and Galia Blum (activity-based probes), and concluded with open discussion sessions for project specific questions.

The workshops were highly enjoyable and sparked many fruitful discussions across career stages and disciplines. The organizers would like to warmly thank all participants for their engagement and enthusiasm.

***- Konstantinos Kalogeropoulos,***
***Assistant Professor,***
***Technical University of Denmark***



# 2025 Lifetime Achievement Award

## Bob Lazarus

Bob has always been a key member of the international protease community. He served as Secretary and then President of the International Proteolysis Society (IPS) between 2011 and 2015. His leadership in the protease field was recognized in October 2025 when he received the prestigious Lifetime Achievement Award for protease research at the International Proteolysis Society meeting in Brazil. At this meeting he also delivered the Keynote address.

Bob's work provides a comprehensive understanding of human tryptase, a critical mediator in allergic inflammatory responses, particularly in asthma. His research illuminates the intricate allosteric regulation of β-tryptase activity, demonstrating that its proteolytic function is dependent on tetramer formation and specific protein-protein interactions. Bob's team has conclusively shown that heparin plays a crucial dual role, both stabilizing the tetramer and allosterically conditioning the active site. Furthermore, his investigations extend to α-tryptase, revealing that while inactive as a homotetramer, it forms active heterotetramers (α/β-tryptase) with β-tryptase. These heterotetramers possess a novel substrate repertoire, activating PAR2 and making mast cells susceptible to vibration-triggered degranulation, offering vital insights into conditions like hereditary α-tryptasemia. Bob's work has delved into therapeutic strategies, identifying that elevated tryptase levels correlate with severe asthma and lead to decreased benefit from anti-IgE treatment. Crucially, he has developed a novel noncompetitive inhibitory antibody that effectively blocks β-tryptase activity by inducing tetramer dissociation into inactive monomers, highlighting a bivalency-driven mechanism for potent inhibition and offering a promising avenue for treating severe asthma. This body of work underscores the significance of tryptase's unique structure and activation mechanisms in disease pathology and its potential as a therapeutic target.

Beyond his foundational work on tryptase, Bob's expertise extends significantly into the broader realm of protease biology and its role in inflammatory diseases, particularly those affecting the skin and airways. His research has shed light on the intricate regulation of Kallikrein-related peptidases (KLKs), specifically KLK7 and KLK5. He has demonstrated that KLK7 undergoes autolysis, leading to a loss of activity, and can cleave mast cell chymase and various cytokines (including interferons and IL-10 family members), suggesting a novel link between KLK7 and mast cell function and cytokine regulation. This work has critical implications for skin barrier integrity, as evidenced by his discovery that imbalances in KLK activity contribute to debilitating conditions like Netherton syndrome and atopic dermatitis. Bob and his team developed inhibitory antibodies against KLK5 and KLK7, including a humanized bispecific antibody, which showed promising results in mouse models by improving skin barrier function and reducing inflammation through an allosteric inhibition mechanism. (continued on next page)

# 2025 Lifetime Achievement Award

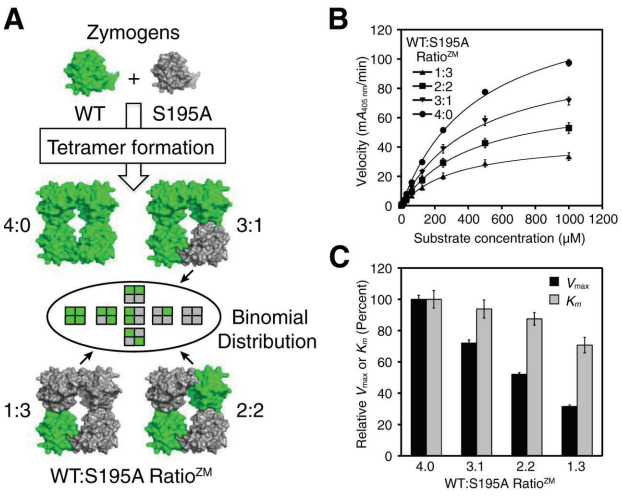
## Bob Lazarus (continued)

Furthermore, their genetic studies identified KLK5 as a causal gene in Type 2-low asthma, where elevated KLK5 expression in the airways can drive neutrophilic inflammation, indicating its potential as a therapeutic target for this unmet clinical need. This collective body of work showcases Bob's profound understanding of protease-mediated mechanisms in various inflammatory pathologies and his innovative approach to developing targeted therapies.

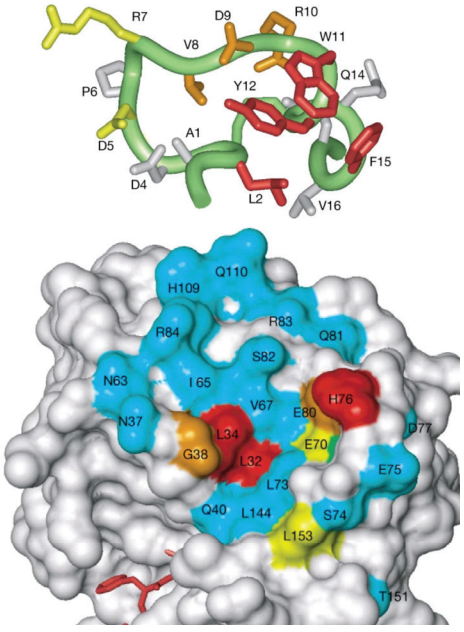
Beyond his work at Genentech, Bob has generously offered his time and expertise to mentoring students at the Pacific Coast Protease Workshop. This annual meeting brings together graduate students and postdocs from across the U.S and Canada. Each trainee at the workshop delivers a 20-minute oral presentation, and Bob has served as an external expert four times (2004, 2012, 2013, and 2016). In this role, he asks insightful questions and provides constructive feedback to the presenters, a role he clearly enjoys. In fact, he has returned to this meeting for the past two years (2024 and 2025) as an attendee, continuing to mentor these trainees even when not formally invited. In addition, Bob organized an ASBMB-sponsored 3-day symposium on "Serine Proteases in Pericellular Proteolysis and Signaling". This symposium was a great success and continues to be held biennially. Beyond organizing research symposiums, Bob has also been an invited speaker at international meetings held in South Africa, Canada, Australia, Italy, Hungary, and Germany.

In summary, Dr. Bob Lazarus is an outstanding collaborator, a highly productive leader in the protease field, an accomplished mentor, and a valued advisor to young scientists. We are very fortunate to have him be part of our protease community, and warmly congratulate him on his lifetime achievement award.

***-Anthony O'Donoghue, University of California, San Diego***




DOI: 10.1074/jbc.M117.812016




DOI: 10.1038/35006574

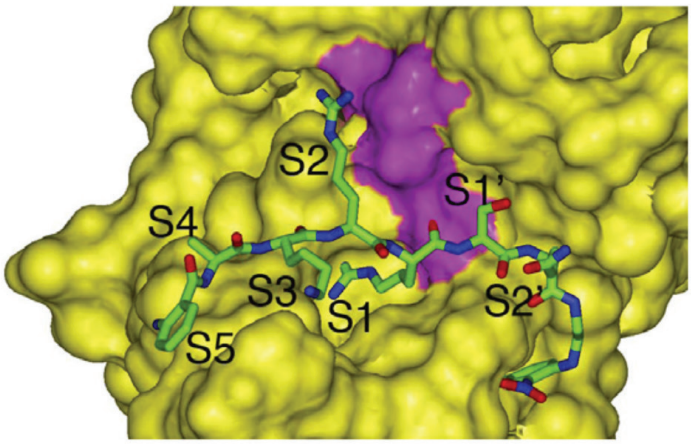
# 2025 Lifetime Achievement Award

## Luiz Juliano


Professor Luiz Juliano Neto has built a distinguished scientific career that places him among the pioneers of modern biochemical research in Brazil, particularly in the fields of peptide chemistry and protease biology. Trained as a physician at the Escola Paulista de Medicina in 1968, he quickly moved beyond traditional disciplinary boundaries, helping to establish a model of scientific "convergence" that integrates medicine with chemistry, physics, and engineering—an approach now widely recognized as essential to innovation in the life sciences.

From the outset of his career, Juliano demonstrated visionary leadership in introducing and advancing peptide synthesis in Brazil. At a time when this field was still emerging internationally, he contributed to the chemical synthesis and functional study of biologically active peptides, particularly those involved in cardiovascular regulation, such as the kallikrein–kinin and renin–angiotensin systems. His early work helped establish the biochemical foundations necessary to understand how peptide mediators regulate blood pressure and inflammation, with implications for hypertension and vascular disease.

A defining feature of Juliano's scientific legacy is his groundbreaking work on proteases—enzymes that play central roles in physiological regulation and disease. Beginning in the 1980s, he pioneered the development of fluorescent peptide substrates, enabling precise measurement of proteolytic activity in complex biological systems. These methodological innovations became widely adopted tools, significantly advancing the study of enzyme kinetics, specificity, and regulation. His research extended to key protease families, including tissue and plasma kallikreins and proprotein convertases such as furin, which are critical in protein processing and cellular signaling. (continued)




Colour representations of the active site region of Dengue NS3 protease with the catalytic triad shown in pink. Enzyme subsites are labelled $S_5$–$S_2'$.
10.1016/j.abb.2006.11.005

# 2025 Lifetime Achievement Award

## Luiz Juliano

Juliano's work has also had broad biomedical impact through its application to infectious diseases and oncology. By investigating the role of proteases in the life cycles of pathogens such as Trypanosoma cruzi, Leishmania, and viruses including dengue, he contributed to a deeper understanding of host–pathogen interactions and potential therapeutic targets. Notably, his earlier studies on coronavirus proteases anticipated later global challenges; during the COVID-19 pandemic, he returned to this field, fostering interdisciplinary collaborations to study viral and host proteases relevant to SARS-CoV-2.

In parallel, Professor Juliano has made significant contributions to cancer research, particularly in elucidating the role of proteolysis in tumor progression. His leadership in establishing metabolomics approaches—supported by advanced mass spectrometry platforms—has enabled new insights into cancer metabolism and biomarker discovery. This work exemplifies his enduring commitment to integrating technologies and disciplines to address complex biomedical problems.

Beyond his research output, comprising over a hundred scientific publications, Juliano has had a profound influence as a mentor and academic leader. As a professor at the Federal University of São Paulo, he has trained generations of scientists and fostered collaborative environments that bridge traditional academic silos. His efforts have not only advanced scientific knowledge but also strengthened Brazil's capacity for high-level biomedical research.

In recognition of his pioneering discoveries, methodological innovations, and commitment to interdisciplinary science, Luiz Juliano Neto's career stands as a model of sustained excellence and impact. His contributions have shaped the understanding of proteolytic systems in health and disease, while his vision of scientific convergence continues to influence the future direction of biomedical research.

**-Marcin Drag, Institute of Physical Chemistry, Polish Academy of Sciences**

# 2025 Ulrich auf dem Keller Young Investigator Award

## Laura Edgington-Mitchell

Dr. Laura Edgington-Mitchell is a leading chemical biologist and protease expert whose accomplishments span fundamental discovery, translational tool development, and international leadership in the proteolysis community. She obtained her Bachelor's degree with a double major in biology and chemistry in 2006 from Transylvania University in the USA. She earned her Ph.D. in 2012 in Chemistry in the Chemical Biology Graduate Program at Stanford University under the guidance of Dr. Matt Bogyo. From 2012–2017, she was a postdoctoral fellow and NHMRC Peter Doherty Fellow at La Trobe University and Monash University. She joined the faculty of the Department of Biochemistry & Pharmacology at the University of Melbourne as a group leader in 2018, and was recently promoted to Associate Professor.

Laura's research group develops and applies chemical activity-based probes, proteomics and degradomics methods that reveal when, where, and how proteases act in vivo. She leverages these technologies to understand and therapeutically target cancer, inflammation, infection, and pain. She truly stands out for her rare combination of deep expertise in the design, synthesis, and rigorous characterization of activity-based probes together with the advanced application of mass spectrometry-based proteomics and degradomics to define protease substrate cleavage events. Her recent work provides a compelling example of how she unites chemical probe development with degradomics to answer biologically and clinically relevant questions. In that work, her team joined forces with the group of Dr. Hayley Newton to investigate Coxiella burnetii, the causative agent of Q fever, using the activity-based probe BMV109 to profile cathepsin activity in infected cells and to quantify infection-induced changes in secreted and lysosomal proteases. They demonstrated that C. burnetii infection profoundly remodels secreted protease levels and drives a marked decrease in active cathepsin B, independent of baseline host expression, revealing a mechanistic link between infection, host protease activation, and pathogen fitness. By establishing a framework to tune virulence through modulation of protease production and activity, this work opens a path for others to dissect similar protease-dependent strategies in a wide range of intracellular pathogens.

**Award History and Selection Process**

In 2019, Ulrich auf dem Keller (IPS President) established the Young Investigator Award. Awardees are selected every two years by the IPS Council to recognise individuals who have made outstanding contributions to the field at an early career stage. In memory of Ulrich, the award was subsequently renamed the Ulrich auf dem Keller Young Investigator Award. In 2025, the IPS Board formalised the nomination and application process. A call for nominations was circulated via email and published on the IPS website https://www.protease.org/young-investigator-award, outlining clearly defined eligibility criteria and submission guidelines. Applications required at least one letter of support, a nomination statement, and a 5-page CV. All applications were reviewed by the IPS Council, with all members participating in the voting process. Where a nominee was a current Council member, they were recused from both discussion and voting related to the award.

## Laura Edgington-Mitchell (continued)

Dr. Edgington-Mitchell has also built a substantial translational portfolio, moving protease imaging and profiling tools from bench to bedside. She is an inventor on five patents, including probes developed with Takeda Pharmaceuticals to monitor cathepsin and elastase activity in clinical samples, which are critical for rational engagement of these proteases in cancer and inflammatory disease. One probe platform she helped develop during her time in the Bogyo Lab was licensed by Vergent Biosciences and progressed through a first-in-human Phase I safety study; it is now in Phase II trials for fluorescence-guided surgical resection of lung cancer and is being extended via a PhD-led clinical trial program in oesophageal and gastric cancers that she co-supervises with surgeons at Peter MacCallum Cancer Centre. She has so far secured ~4.2 million AUD in competitive research funding, including NHMRC Ideas Grants (as lead CI), an ARC DECRA Fellowship, the Grimwade Research Fellowship, a Cancer Australia/Cure Cancer Young Investigator Award, philanthropic support, and multiple industry contracts with Roche, Medivir, Clarity, and Advinus. This diverse funding base underscores her ability to position protease biology at the interface of basic science, drug discovery, and clinical translation.

Laura's work has so far resulted in 69 publications that have been cited ~3,200 times, which is exceptional for her career stage. She has received numerous awards among which include the Chinese Academy of Sciences President's International Fellowship Initiative (PIFI) Award 2025, a Lorne Protein Conference Sparrow Award in 2023, a MJ Gething Gender Equity Award in 2022, and Monash University Deans Award for Early Career Research in 2017. She is a member of the Early Career Advisory Board for ACS Chemical Biology. Laura is an active member of the protease community, having given numerous invited talks at both IPS and protease Gordon Conferences. In 2018 and 2014, she was elected to Chair and co-Chair the Gordon Research Seminar on Proteolytic Enzymes and their Inhibitors. We congratulate Laura on her accomplishments and thank her for her leadership in the society.

***-Antoine Dufour, University of Calgary***
***Jeanne Hardy, University of Massachusetts, Amherst***

# IPS 2025 Awards

## Poster Prizes

Alexandre Aubert
Andre Luis Lira da Silva
André Luiz Pinto Guedes Lourenço
Caio Nobrega Zanotto
Christopher Bourne
Daniel Alexandre de Souza
Gabriel Lemieux
Giovana de Castro Fiorini Maia
Julian Nguyen
Kinda Sharrouf
Ruggiero Pio Cassatella
Victoria Eugenia Garcia Perez



## Travel Awards

Atsumi Ota
Ana Maria Filipe
André Luis Lira da Silva
Anna Siewerth
Bartlomiej Skinderowicz
Bartmann Johannes
Caterina Travisan
Dennis_Cydney
Diego Trujillo
Eline Bernaerts
Elisa Nightingale
Gabriel Lemieux
Jonathan Coene
Matthieu Lepage
Miguel Cosenza
Nathalia Thompson
Ruggiero Pio Cassatella
Samuel Zolg
Tamas Dobai
Victoria Garcia

# Meeting Report

## *The 43rd Winter School on Proteases and Their Inhibitors in Tiers*

From 11 to 15 March 2026, young protease researchers and leading scientists gathered at the Winter School in Tiers, held in the beautiful setting of the Italian Alps (South Tyrol). What sets the Winter School in Tiers apart is that the vast majority of talks are delivered by early-career scientists, primarily PhD students. The scientific sessions covered fundamental questions such as protease substrate discovery and interactomes; immunity, inflammation and metabolism; cancer; pathogens and infectious diseases; sheddases and membrane proteolysis; and natural and pharmaceutical inhibitors, including impressive presentations on drug discovery projects in the area of allergy by Chiesi Pharma and Genentech.

During the lively careers session, aspects of academic and industrial research were discussed. Henry Maun gave a stimulating presentation on Genentech's unique situation and the San Francisco biotech scene in general. Henry's contributions earned him one of the highest accolades given at the Winter School: a Green Influencer Fritzi Award. Fritzi awards are presented by the anonymous Winter School committee and handed out by their dedicated assistants.

The Henner Graeff Foundation (https://www.henner-graeff-stiftung.de) presented Young Investigator Awards to three outstanding scientists: Michel Hendel (Technical University of Munich), Chelsea Kaden (University of Greifswald) and Kira Kutschheit (University of Freiburg).


The scientific sessions held in Tiers' town hall were excellent, as was the food at the Hotel Paradies, a venue that attracts celebrities from all over the world.

Make sure you don't miss the next Winter School, taking place from 3 to 7 March 2027.

Visit https://plus.ac.at/tiers to keep up to date.

***- Klaudia Brix and Hans Brandstetter***

# Meeting Announcements

***3-6 June 2026***

## *International Society of Protein Termini (ISPT)*


The International Society of Protein Termini (ISPT) is pleased to announce that regist International Society of Protein Termini (ISPT) ration and abstract submission are now open for the Protein Termini Conference 2026: From Mechanisms to Biological Impact, to be held 3–6 June 2026 in Palermo, Italy, with FEBS endorsement.

You can now find all practical information, register, and submit your abstract via the conference website:Conference website (registration & abstracts):

https://proteintermini.org/meeting/

The conference will gather global leaders and emerging researchers to discuss cutting-edge advances in protein terminal biology, spanning translational regulation, co- and post-translational modifications, proteolytic pathways, proteostasis mechanisms, and targeted protein modulation.

We are particularly excited that the conference will take place at the magnificent Palazzo dei Normanni, the Royal Palace of Palermo — a UNESCO World Heritage site and home to one of the oldest parliamentary institutions in the world.Evening poster sessions will be held in the nearby beautiful Oratorio San Mercurio, and the Gala Dinner will take place in the magnificent aristocratic Villa Chiaromonte Bordonaro.Registration fees are very low and all-inclusive, covering accommodation, meals, and the Gala Dinner.

In addition, numerous fellowships and awards will be offered to support the participation of young researchers, reflecting ISPT's strong commitment to accessibility and to fostering early-career scientists. Registration and abstract submission:

https://www.conferencecentral.org/webpage/view/45

# Meeting Announcements

***June 21 - 26, 2026***

## *The Power of Proteases and their Inhibitors, Bridging Mechanisms and Therapeutics*

The Proteases, Inhibitors and Therapeutics GRC is a premier, international scientific conference focused on advancing the frontiers of science through the presentation of cutting-edge and unpublished research, prioritizing time for discussion after each talk and fostering informal interactions among scientists of all career stages. The conference program includes an array of speakers and discussion leaders from institutions and organizations worldwide, concentrating on the latest developments in the field. The conference is five days long and held in a remote location to increase the sense of camaraderie and create scientific communities, with lasting collaborations and friendships. In addition to premier talks, the conference has designated time for poster sessions from individuals of all career stages, and afternoon free time and communal meals allow for informal networking opportunities with leaders in the field.

Proteases, Inhibitors and Therapeutics
*Gordon Research Conference*

**The Power of Proteases and their Inhibitors, Bridging Mechanisms and Therapeutics**

June 21 - 26, 2026

Apply Now

**GRC Education Requirements:** Undergraduates or those who have not obtained a bachelor's degree in science/engineering (or acceptable equivalent) are not eligible to apply to attend Gordon Research Conferences or Seminars.

**Chair**
Galia Blum

**Vice Chairs**
Lakshmi C. Wijeyewickrema and
Anthony J. O'Donoghue

Proteases, Inhibitors and Therapeutics (GRS)
*Gordon Research Seminar*

**Advancing Protease Biology: Enzymatic Mechanisms and Therapeutic Strategies**

June 20 - 21, 2026

Apply Now

**GRC Education Requirements:** Undergraduates or those who have not obtained a bachelor's degree in science/engineering (or acceptable equivalent) are not eligible to apply to attend Gordon Research Conferences or Seminars.

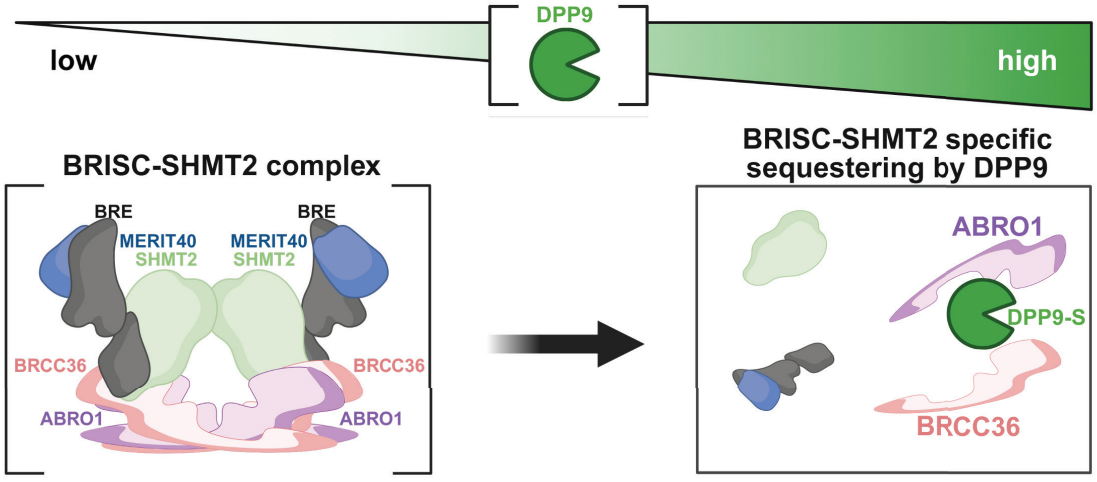
**Chairs**
Samantha Martinusen and
Rawad Hanna

For 2026, the conference will place a special emphasis on the mechanisms, functions, and translational implications of proteases and their inhibitors, highlighting their roles in health, disease, and therapeutic innovation. Sessions will explore the latest advances in protease biology, the development of next-generation inhibitors, and the impact of these molecules on drug discovery and patient care. Emerging technologies for monitoring protease activity and novel strategies for targeting proteolysis will be featured, as those that have led to recent breakthroughs, in SARS-CoV-2 main protease inhibitors in infectious disease, cancer, and cardiovascular research. The program will showcase world-renowned experts in protease structure, function, and inhibition, whose work spans innovative analytical platforms, the dynamics of proteases in complex biological systems, and the translation of fundamental discoveries into impactful therapies. The conference continues its tradition of fostering interdisciplinary collaborations, welcoming new researchers, and supporting the growth of promising scientists. A dedicated seminar will accompany the 2026 meeting, focused on mentoring and attracting junior scientists, graduate students, and postdoctoral fellows to this vibrant field. Whether your interests are in basic enzyme biochemistry, structural and chemical biology, or translational drug discovery, this conference offers a unique environment to explore the exciting intersection of protease research and therapeutic innovation.

# Protease Paper Highlight

Wirtgen VE, Saied L, Zolg S, Alonso MC, Mayer B, Donzelli L, Maurer U, Timmers HTM, Knobeloch KP, Kleifeld O, Geiss-Friedlander R (2026) **Proximity labeling reveals non-catalytic interactions between DPP9 and ubiquitin signaling complexes.** Cell Mol Life Sci. DOI: 10.1007/s00018-025-06021-z

Dipeptidyl peptidase 9 (DPP9) is an amino-peptidase with roles in immunity, DNA-repair, cell signaling, memory and neonatal survival; its dysregulation is linked to cancer and immune-related disorders. While many studies focus on its catalytic activity, scaffolding functions of DPP9 are emerging. Here, we mapped the DPP9 interactome using TurboID-based proximity labeling in DPP9 knock-out HEK293 cells reconstituted with doxycycline-inducible miniTurboID-DPP9, allowing fine-tuned expression that approximates physiological levels. Besides known partners, proteins involved in autophagy, mRNA decay and ubiquitin signaling along with DPP8, were strongly enriched among the identified DPP9 binding partners. Notably, we validated DPP8, the E3 ligase CBL, the deubiquitinase complexes CYLD-SPATA2 and the BRISC complex components BRCC36/BRCC3 and ABRO1/ABRAXAS2 as novel DPP9 interactors. Furthermore, NanoBRET assays in living cells demonstrated that DPP9 disrupts the binding between BRCC36/BRCC3 and ABRO1/ABRAXAS2, and the interaction of CYLD with SPATA2, thereby compromising these protein-protein interactions. Mechanistically, these findings reveal physical and potentially regulatory interactions between DPP9 and components of the ubiquitin system and provide a basis for dissecting the non-catalytic functions of DPP9.

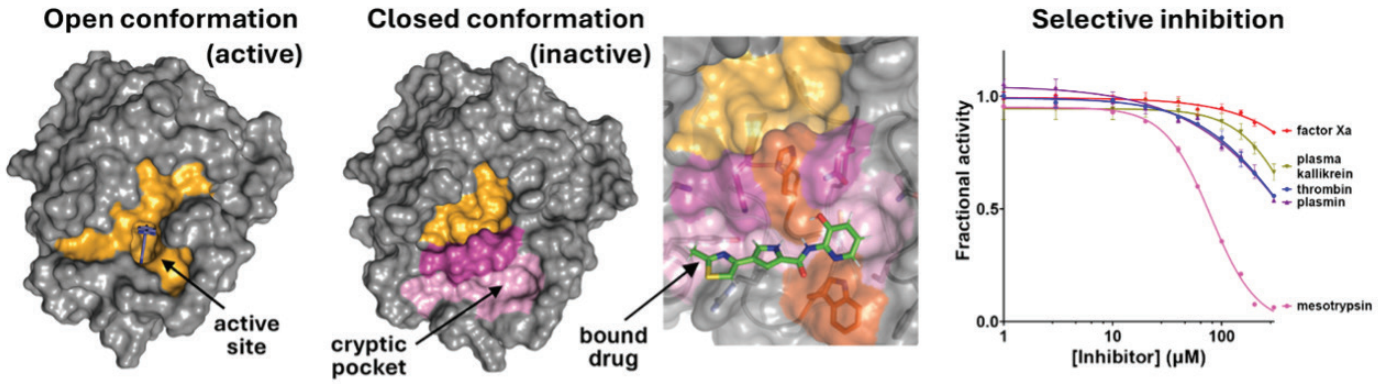



Proposed model for DPP9-mediated modulation of the deubiquitinase BRISC complex assembly. Under normal conditions BRCC36 assembles with ABRO1, BRE, MERIT40 (and SHMT2) to form the BRISC-SMHT2 complex. We propose that DPP9 binding to BRCC36 and ABRO1 disrupts these interactions either by preventing BRISC complex formation or destabilization of the existing complex

# Protease Paper Highlight

Coban M, Gokara M, Forero Vargas LM, Tanzer SD, Zhou SX, Hockla A, Sankaran B, Caulfield TR, Radisky ES. (2026). **Discovery of an autoinhibited conformation in mesotrypsin reveals a strategy for selective serine protease inhibition.** Science Advances.
DOI: [10.1126/sciadv.adu9129](https://doi.org/10.1126/sciadv.adu9129)

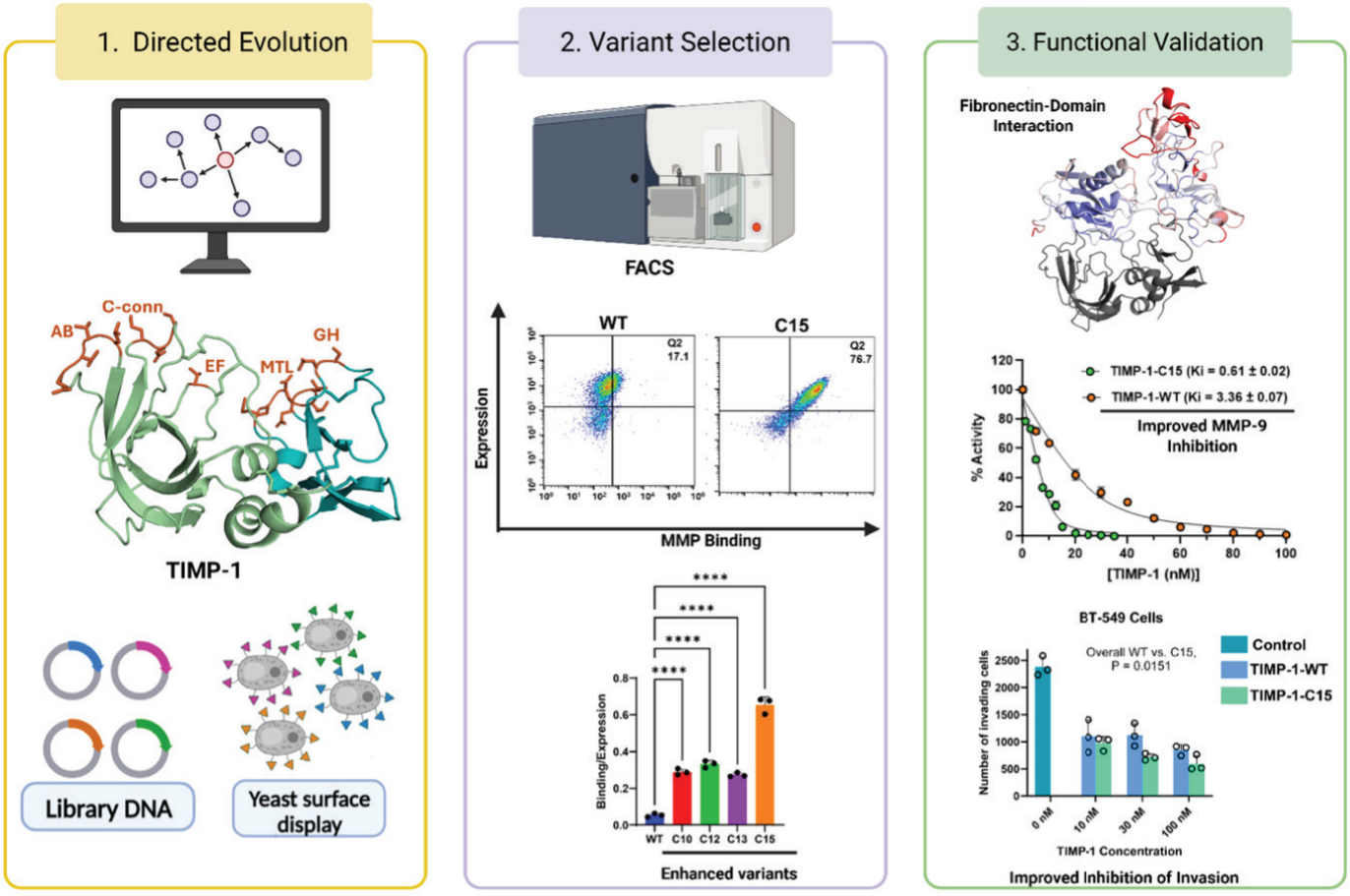
Mesotrypsin (PRSS3), a trypsin isoform linked to invasion and poor outcome in prostate, pancreatic, lung, and other cancers, has been difficult to inhibit selectively because trypsin-family active sites are highly conserved. Coban et al. captured mesotrypsin in crystal structures of both an open, active conformation and an unexpected closed, autoinhibited conformation that reveals a previously unknown cryptic pocket adjacent to the active site. Using structure-guided virtual screening against this pocket, they identified a proof-of-concept small-molecule allosteric inhibitor that stabilizes the inactive state and selectively inhibits mesotrypsin over related proteases. The study opens a new strategy for targeting this cancer-associated protease, while also suggesting that analogous cryptic pockets across the S1 serine protease family could provide a broader route to selective inhibitor discovery.



# Protease Paper Highlight

Shoari A, Coban MA, Hockla A, Rezhdo A, Dimesa AM, Raeeszadeh-Sarmazdeh M, Van Deventer JA, Radisky ES. (2026). **Directed evolution of metalloproteinase inhibitor TIMP-1 for selective inhibition of MMP-9 exploits catalytic and fibronectin domain interactions.** Journal of Biological Chemistry. DOI: [10.1016/j.jbc.2025.110258](https://doi.org/10.1016/j.jbc.2025.110258)

Matrix metalloproteinase-9 (MMP-9) is a key driver of extracellular matrix remodeling, invasion, and metastasis in triple-negative breast cancer and other aggressive diseases, but selective inhibition has been difficult because MMP catalytic sites are highly conserved. Shoari et al. used yeast surface display and directed evolution to engineer the natural broad-spectrum inhibitor TIMP-1 into a variant, TIMP-1-C15, with enhanced affinity and selectivity for MMP-9. The engineered inhibitor achieves this specificity by engaging not only the catalytic domain but also the unique fibronectin domains of MMP-9, leveraging multidomain interactions beyond the active site. TIMP-1-C15 showed improved selectivity over related MMPs and improved suppression of MMP-9-dependent invasion in triple-negative breast cancer cells, highlighting a protein-engineering route to more precise metalloproteinase inhibitors.



# Protease Paper Highlight

Ziegler AR, Scott NE, Edgington-Mitchell LE (2026). **Advances in degradomics technologies to assess proteolytic cleavage events.** Cell Chem Biol.
DOI: [10.1016/j.chembiol.2026.01.001](https://doi.org/10.1016/j.chembiol.2026.01.001)

Proteases contribute to essential cellular processes through catalyzing proteolysis, resulting in peptide bond hydrolysis and the generation of novel polypeptide species. Identification of proteolytic cleavage events is crucial for discerning proteolytic networks in biological systems, including the contribution of individual proteases to specific disease states. As such, various mass spectrometry-based workflows have been exploited for the sensitive identification of cleavage sites. To date, a range of enrichment strategies have been developed, focusing on increasing sensitivity, ease, and throughput for protease substrate discovery. Recent advances in mass spectrometry instrumentation have also permitted enrichment-free workflows for degradomics analysis, providing simultaneous and systematic assessment of the proteome and degradome. In this review, we discuss current technologies for the enrichment and identification of both N- and C-termini, as well as their application to profile protease specificity and decipher individual substrate repertoires in diverse biological conditions.