

CV date	15.09.2021
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Part A. PERSONAL INFORMATION

First and Family name	Ulrich ECKHARD		
DNI/NIE	Y7570115-R	Age:	38
Researcher codes	WoS Researcher ID	L-3733-2016	
	SCOPUS Author ID	8706725900	
	Open Researcher and Contributor ID (ORCID)	0000-0001-5863-4514	

A.1. Current position

Name of University/Institution	Instituto de Biología Molecular de Barcelona, Consejo Superior de Investigaciones Científicas (IBMB-CSIC)		
Department	Department of Structural Biology		
Address and Country	Carrer de Baldiri Reixac 15, 08028 Barcelona, España		
Phone number	+34 (0)644 562438	E-mail	ueccri@ibmb.csic.es
Current and future position	Beatriu de Pinos Post-doctoral Fellow Ramon y Cajal Research Investigator	From	01.10.2019 Mid 2022
Key words	protease research; structural biochemistry; proteomics; health sciences		

A.2. Education

PhD (Dr. rer. nat.)	University of Salzburg (Natural Sciences, Genetics)	2011
MSc (Mag. rer. nat.)	University of Salzburg / University of Linz (Molecular Biology)	2011
MSc (Mag. biol.)	University of Salzburg (Biology, Genetics)	2007
BSc (Bakk. rer. nat.)	University of Salzburg / University of Linz (Molecular Biosciences)	2006
BSc (Bakk. biol.)	University of Salzburg (Biology, Genetics and Molecular Biology)	2005

A.3. JCR articles, citations, h Index

Database: Web of Science (Clarivate Analytics; 15.09.2021) Index-h / h-index: **18**

Total number of citations: **996**

Total number of articles: **33**

Database: Google Scholar (15.09.2021) Index-h / h-index: **20**

Total number of citations: **1369**

i10-index: **25**

Total number of articles: **34**

A.4. Employment History

- 10/2019–present: Post-doctoral researcher in the Proteolysis Lab of Prof. F. Javier Gomis-Rüth at IBMB-CSIC, Barcelona, Spain. *Funded by a Beatriu de Pinós post-doctoral fellowship.*
- 10/2017–09/2019: Post-doctoral researcher in the Structural Biology Lab of Prof. Hans Brandstetter, Department of Biosciences, University of Salzburg, Austria. *Funded by a post-doc fellowship from the Peter and Traudl Engelhorn Foundation (PTES).*
- 09/2016–09/2017: Post-doctoral researcher in the laboratory of Prof. Maria Selmer, Department of Cell and Molecular Biology, Uppsala University, Sweden.
- 05/2012–08/2016: Post-doctoral fellow in the lab of Prof. Chris Overall, Centre for Blood Research, University of British Columbia, Vancouver, Canada. *Funded by a postdoctoral fellowship from the Michael Smith Foundation for Health Research (MSFHR).*
- 12/2011–04/2012: Post-doctoral fellow in the Structural Biology Lab of Prof. Hans Brandstetter, Department of Molecular Biology, University of Salzburg, Austria.
- 01/2008-11/2011: PhD position within the FWF project P20582 at the University of Salzburg. Thesis: "Biochemical and structural characterization of collagenase G reveals a chew and digest mechanism of bacterial collagenolysis". Graduation as Doctor of Natural Sciences: 28.11.2011.

Part B. CV SUMMARY

During my PhD in the lab of [Prof. Hans Brandstetter](#) at the University of Salzburg, I focused on the cloning, expression, purification, and biochemical and structural characterization of clostridial collagenases, resulting in 6 peer reviewed articles, including first author publications in *The Journal of Biological Chemistry* and *Nature Structural & Molecular Biology*. I succeeded in solving the long-standing puzzle of clostridial collagenolysis by determining the crystal structure of the collagenase unit of ColG and its accessory PKD-like domain, and deposited a total of 10 structures to the PDB, including the very first one of clostridial collagenases.

In May 2012, I joined the degradomics lab of [Prof. Chris Overall](#) at the UBC Centre for Blood Research in Vancouver, Canada, where I focused on proteomics whilst staying in close contact with protease research. I acquired several mass spectrometry techniques and participated in multiple interdisciplinary and collaborative projects; e.g. I developed a MALDI-TOF based bradykinin release assay, profiled clostridial collagenases using PICS proteomics, and lead the collaborative task to profile human MMPs, and corroborated our results using a panel of fluorescent peptides, molecular modelling and molecular docking. By employing positional proteomics, I assessed the proteome and N-terminome of human pulp and contributed in the degradomic analysis of human platelets and murine pancreatic tumors. Moreover, I established a strong collaboration with [Prof. Andrew C. Doxey](#) at the University of Waterloo, focusing on a subgroup of bacterial flagellins that harbor a peptidase-like domain, and we are now directing the project towards biofilm biology.

In September 2016, I joined the lab of [Prof. Maria Selmer](#) at Uppsala University within a newly started protein evolution project, where I tackled the overarching question how protein structure and function are intertwined. My main project focused on the characterization of various Atlantic and Baltic herring proteins that are involved in ecological adaptation, I solved the crystal structures of both variants of phosphoglucomutase 5, and corroborated our findings using e.g. SAXS, CD, and differential scanning fluorimetry. Furthermore, I characterized a phage-encoded SAM-hydrolase, solved its apo structure, and determined together with an Erasmus Plus student the structure of two HisA variants of *Salmonella enterica* with divergent substrate specificities.

In 2017, I secured a prestigious two-year fellowship from the [Peter and Traudl Engelhorn Foundation](#), allowing me to start my own research project at the University of Salzburg. I succeeded to establish expression and purification strategies for various active and inactive flagellinolytic variants, performed biochemical characterizations, while the structural studies are still ongoing. Furthermore, I focused on a peculiar and highly heterogeneous family of so-called U32 collagenases. In fall 2019, I was awarded a 3-year Beatriu de Pinós post-doctoral fellowship to join the Proteolysis Lab of [Prof. Xavier Gomis-Rüth](#) at IBMB-CSIC in Barcelona, where I am continuing my research in the field of proteolysis and extend my skill-set to CryoEM, and where I am currently developing my own research line as a future *Ramon y Cajal* independent research fellow at the interface of molecular biochemistry and structural biotechnology.

Part C. RELEVANT MERITS**C.1. Publications (*contributed equally)**

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- 34 Eckhard U*, Körschgen H*, von Wiegen N, Stöcker W, and Gomis-Rüth FX (2021). The crystal structure of a 250-kDa heterotetrameric particle explains inhibition of sheddase meprin β by endogenous fetuin-B. **PNAS**, 118(14):[e2023839118](#).
 - 33 Godoy-Gallardo M, Eckhard U, Delgado LM, Puente YJD de R, Hoyos-Nogués M, Gil FJ, and Perez RA. Antibacterial approaches in tissue engineering using metal ions and nanoparticles: From mechanisms to applications. **Bioactive Materials**, 6(12):[4470-4490](#).
 - 32 Guo X, Söderholm A, Kanchugal P S, Isaksen GV, Warsi O, Eckhard U, Trigüis S, Gogoll A, Jerlström-Hultqvist J, Åqvist J, Andersson DI, and Selmer M (2021). Structure and mechanism of a phage-encoded SAM lyase revises catalytic function of enzyme family. **eLife**, 10:[e61818](#).
 - 31 Gustafsson R*, Eckhard U*, Ye W, Enbody ED, Pettersson M, Jemth P, Andersson L, and Selmer M (2020). Structure and Characterization of Phosphoglucomutase 5 from Atlantic and Baltic Herring—An Inactive Enzyme with Intact Substrate Binding. **Biomolecules**, 10(12):[1631](#).
 - 30 Eckhard U, Blöchl C, Jenkins BGL, Mansfield MJ, Huber CG, Doxey AC, and Brandstetter H (2020). Identification and characterization of the proteolytic flagellin from the common freshwater bacterium *Hylemonella gracilis*. **Scientific Reports**, 10(1):[19052](#).
 - 29 Tharmarajah G, Eckhard U, Jain F, Marino G, Prudova A, Urtatiz O, Fuchs H, Hrabe de Angelis M, Overall CM, and Van Raamsdonk CD (2018). Melanocyte development in the mouse tail epidermis requires the Adamts9 metalloproteinase. **Pigment Cell & Melanoma Research**, 31(6):[693-707](#).
 - 28 Jerlström-Hultqvist J, Warsi O, Knopp M, Söderholm A, Eckhard U, Vorontsov E, Selmer M, and Andersson DI. A bacteriophage enzyme induces bacterial metabolic perturbation that confers a novel promiscuous function. **Nature Ecology & Evolution**, 2(8):[1321-1330](#).

- 27 Dufour A, Bellac CL, **Eckhard U**, Solis N, Klein T, Kappelhoff R, Fortelny N, Jobin P, Rozmus J, Mark J, Pavlidis P, Dive V, Barbour SJ, and Overall CM (2018). C-terminal truncation of IFN- γ inhibits proinflammatory macrophage responses and is deficient in autoimmune disease. **Nature Communications**, 9(1):[2416](#).
- 26 King SL*, Goth CK*, **Eckhard U**, Joshi HJ, Haue AD, Vakhrushev SY, Schjoldager K, Overall CM, and Wandall HH (2018). TAILS N-terminomics and proteomics reveal complex regulation of proteolytic cleavage by O-glycosylation. **The Journal of Biological Chemistry**, 293(20):[7629-7644](#).
- 25 Abbey SR*, **Eckhard U***, Marino G, Solis N, Matthew I, and Overall CM (2018). The Human Odontoblast Cell Layer and Dental Pulp Proteomes and N-Terminomes. **Journal of Dental Research**, 97(3):[338-346](#).
- 24 Klein T, **Eckhard U**, Dufour A, Solis N, and Overall CM. Proteolytic cleavage – Mechanisms, function and “omic” approaches for a near ubiquitous posttranslational modification (2018). **Chemical Reviews**, 118(3):[1137-1168](#).
- 23 **Eckhard U***, Bandukwala H*, Mansfield MJ*, Marino G, Cheng J, Wallace I, Holyoak T, Charles TC, Austin J, Overall CM, and Doxey AC (2017). Discovery of a proteolytic flagellin family in diverse bacterial phyla that assembles enzymatically active flagella. **Nature Communications**, 8(1):[521](#).
- 22 Butler GS, Connor AR, Sounni NE, **Eckhard U**, Morrison CJ, Noël A, and Overall CM (2017). Proteolytic Processing of the CCN3 (Nov/nephroblastoma overexpressed) and CCN5 (WISP2/WNT1 inducible signaling pathway 2) by membrane-type 1 matrix metalloproteinase (MT1 MMP, MMP14). **Matrix Biology**, 59:[23-38](#).
- 21 Prudova A*, Gocheva V*, Auf dem Keller U*, **Eckhard U***, Olson OC, Akkari L, Butler GS, Fortelny N, Lange PF, McLeod J, Joyce JA, and Overall CM (2016). TAILS N-terminomics and proteomics show protein degradation dominates over proteolytic processing by cathepsins in pancreatic tumors. **Cell Reports**, 16(6):[1762-1773](#).
- 20 **Eckhard U**, Marino G, Butler GS, and Overall CM (2016). Positional proteomics in the era of the human proteome project on the doorstep of precision medicine. **Biochimie**, 122:[110-118](#).
- 19 **Eckhard U***, Huesgen PF*, Schilling O*, Bellac CL, Butler GS, Cox JH, Dufour A, Goebeler V, Kappelhoff R, Auf dem Keller U, Klein T, Lange PF, Marino G, Morrison CJ, Prudova A, Rodriguez D, Starr AE, Wang Y, and Overall CM (2016). Active site specificity profiling datasets of matrix metalloproteinases (MMPs) 1, 2, 3, 7, 8, 9, 12, 13 and 14. **Data in Brief**, 7:[299-310](#).
- 18 **Eckhard U***, Huesgen PF*, Schilling O*, Bellac CL, Butler GS, Cox JH, Dufour A, Goebeler V, Kappelhoff R, Auf dem Keller U, Klein T, Lange PF, Marino G, Morrison CJ, Prudova A, Rodriguez D, Starr AE, Wang Y, and Overall CM (2016). Active site specificity profiling of the matrix metalloproteinase family: Proteomic identification of 4300 cleavage sites by nine MMPs explored with structural and synthetic peptide cleavage analyses. **Matrix Biology**, 49:[37-60](#).
- 17 **Eckhard U**, Marino G, Abbey SR, Matthew I, and Overall CM (2015). TAILS N-terminomic and proteomic datasets of healthy human dental pulp. **Data in Brief**, 5:[542-548](#).
- 16 **Eckhard U**, Marino G, Abbey SR, Tharmarajah G, Matthew I, and Overall CM (2015). The human dental pulp proteome and N-terminome: leveraging the unexplored potential of semitryptic peptides enriched by tails to identify missing proteins in the human proteome project in underexplored tissues. **Journal of Proteome Research**, 14(9):[3568-3582](#).
- 15 Marino G, **Eckhard U**, and Overall CM (2015). Protein termini and their modifications revealed by positional proteomics. **ACS Chemical Biology**, 10(8): [1754-1764](#).
- 14 Huesgen PF, Lange PF, Rogers LD, Solis N, **Eckhard U**, Kleifeld O, Goulas T, Gomis-Rüth FX, and Overall CM (2015). LysargiNase mirrors trypsin for protein C-terminal and methylation-site identification. **Nature Methods**, 12:1, [55-58](#).
- 13 Prudova A, Serrano K, **Eckhard U**, Fortelny N, Devine DV, and Overall CM (2014). TAILS N-terminomics of human platelets reveals pervasive metalloproteinase-dependent proteolytic processing in storage. **Blood**, 124:26, [e49-60](#).
- 12 Barré O*, Dufour A*, **Eckhard U***, Kappelhoff R*, Béliveau F, Leduc R, and Overall CM (2014). Cleavage specificity analysis of six type II transmembrane serine proteases (TTSPs) using PICS with proteome-derived peptide libraries. **PLoS One**, 9:9, [e105984](#).
- 11 **Eckhard U**, Huesgen PF, Brandstetter H, and Overall CM (2014). Proteomic protease specificity profiling of clostridial collagenases reveals their intrinsic nature as dedicated degraders of collagen. **Journal of Proteomics**, 100, [102-114](#).
- 10 Marino G, Huesgen PF, **Eckhard U**, Overall CM, Schröder WP, and Funk C (2014). Family-wide characterization of Matrix Metallo-proteinases from *Arabidopsis thaliana* reveals their distinct proteolytic activity and cleavage site specificity. **Biochemical Journal**, 457:2, [335-346](#).
- 9 **Eckhard U***, Schönauer E*, and Brandstetter H (2013). Structural basis for activity regulation and substrate preference of clostridial collagenases G, H, and T. **The Journal of Biological Chemistry**. 288:28, [20184-20194](#).
- 8 Auf dem Keller U*, Prudova A*, **Eckhard U**, Fingleton B, and Overall CM (2013). Systems-level analysis of proteolytic events in increased vascular permeability and complement activation in skin inflammation. **Science Signaling**, 6:[258, rs2](#).

- 7 Kofler S, Asam C, **Eckhard U**, Wallner M, Ferreira F, and Brandstetter H (2012). Crystallographically Mapped Ligand Binding Differs in High and Low IgE Binding Isoforms of Birch Pollen Allergen Bet v 1. **Journal of Molecular Biology**, 422:1, [109-123](#).
- 6 **Eckhard U** and Brandstetter H (2011). Polycystic kidney disease-like domains of clostridial collagenases and their role in collagen recruitment. **Biological Chemistry**, 392:11, [1039-1045](#).
- 5 **Eckhard U**, Schönauer E, Nüss D, and Brandstetter H (2011). Structure of collagenase G reveals a chew-and-digest mechanism of bacterial collagenolysis. **Nature Structural & Molecular Biology**, 18:10, [1109-1114](#).
- 4 Ducka P*, **Eckhard U***, Schönauer E*, Kofler S, Gottschalk G, Brandstetter H, and Nüss D (2009). A universal strategy for high-yield production of soluble and functional clostridial collagenases in E. coli. **Applied Microbiology and Biotechnology**, 83:6. [1055-1065](#).
- 3 **Eckhard U***, Schönauer E*, Ducka P*, Briza P, Nüss D, and Brandstetter H (2009). Biochemical characterization of the catalytic domains of three different clostridial collagenases. **Biological Chemistry**, 390:1, [11-18](#).
- 2 **Eckhard U**, Nüss D, Ducka P, Schönauer E, and Brandstetter H (2008). Crystallization and preliminary X-ray characterization of the catalytic domain of collagenase G from *Clostridium histolyticum*. **Acta Crystallographica Section F** 64:5, [419-421](#).
- 1 Stolba R, Rezanka E, **Eckhard U**, and Wider G (2005). Genotyping of the LCT (T/C-13910) polymorphism on the LightCycler using fluorescent hybridisation probes. **Journal of Laboratory Medicine**, 29 (3), [194-197](#).

C.2. Research projects, grants, awards, conference participations

Post-doctoral fellowships and grants

- 02/2020–01/2023: Post-doctoral fellowship within the Beatriu de Pinós (COFUND program of the Marie Skłodowska Curie action) mobility program, Generalitat de Catalunya, Spain (144,300 EUR).
- 10/2017–09/2019: Post-doctoral fellowship from the Peter and Traudl Engelhorn Foundation (PTES), Weilheim, Germany (134,773 EUR).
- 05/2016: Transition grant from the UBC Centre for Blood Research, Vancouver, Canada. Co-funding of an external stay at the University of Waterloo, Canada, and research reagents (3,500 CAD).
- 09/2013–08/2016: Post-doctoral fellowship from the Michael Smith Foundation for Health Research (MSFHR), British Columbia, Canada (124,000 CAD).

Selected travel bursaries, academic excellence awards, and workshop participations

- 02/2020: Selected participant of the “Vienna BioCenter Cryo-EM Winter School” in Vienna, Austria.
- 11/2019: Selected participant of the “Cryo-EM Sample Preparation Workshop” in Grenoble, France.
- 06/2018: Runner-up for the Best Oral Presentation at the 22nd Swedish Conference on Macromolecular Structure and Function, Tällberg, Sweden.
- 10/2017: Poster award at the MX and Cryo-EM conference in Barcelona, Spain (500 EUR).
- 06/2016: Selected participant of the “EMBO Global Exchange Lecture Course – Structural and biophysical methods for biological macromolecules in solution” in Suwon, Korea.
- 07/2015: BCPN travel award for Max Quant Summer School in Munich (750 CAD).
- 06/2015: UBC Centre for Blood Research travel bursary: EuPA conference, Milan, Italy (1,000 CAD).
- 04/2014: Travel bursary from HUPO to attend US HUPO, Seattle, WA, USA (500 USD).
- 02/2014: ÖGMBT travel grant for the Winter School on Proteases & Inhibitors, Tiers, Italy (500 EUR).
- 09/2013: BCPN travel grant for the World HUPO Congress in Yokohama, Japan (1,500 CAD).
- 01/2013: Kurt Zopf Award to my PhD supervisor Prof. Hans Brandstetter for our Nature Structural & Molecular Biology publication (Eckhard et al. 2011, NSMB; 10,000 EUR).
- 06/2012: Selected participant of the proteomics informatics course “The Trans-Proteomic Pipeline (TPP) – MS2 proteomics validation and analysis. Seattle Proteome Center, WA, USA.
- 10/2011: ÖGMBT travel award to attend the IPS meeting in San Diego, CA, USA (500 EUR).
- 09/2010: Selected participant of the “EMBO Practical Course – Computational aspects of protein structure determination and analysis” at the EBI in Hinxton, United Kingdom.
- 08/2009: FEBS travel bursary for the IUBMB and FAOBMB congress in Shanghai, China (800 EUR).
- 04/2009: Selected participant of the “Protein crystallography course on the practical and theoretical aspects of data-collection and data-processing” at the BIOXHIT Centre in Oulu, Finland.
- 09/2008: Selected participant of the “Protein Expression, Purification and Crystallization” (PEPC6) workshop at the EMBL in Hamburg, Germany.
- 10/2007: Academic Excellence Scholarship (MSc), University of Salzburg, Austria (764 EUR).
- 05/2005: Academic Excellence Scholarship (BSc), University of Salzburg, Austria (727 EUR).