

Curriculum Vitae

Claudia Ctortecka, Ph.D.

Personal Information

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Education and Training

- 01/2018 – 12/2021 **Ph.D. Doctoral Program in Molecular Biology**, University of Vienna, AT
- 09/2015 – 12/2017 **Master of Science in Natural Sciences**, Molecular Biotechnology – Specialization: Drug Discovery, University of Applied Sciences, Vienna, AT
- 09/2012 – 07/2015 **Bachelor of Science in Natural Sciences**, Molecular Biotechnology, University of Applied Sciences, Vienna, AT

Relevant Work Experience

- 02/2025 – Present **CLP Translational Proteomics Fellow**, Group of Neil Kelleher, Northwestern University, Evanston, IL, USA
- Spatial and single cell global proteomics and proteoform technology development
 - Mechanistic evaluation of small molecule treatment effects in neurodegeneration
 - Computational intersection of bottom-up, top-down and MALDI MS entities
- 01/2022 – 01/2025 **Postdoctoral Fellow**, Group of Steven A. Carr, Broad Institute of MIT and Harvard, Cambridge, MA, USA
- Single-cell and low-input mass spectrometry-based global proteome profiling
 - Post-translational modification enrichments of small cell populations
 - Low-input HLA-I and HLA-II immunopeptidomics
- 01/2018 – 12/2021 **Ph.D. Student**, Groups of Karl Mechtler/Sasha Mendjan, IMP/IMBA – Vienna BioCenter PhD program, Vienna, AT
- Thesis: ‘Mass spectrometry based single cell proteomics’
 - Acquisition strategy to define proteome expression profiles of ultra-low input samples using mass spectrometry-based proteomics in large cohorts
 - Development of a custom data processing pipeline for multiplexed DIA measurements
 - Industry collaboration on a commercial workflow for single cell proteomics sample preparation using a piezo acoustic picoliter dispensing robot
- 01/2019 – 12/2021 **Teaching tutor** at University of Applied Sciences, Vienna, AT
- Integrative Master course in ‘Mass spectrometry’ combining lectures and laboratory classes
 - Assisted in conceptualizing the course, teaching and generation of materials
- 01/2017 – 12/2017 **Master Internship**, Group of Uwe Rix, H. Lee Moffitt Cancer Center - Department of Drug Discovery, Tampa, FL, USA
- Thesis: ‘A functional proteomics approach towards elucidating the mechanism of action of midostaurin in lung cancer’
- 01/2016 – 12/2016 **Technical Assistant**, Group of Keiryn Bennett, Research Center for Molecular Medicine of the Austrian Academy of Sciences (CeMM), Vienna, AT
- 01/2015 – 06/2015 **Bachelor Internship**, Group of Christos Samakovlis, Stockholm University, Stockholm, SE
- Thesis: ‘Emp (epithelial membrane protein) is required for functional airways in Drosophila’

Funding and Awards

2025	Best Young Investigator oral presentation, iSCMS 2025
2024	PTRC technology grant within the Clinical Proteomic Tumor Analysis Consortium by the National Cancer Institute, total volume: \$40,000
2023	SPARC (Scientific Projects to Accelerate Research and Collaboration) grant by the Broad Institute of MIT and Harvard, total volume: \$100,000
2021	Best PhD thesis award by the European Proteomics Association
2017	Marshall Plan Scholarship of the Austrian Marshall Plan Foundation (Field Report)
2015	Erasmus+ traineeship
2014	FEMtech fellowship

Leadership and Management Experience

2022 - present	Peer review activities: Nature Methods, Analytical Chemistry, Molecular and Cellular Proteomics, Journal of Proteome Research, Nature Communications, Clinical Proteomics
2020 - present	Supervision and co-supervision of multiple technical assistants (2), Master (1) and Bachelor (1) students, research associates (3) and short-term interns (2)
2019 - 2020	Student representative at the Vienna Biocenter Campus Ph.D. program
2018 - 2021	Head of organization and outreach: EuPA summer school on practical proteomics 2018; European Single Cell Proteomics Conference 2019 and the European Single Cell Proteomics Conference 2021
2018	Participation in the Single cell RNAseq course; EMBL Heidelberg, DE
2013 - 2017	Student representative at University of Applied Sciences

Memberships

2025 - present	Chair of the Single Cell Proteomics Initiative (SCI) at HUPO
2022 - 2024	Early Career Researcher and Ambassador of the SCI at HUPO
2022 - present	National Postdoctoral Association
2018 - present	American Society of Mass Spectrometry

Additional qualifications

Languages:	German (native speaker), English (fluent)
Computing skills:	R (proficient), python (beginner), Matlab (beginner)
Data analysis tools:	Biognosys software tools, Proteome Discoverer software suite, MSFragger, DIA-NN, Bruker Proteoscape computing platform, SpectrumMill, ProteoWizard tools, Skyline, Proteinaceous tools
Liquid handlers:	cellenONE, Agilent Bravo, SPT Labtech mosquito, Opentrons OT-2
Liquid chromatography:	Ultimate Dionex U3000, Agilent 1200/1260, Easy LC 1000/1200, nanoElute, nanoElute2, Evosep, Vanquish Neo
Mass Spectrometers:	LTQ Orbitrap Velos, Q Exactive Plus, Q Exactive HF, Q Exactive HFX, Orbitrap Fusion Lumos Tribrid, Orbitrap Eclipse Tribrid, Orbitrap Exploris 480 + FAIMS Pro and FAIMS Pro Duo, Orbitrap Astral, timsTOF Pro, timsTOF SCP, timsTOF HT, timsTOF Ultra, timsTOF Ultra2
Other:	Laser capture microdissection system Leica LMD7, Sony SH800 cell sorter

Selected oral presentations

2025 - iHUPO, Toronto, CA – keynote
2025 - iHUPO Single-Cell Proteomics Workshop, Toronto, CA – panelist
2025 - International Single Cell Mass Spectrometry Meeting, Chicago, IL - invited
2025 - ASMS2025; Baltimore, MD, USA - selected
2024 - EMBO Practical Course Targeted proteomics, Barcelona, ES - closing keynote

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2024 - international single cell mass spectrometry meeting, Copenhagen, DK - **invited**
2024 - International Human Proteome Organization, Dresden, DE - **keynote**
2024 - Bruker Exceed Symposium at HUPO 2024, Dresden, DE - **invited**
2024 - Evosep User Meeting, Cambridge, MA, USA - **invited**
2024 - Lunch and Learn at Whitehead Institute, Cambridge, MA, USA - **invited**
2024 - ASMS2024; Anaheim, CA, USA - **selected**
2024 - BroadE; Boston, MA, USA - **teaching course**
2023 - Broad Institute annual retreat; Boston, MA, USA - **invited**
2023 - Evosep Breakfast seminar at ASMS2023; Houston, TX, USA - **invited**
2023 - Annual meeting of ABRF; Boston, MA, USA - **keynote speaker**
2023 - HUPO Single Cell Initiative, Webinar; online event - **invited**
2022 - Single Cell Proteomics Technology Workshop; Cancun, MX – **session chair**
2022 - Evosep Webinar on Single Cell Proteomics; online event - **invited**
2022 - HUPO B/D-HPP Single Cell Day; online event – **invited** ([recording available](#))
2022 - Italian Mass Spectrometry Society – Single Cell Day; Parma, IT – **invited** ([recording available](#))
2022 - 37th Asilomar Conference on Mass Spectrometry (ASMS); Asilomar, CA, USA - **invited**
2022 - Bruker Lunch Workshop at ASBMB2022; Cambridge, MA, USA – **invited**
2022 - The 14th ASBMB 2022 Cambridge, MA, USA – **invited**
2022 - ASMS2022; Minneapolis, MN, USA – **selected**
2022 - Bruker eXceed symposium 2022; Minneapolis, MN, USA – **invited**
2021 - ASMS2021 - Cellenion; Philadelphia, IL, USA – **invited** ([recording available](#))
2021 - SCP2021; Boston, MA, USA – **invited**
2021 - ESCP2021; Vienna, AT – **invited**
2021 - MSB2021; Boston, MA, USA – **selected**
2019 - LifeTime Launch Event 2019; Berlin, DE – **selected** ([recording available](#))

Full publication list

Manakongtreecheep K.*, **Ctortecka C.***, Correa-Medero L.O., Zhu T., Lippincott I., Lawrence G.M., Howard A., Hernandez G.M., Forman C., Duggan E.C., Wilbrink M.A., Verzani E.K., Afeyan A.B., Li J., Nesvizhskii A.I., Oliveira G., Keskin D.B., Ott P.A., Clauser K.R., Bakalar M., Sarkizova S., Hacohen N.#, Carr S.A.#, Abelin J.G.#, Wu C.J.#. Sensitive detection of cancer antigens enabled by user-defined peptide libraries. *Nat Biotechnol*, 2026 Feb 09, doi: 10.1038/s41587-026-03003-9 (* equal contribution; # co-correspondence)

Deutsch E.W., Lindskog C., Budnik B., **Ctortecka C.**, Guo T., Pineau C., Zhang G., Andken M., Zheng C., Sun Z., Mudge J.M., Orchard S., Overall C.M., Packer N.H., Weintraub S.T., Roehrl M.H.A., Nice E., Van Eyk J.E., Völker U., Bandeira N., Aebersold R., Moritz R.L., Omenn G.S. The 2025 Report on the Human Proteome from the HUPO Human Proteome Project. *J Proteome Res.* 2026 Jan 5. doi: 10.1021/acs.jproteome.5c00759. PMID: 41490290.

Cutler, R*, Corveleyn L*, **Ctortecka C***, Cantlon J, Vaca SAJ, Deforce D, Vijg J, Dhaenens M, Papanastasiou M, Carr SA, Sidoli S. Mass Spectrometry-Based Profiling of Single-Cell Histone Post-Translational Modifications to Dissect Chromatin Heterogeneity. *Nat Commun.*, 2025 Dec 12. doi: 10.1038/s41467-025-66031-0. PMID: 41387402; PMCID: 12700877 (* equal contribution)

Haines M, Thorup J.R., Gohsman S., **Ctortecka C.**, Newton C., Rohrer D.C., Hostetter G., Mani D.R., Gillette M.A., Satpathy S., Carr S.A. High-throughput proteomic and phosphoproteomic analysis of formalin-fixed paraffin-embedded tissue. *Mol Cell Proteomics*, 2025 Jul, doi: 10.1016/j.mcpro.2025.101044. PMID: 40744364; PMCID: 12450643

Ctortecka C[§], Clark NM, Boyle BW, Seth A, Mani DR, Udeshi ND, Carr SA[§]. Automated single-cell proteomics providing sufficient proteome depth to study complex biology beyond cell type

classifications. *Nat Commun.* 2024 Jul 8;15(1):5707. doi: 10.1038/s41467-024-49651-w. PMID: 38977691; PMCID: PMC11231172. (§ corresponding authors)

Ctortecka C*,[§], Hartlmayr D*, Seth A, Mendjan S, Tourniaire G, Udeshi ND, Carr SA, Mechtler K. An Automated Nanowell-Array Workflow for Quantitative Multiplexed Single-Cell Proteomics Sample Preparation at High Sensitivity. *Mol Cell Proteomics.* 2023 Dec;22(12):100665. doi: 10.1016/j.mcpro.2023.100665. Epub 2023 Oct 14. PMID: 37839701; PMCID: PMC10684380. (* equal contribution; § corresponding authors)

Phulphagar KM*, **Ctortecka C***, Vaca SAJ, Klaeger S, Verzani EK, Hernandez GM, Udeshi ND, Clauser KR, Abelin JG[§], Carr SA[§]. Sensitive, High-Throughput HLA-I and HLA-II Immunopeptidomics Using Parallel Accumulation-Serial Fragmentation Mass Spectrometry. *Mol Cell Proteomics.* 2023 Jun;22(6):100563. doi: 10.1016/j.mcpro.2023.100563. Epub 2023 May 3. PMID: 37142057; PMCID: PMC10326702. (* equal contribution; § corresponding authors)

Ctortecka C, Mechtler K. The rise of single-cell proteomics. *Anal Sci Adv.* 2021 Feb 1;2(3-4):84-94. doi: 10.1002/ansa.202000152. PMID: 38716457; PMCID: PMC10989620

Ctortecka C[§], Stejskal K, Krššáková G, Mendjan S, Mechtler K[§]. Quantitative Accuracy and Precision in Multiplexed Single-Cell Proteomics. *Anal Chem.* 2022 Feb 8;94(5):2434-2443. doi: 10.1021/acs.analchem.1c04174. Epub 2021 Dec 30. PMID: 34967612; PMCID: PMC8829824. (§ corresponding authors)

Hofbauer P, Jahnel SM, Papai N, Giesshammer M, Deyett A, Schmidt C, Penc M, Tavernini K, Grdseloff N, Meledeth C, Ginistrelli LC, **Ctortecka C**, Šalic Š, Novatchkova M, Mendjan S. Cardioids reveal self-organizing principles of human cardiogenesis. *Cell.* 2021 Jun 10;184(12):3299-3317.e22. doi: 10.1016/j.cell.2021.04.034. Epub 2021 May 20. PMID: 34019794.

Ctortecka C, Krššáková G, Stejskal K, Penninger JM, Mendjan S, Mechtler K, Stadlmann J. Comparative Proteome Signatures of Trace Samples by Multiplexed Data-Independent Acquisition. *Mol Cell Proteomics.* 2022 Jan;21(1):100177. doi: 10.1016/j.mcpro.2021.100177. Epub 2021 Nov 15. PMID: 34793982; PMCID: PMC8717550.

Stadlmann J, Hudecz O, Krššáková G, **Ctortecka C**, Van Raemdonck G, Op De Beeck J, Desmet G, Penninger JM, Jacobs P, Mechtler K. Improved Sensitivity in Low-Input Proteomics Using Micropillar Array-Based Chromatography. *Anal Chem.* 2019 Nov 19;91(22):14203-14207. doi: 10.1021/acs.analchem.9b02899. Epub 2019 Oct 31. PMID: 31612716; PMCID: PMC6873107.

Sumi NJ, **Ctortecka C**, Hu Q, Bryant AT, Fang B, Remsing Rix LL, Ayaz M, Kinose F, Welsh EA, Eschrich SA, Lawrence HR, Koomen JM, Haura EB, Rix U. Divergent Polypharmacology-Driven Cellular Activity of Structurally Similar Multi-Kinase Inhibitors through Cumulative Effects on Individual Targets. *Cell Chem Biol.* 2019 Sep 19;26(9):1240-1252.e11. doi: 10.1016/j.chembiol.2019.06.003. Epub 2019 Jun 27. PMID: 31257184; PMCID: PMC6754293.

Ctortecka C, Palve V, Kuenzi BM, Fang B, Sumi NJ, Izumi V, Novakova S, Kinose F, Remsing Rix LL, Haura EB, Koomen JM, Rix U. Functional Proteomics and Deep Network Interrogation Reveal a Complex Mechanism of Action of Midostaurin in Lung Cancer Cells. *Mol Cell Proteomics.* 2018 Dec;17(12):2434-2447. doi: 10.1074/mcp.RA118.000713. Epub 2018 Sep 14. PMID: 30217950; PMCID: PMC6283294.

Weißer J, **Ctortecka C**, Busch CJ, Austin SR, Nowikovsky K, Uchida K, Binder CJ, Bennett KL. A Comprehensive Analytical Strategy To Identify Malondialdehyde-Modified Proteins and Peptides. *Anal Chem.* 2017 Apr 4;89(7):3847-3852. doi: 10.1021/acs.analchem.6b05065. Epub 2017 Mar 15. PMID: 28248083.

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Gogalic S., Hageneder S., **Ctortecka C.**, Bauch M., Kahn I, Preininger C., Sauer U., Dostalek J.; Plasmonically amplified fluorescence bioassay with microarray format; SPIE.; 2015 May, Vol. 9506, doi: 10.1117/12.2179470

[Book Chapter](#)

Hartlmayr D, **Ctortecka C**, Mayer R, Mechtler K, Seth A. Label-Free Sample Preparation for Single-Cell Proteomics, Methods Mol. Biol. 2024 June, Vol. 2817, doi: 10.1007/978-1-0716-3934-4_1