Matthew The

Group Leader Bioinformatics

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I'm a bioinformatics research group leader specializing in proteomics—the study of proteins on a large scale. My work focuses on developing smarter computational tools to make sense of complex biological data. One of my key contributions has been maintaining and improving Percolator, a machine-learning tool that helps researchers identify proteins more accurately from mass spectrometry data. Recently, my team and I developed software tools like PTMNavigator to explore protein modifications and CurveCurator to analyze drug response patterns. By combining computer science, statistics, and biology, I aim to make proteomics research more reliable and insightful. Ultimately, my goal is to help uncover new biological discoveries that could lead to better disease treatments and a deeper understanding of how life works at the molecular level.

EDUCATION / RESEARCH EXPERIENCE

2019-now **Group Leader Bioinformatics** (since 2021) / **Postdoctoral researcher**
TU Munich, Chair of Proteomics and Bioanalytics
Research group of Prof. Dr. Bernhard Kuster

- Supervising a team of 1 Postdoc and 4 PhDs, as well as 15+ student projects
- Phosphoproteomic data analysis tools for personalized drug recommendation and drug perturbation experiments
- Frontend and backend development for ProteomicsDB (SAP HANA)

2014-2018 **PhD in Bioinformatics / Open Source Developer**
KTH Royal Institute of Technology
Supervisor: Prof. Dr. Lukas Käll
Statistics and machine learning for large-scale mass spectrometry data

- Maintaining and extending the Percolator software package
- Unsupervised clustering of shotgun proteomics data
- Bayesian graphical models for protein quantification

2011-2013 **MSc in Applied Mathematics / Scientific Computing** (with distinction)
TU Berlin/KTH Royal Institute of Technology (double degree)
Focus: Numerical linear algebra, Computational biology

2007-2011 **BSc in Physics** (with distinction)
Leiden University
Focus: Quantum mechanics, Experimental physics

2007-2010 **BSc in Industrial and Applied Mathematics** (with distinction)
Delft University of Technology
Focus: Numerical methods, Partial Differential Equations

SELECTED PUBLICATIONS

peer-reviewed publications: 28 | citations: 918 | h-index: 17

Müller, J., Bayer, F. P., Wilhelm, M., Schuh, M. G., Kuster, B., & The, M. (2025). PTMNavigator: interactive visualization of differentially regulated post-translational modifications in cellular signaling pathways. ***Nature Communications***, https://doi.org/10.1038/s41467-024-55533-y.

Picciani, M., Gabriel, W., Giurcoiu, V. G., Shouman, O., Hamood, F., Lautenbacher, L., … The, M. & Wilhelm, M. (2024). Oktoberfest: Open-source spectral library generation and rescoring pipeline based on Prosit. ***Proteomics***, https://doi.org/10.1002/pmic.202300112.

Bayer, F. P., Gander, M., Kuster, B., & The, M. (2023). CurveCurator: a recalibrated F-statistic to assess, classify, and explore significance of dose–response curves. ***Nature Communications***, doi:10.1038/s41467-023-43696-z.

Zecha, J., Bayer, F. P., Wiechmann, S., Woortman, J., Berner, N., Müller, J., ... The, M., Wilhelm, M., & Kuster, B. (2023). Decrypting drug actions and protein modifications by dose-and time-resolved proteomics. ***Science***, doi:10.1126/science.ade3925.

The, M., Samaras, P., Kuster, B., & Wilhelm, M. (2022). Re-analysis of ProteomicsDB using an accurate, sensitive and scalable false discovery rate estimation approach for protein groups. ***Molecular & Cellular Proteomics***, doi:10.1016/j.mcpro.2022.100437.

Hamood, F., Bayer, F. P., Wilhelm, M., Kuster, B., & The, M. (2022). SIMSI-Transfer: Software-assisted reduction of missing values in phosphoproteomic and proteomic isobaric labeling data using tandem mass spectrum clustering. ***Molecular & Cellular Proteomics***, doi:10.1016/j.mcpro.2022.100238.

The, M., Käll, L. (2020). Focus on the spectra that matter by clustering of quantification data in shotgun proteomics. ***Nature Communications***, doi:10.1038/s41467-020-17037-3.

The, M., Käll, L. (2019). Integrated identification and quantification error probabilities for shotgun proteomics. ***Molecular & Cellular Proteomics***, doi:10.1074/mcp.RA118.001018.

The, M., MacCoss, M.J., Noble, W.S., Käll, L. (2016). Fast and accurate protein false discovery rates on large-scale proteomics data sets with Percolator 3.0. ***J. Am. Soc. Mass Spectrom.***, doi:10.1007/s13361-016-1460-7.

The, M., Käll, L. (2016). MaRaCluster: A Fragment Rarity Metric for Clustering Fragment Spectra in Shotgun Proteomics. ***J. Proteome Res.***, doi:10.1021/acs.jproteome.5b00749.

GRANTS

PI, “Tripling human Phosphorylation Site functional Annotation to enhance Individualized treatment recommendations from Clinical phosphoproteomics data (PhoSAIC)”. **DFG** (Germany) 537476536, **€221.155**, 01/2024 - 12/2026.

PI, co-applicant, “DROP^{2}AI: Drug Response Prediction using Proteomics and AI”. **BMBF** (Germany) 031L0305A, **€824,000**, 03/2023 - 02/2026.

SELECTED PRESENTATIONS

Invited speaker, “DecryptM: decrypting drug actions and protein modification by dose- and time-resolved proteomics.” Weihenstephan Bioinformatics Symposium 2022, October 20, 2022, Freising, Germany.

Keynote speaker, “Developing and maintaining tools in a multidisciplinary research team”. EuBIC-MS Winter School 2022, March 21-24, 2022, Oeiras, Portugal.

Oral Presenter, “DecryptM: decrypting drug actions and protein modification by dose- and time-resolved proteomics.” 22nd Human Proteome Organization (**HUPO)** World Congress, September 17-21, 2023, Busan, South Korea.

Oral Presenter, “Focus on the spectra that matter by clustering of quantification data in shotgun proteomics.” 28th Conference on Intelligent Systems for Molecular Biology (**ISMB**), July 13-16, 2020, Virtual Conference.

Oral Presenter, “A combined identification and quantification error model of label-free protein quantification.” 66th **ASMS** Conference on Mass Spectrometry and Allied Topics, June 3-7, 2018, San Diego, CA, USA.

Oral Presenter, “Clustering spectra based on fragment rarity.” 63rd **ASMS** Conference on Mass Spectrometry and Allied Topics, May 30-June 4, 2015, St. Louis, MO, USA.

TEACHING EXPERIENCE

2022-now	**Course responsible & developer**, “Analysis of High-Throughput Datasets for Biologists”, 3 course rounds, ~60h/round, TU Munich.
2023-now	**Instructor**, “Proteomics module DKTK Munich OncoTrack”, 2 course rounds, ~4h/round, TU Munich.
2019-2022	**Instructor**, “Intensive Course Proteomics”, 7 course rounds, ~4h/round, TU Munich.
2015-2018	**Computer exercise instructor & developer**, “Bioinformatics and Biostatistics”, 4 course rounds, ~10h/round, KTH Royal Institute of Technology.

AWARDS / GRANTS

2023	**Travel grant** for Human Proteome Organization World Congress
2018	**Travel grant** for EuBIC developers' meeting
2017	**Travel grant** for Human Proteome Organisation World Congress
2015	**Travel grant** for American Society for Mass Spectrometry Annual Conf.
2011-2013	**Erasmus Mundus Scholarship (Joint Masters Degree)** 2-year scholarship, Awarded by European Commission
2008	**Young Talent Encouragement Award for Physics** Awarded by The Royal Holland Society of Sciences and Humanities

TRAININGS

2025	Persuasive Grant Writing (Nature Masterclasses, 8h)
2025	Networking for Researchers (Nature Masterclasses, 8h)
2025	Interview and Media training (TUM Institute for LifeLong Learning, 16h)
2023-2024	TUM Research Level 2 program (TUM Institute for LifeLong Learning, 100h+)
2022	Onboarding Program for new instructors (ProLehre, 16h)
2021	Grant writing workshop (ProSciencia, 16h)
2021	Time and career management course (NaturalScience.Careers, 16h)

2020-now	Participation in 6 Postdoc101 talks (TUM ForTe, 10h+)

SKILLS

IT	Highly skilled in Python, C++, SQL, LaTeX, PHP, Git, Bash Skilled in Java, C, Scala, R, JavaScript, Go, Matlab
Language	Dutch (native), English (TOEFL:112/120), German (C1), Danish (B2), Swedish (B2)

SCIENTIFIC EVENTS / ACTIVITIES

2024	**Meeting organizer**, EuBIC organizational meeting, Barcelona.
2023	**Hackathon project lead**, “Easy-to-use interactive HTML plots collection for data exploration and web tools”, EuBIC developers' meeting, Ascona.
2023-now	**Peer-reviewed 2 grant proposals** for 2 funding agencies: Swiss National Science Foundation, Knut and Alice Wallenberg Foundation.
2018-now	**Peer-reviewed 20+ articles** for 8 scientific journals: Nature Communications, Scientific Data, Bioinformatics, Molecular and Cellular Proteomics, Journal of Proteome Research
2015	**Executive Board**, Swedish Bioinformatics Workshop.