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Mathias Wilhelm

Mathias Wilhelm

Education

08/12 – 05/17	**Doctor of Natural Sciences (Dr. rer. nat.)**, *Chair of Proteomics and Bioanalytics, Technical University of Munich, Bavaria, Germany*, In collaboration with SAP SE (Walldorf, Baden-Württemberg, Germany) and ICP (Potsdam, Brandenburg, Germany), distinction: *summa cum laude* (with highest honor)
10/09 – 10/11	**Master of Science, Informatics in the Natural Sciences**, *Bielefeld University, Bielefeld, Germany*, In collaboration with Children's Hospital/Harvard Medical School, Boston, MA, USA, final average: 1.0
10/06 – 10/09	**Bachelor of Science, Bioinformatics and Genome Research**, *Bielefeld University, Bielefeld, Germany*, final average: 1.5

Work and Research Experiences

03/21 – current	**Tenure Track Assistant Professor**, *Computational Mass Spectrometry, Technical University of Munich, Bavaria, Germany*
08/19 – current	**Co-founder of MSAID GmbH**, *Garching, Bavaria, Germany*
05/17 – 02/21	**Group leader bioinformatics at Technical University of Munich**, *Chair of Proteomics and Bioanalytics, Technical University of Munich, Bavaria, Germany*
06/14 – current	**Co-founder of OmicScouts GmbH**, *Freising, Bavaria, Germany*
11/15 – 05/17	**PhD position at Technical University of Munich**, *Chair of Proteomics and Bioanalytics, Technical University of Munich, Bavaria, Germany*
08/12 – 10/15	**PhD position at SAP SE**, *Walldorf, Baden-Württemberg, Germany*
02/12 – 07/12	**Research assistant at Boston Children's Hospital/Harvard Medical School**, *Boston, MA, USA*

Awards and Honors

2023	**Nominated for the Bavarian-wide award of good teaching of the "Bayerisches Staatsministerium für Wissenschaft und Kunst" (StMWK)**
2023	**Winner of the GC LS TUM Graduate Council Supervisory Award**
04/2017	**Dissertation Award by the DGPF (Deutsche Gesellschaft für Proteomforschung; German Society for Proteome Research)**
07/2015	**Invited participant of the 65th Lindau Nobel Laureate Meeting**
2009/2011	**Top of the class of the Bachelor Program Bioinformatics and Genome Research and Master Program Informatics in the Natural Sciences**

Grants

2023-2028	**ORIGIN - Learning Isoform Fingerprints to Discover the Molecular Diversity of Life**, *PI*, ERC Starting Grant
2023-2026	**Drop2AI - Drug Response Prediction using Proteomics and AI**, *PI*, BMBF/CompLS

2023-2025 **Improving chemical proteomics with AI**, *PI*, Industry R&D project

2023-2023 **DL4DNPS - Deep Learning for de novo peptide sequencing**, *PI*, MDSI Seed Fund

2022-2026 **The Proteomes that Feed the World – International Graduate School**, *PI*, Elite Network Bavaria

2021-2024 **PROTrEIN - Computational Proteomics Training European Innovative Network**, *PI*, EU (No 956148)

2019-2021 **DIAS - Data integration, Analytics and Services in ProteomicsDB**, *Project Leader/PI*, BMBF/CompLS

2018-2023 **EPIC-XS - European Proteomics Infrastructure Consortium providing Access**, *Project Leader*, EU project (No 823839)

2014-2019 **ProteomicsDB - Proteomics Analytics, Multi Omics Integration and Drug Sensitivity and Resistance**, *Project Leader*, third-party funding

2014-2019 **ProteomeTools - Translating the human proteome into molecular and digital tools for drug discovery, personalized medicine and life science research**, *Project Leader*, BMBF (No 031L0008A)

Reviewing

Appointments, *Professorship Functional Phytometabolomics at TUM, Conceptualization of Bioinformatics of Infection Prevention at TUM, Recognition of Distinction at Oxford, apl. Prof. at Ruhr-Universität Bochum, Habilitation at the Federal Institute for Materials Research and Testing*

Grant reviews, *ERC Consolidator grant, Emmy-Noether, DFG, DAAD*

Journal reviews, *Analytical Chemistry, Bioinformatics, BMC Bioinformatics, Briefings in Bioinformatics, Chromatography A, Cell Discovery, Cell Host Microbe, Cell reports methods, Expert Review Proteomics, Journal of chemical information and modeling, Journal of Chromatography A, Journal of Proteome Research, Journal of Proteomics, Molecular and Cellular Proteomics, Molecular Systems Biology, Nature Biotechnology, Nature Communications, Nature Medicine, Nature Protocols, Nature, NeurIPS, Science, PLOS One, Scientific Data*, 20 per year on average

Teaching

2016-2023 **Doctoral candidates**, *Supervisor of 9 PhD candidates and Co-supervisor of 8 PhD candidates*

2012-2023 **Student theses**, *>30 bachelor, >15 internship, >20 master*

2012-2023 **BSc level teaching @ TUM**, *Intensive Course Proteomics (Molecular Biotechnology), Fachspezifische Qualifikation Life Sciences (Biology), Hot Topics (Biology), Advanced Bioinformatics (Bioinformatics), Problem-based learning (Bioinformatics), Applied Data Science (Biology Life Sciences)*

2021-2023 **MSc level teaching @ TUM**, *Systems BioMedicine (Bioinformatics), Masterpraktikum (Bioinformatics), Fortgeschrittenen-Praktikum Bioinformatik (Bioinformatics), Interdisciplinary Projects (Informatics)*

2008-2012 **BSc level teaching @ Bielefeld**, *Computer Science Preparation Course (Bioinformatics), Advanced Java Programming (Bioinformatics)*

Academic Engagement

2023-current **Conference organization**, *Assiting organization of DGMS 2024 in Freising, Co-organizer Dagstuhl Computational Proteomics Seminar (2025)*

2023-2029 **Member of the examination board**, *Bioinformatics study course*

2020-current **Editorial Board Member**, *Molecular and Cellular Proteomics*

2007-2011 **Member of the student council**, *Faculty of Technology, Bielefeld University*,
Member of the “Faculty committee for research and young academics“, “Committee for the appointment of tutors“, “Committee for the master program Bioinformatics and Genome research“

2009-2010 **Member of the committee for the reorganization of all informatics bachelor study programs**, Faculty of Technology, Bielefeld University

2008-2010 **Elected member of the faculty conference and committee for habilitations**, Faculty of Technology, Bielefeld University

Research highlights

2021 - 2023 **>2.2 M research funding acquired (incl. ERC starting grant)**

2021 - current **>50 talks at national and international conferences, symposia, and workshops**

>60 publications in peer-reviewed international journals, *7705 citations, h-index of 33, and i10-index of 48*, according to Google Scholar

Top 5 Publications

* Authors contributed equally. $^{\#}$ Corresponding author.

2021 June
Nature Communications
Deep learning boosts sensitivity of mass spectrometry-based immunopeptidomics,
Wilhelm M$^{*\#}$, Zolg DP*, Graber M, Gessulat S, Schmidt T, Schnatbaum K, Schwencke-Westphal C, Seifert P, de Andrade Krätzig N, Zerweck J, Knaute T, Bräunlein E, Samaras P, Lautenbacher L, Klaeger S, Wenschuh H, Rad R, Delanghe B, Huhmer A, Carr SA, Clauser KR, Krackhardt AM, Reimer U, Kuster B$^{\#}$
Journal Impact Factor: 17.7 – Citations according to Google Scholar: 100 – doi: 10.1038/s41467-021-23713-9

2019 May
Nat Methods
PROSIT: Proteome-wide prediction of peptide tandem mass spectra by deep learning,
Gessulat S*, Schmidt T*, Zolg DP, Samaras P, Schnatbaum K, Zerweck J, Knaute T, Rechenberger J, Delanghe B, Huhmer A, Reimer U, Ehrlich HC, Aiche S, Kuster B$^{\#}$, Wilhelm M$^{\#}$
Journal Impact Factor: 26.9 – Citations according to Google Scholar: 583 – doi: 10.1038/s41592-019-0426-7

2018 Jan
Nucleic Acids Res
ProteomicsDB,
Schmidt T*, Samaras P*, Frejno M, Gessulat S, Barnert M, Kienegger H, Krcmar H, Schlegl J, Ehrlich HC, Aiche S, Kuster B$^{\#}$, Wilhelm M$^{\#}$
Journal Impact Factor: 10.1 – Citations according to Google Scholar: 214 – doi: 10.1093/nar/gkx1029

2017 Dec
Science
The target landscape of clinical kinase drugs,
Klaeger S*, Heinzlmeir S*, Wilhelm M*, Polzer H, Vick B, Koenig PA, Reinecke M, Ruprecht B, Petzoldt S, Meng C, Zecha J, Reiter K, Qiao H, Helm D, Koch H, Schoof M, Canevari G, Casale E, Depaolini SR, Feuchtinger A, Wu Z, Schmidt T, Rueckert L, Becker W, Huenges J, Garz AK, Gohlke B, Zolg DP, Kayser G, Vooder T, Preissner R, Hahne H, Tõnisson N, Kramer K, Götze K, Bassermann F, Schlegl J, Ehrlich HC, Aiche S, Walch A, Greif PA, Schneider S, Felder ER, Ruland J, Médard G, Jeremias I, Spiekermann K, Kuster B
Journal Impact Factor: 37.2 – Citations according to Google Scholar: 715 – doi: 10.1126/science.aan4368

2017 Jan
Nat Methods
Building ProteomeTools based on a complete synthetic human proteome,
Zolg DP*, Wilhelm M*, Schnatbaum K, Zerweck J, Knaute T, Delanghe B, Bailey DJ, Gessulat S, Ehrlich HC, Weininger M, Yu P, Schlegl J, Kramer K, Schmidt T, Kusebauch U, Deutsch EW, Aebersold R, Moritz RL, Wenschuh H, Moehring T, Aiche S, Huhmer A, Reimer U, Kuster B
Journal Impact Factor: 25.3 – Citations according to Google Scholar: 208 – doi: 10.1038/nmeth.4153

2014 May
Nature
Mass-spectrometry-based draft of the human proteome,
Wilhelm M*, Schlegl J*, Hahne H*, Moghaddas Gholami A*, Lieberenz M, Savitski MM, Ziegler E, Butzmann L, Gessulat S, Marx H, Mathieson T, Lemeer S, Schnatbaum K, Reimer U, Wenschuh H, Mollenhauer M, Slotta-Huspenina J, Boese JH, Bantscheff M, Gerstmair A, Faerber F, Kuster B
Journal Impact Factor: 42.3 – Citations according to Google Scholar: 2028 – doi: 10.1038/nature13319

Invited Talks

2024 (2) **Australia Bioinformatics Community, Lorne Proteomics**

2023 (5) **EuBIC-MS Developers Meeting, 2nd Winter School Ghent, BSPR-EuPA, Joint 11th AOHUPO and 7th AOAPO Congress, Annual Danish Bioinformatics Conference**

2022 (8) **The Pioneers of Omics webinar, Lorentz Center Workshop on Proteomics and Machine Learning, EPIC-XS/EuPA webinar Computational Proteomics, 14th International Symposium on Mass Spectrometry in the Health and Life Sciences, 2nd HUPO-HIPP summer school, ACS Measurement Science Symposium, MHC-bound peptides as candidate T cell epitopes, London Proteomics Discussion Group**

2021 (6)	**Proteomics Workshop at IIT (Bombay), 6th HPP 2.0 webinar, PROTrEIN Summer School 2021, de.NBI Summer School 2021, MSCORESYS summer school, EMBO PRactical Course on Targeted Proteomics**
2020 (2)	**Personalized and Precision Medicine International Conference (Munich, Germany); Proteomics in Cell Biology and Disease Mechanisms (Wellcome Genome Campus, UK)**, *Deep learning to assist the identification pf neoantigens, Deep learning to assist the identification of neoantigens*
2019 (7)	**EuBIC WinterSchool (Zakopane, Poland); 13th International Symposium on Mass Spectrometry in the Health and Life Sciences (San Francisco, CA, USA); de.NBI Summerschool (Bio)Data Science (Gatersleben, Germany); Workshop (Taipei, Taiwan); EMBO course - Targeted Proteomics (Barcelona, Spain); Seminar (Bochum, Germany), ProteomeDiscoverer User Meeting (Bremen, Germany)**
2018 (7)	**TUM/LMU quantitative biology symposium (Munich, Germany); Webinar for Biognosys (Zurich, Switzerland); Treffpunkt Bioinformatik, Big Data for Genomics and Medicine(Berlin, Germany); Advanced Mass Spectrometry Seminar (Freising, Germany); EMBO Practical Course: Targeted Proteomics (Barcelona, Spain); Quantitative Proteomics - Strategic Workflow and Data Analysis (Taipei, Taiwan); Proteome Discoverer Users Meeting (Bremen, Germany)**
2017 (1)	**EMBL-EBI Industry workshop on Bio-pharmaceutical opportunities in proteomics (Cambridge, England)**
2015 (1)	**Thermo Scientific User Meeting(Munich, Germany)**
2014 (2)	**10th Siena Meeting (Siena, Italy); Thermo Scientific User Meeting (Berlin, Germany)**

Publication list

2024 Jan
Nature Communications
Deep learning-driven fragment ion series classification enables highly precise and sensitive de novo peptide sequencing,
Klaproth-Andrade D, Hingerl J, Bruns Y, Smith NH, Träuble J, Wilhelm M, Gagneur J
doi: 10.1038/s41467-023-44323-7

2023 Oct
Nature Chemical Biology
Chemical proteomics reveals the target landscape of 1,000 kinase inhibitors,
Reinecke M, Brear P, Vornholz L, Berger BT, Seefried F, Wilhelm S, Samaras P, Gyenis L, Litchfield DW, Medard G, Müller S, Ruland J, Hyvönen M, Wilhelm M, Kuster B
doi: 10.1038/s41589-023-01459-3

2023 Sep
Analytical Chemistry
Assessment and Prediction of Human Proteotypic Peptide Stability for Proteomics Quantification,
Chiva C, Elhamraoui Z, Sole A, Serret M, Wilhelm M, Sabido E
doi: 10.1021/acs.analchem.3c02269

2023 Sep
Proteomics
Oktoberfest: Open-source spectral library generation and rescoring pipeline based on Prosit,
Picciani M, Gabriel W, Giurcoiu VG, Shouman O, Hamood F, Lautenbacher L, Jensen CB, Müller J, Kalhor M, Soleymaniniya A, Kuster B, The M, Wilhelm M
doi: 10.1002/pmic.202300112

2023 Aug
Nature Communications
Proteogenomic analysis reveals RNA as a source for tumor-agnostic neoantigen identification,
Tretter C, Krätzig NA, Pecoraro M, Lange S, Seifert P, von Frankenberg C, Untch J, Zuleger G, Wilhelm M, Zolg DP, Dreyer FS, Bräunlein E, Engleitner T, Uhrig S, Boxberg M, Steiger K, Slotta-Huspenina J, Ochsenreither S, von Bubnoff N, Bauer S, Boerries M, Jost PJ, Schenck K, Dresing I, Bassermann F, Friess H, Reim D, Grützmann K, Pfütze K, Klink B, Schröck E, Haller B, Kuster B, Mann M, Weichert W, Fröhling S, Rad R, Hiltensperger M, Krackhardt AM
doi: 10.1038/s41467-023-39570-7

2023 Jul
Science
Decrypting drug actions and protein modifications by dose-and time-resolved proteomics,
Zecha J, Bayer FP, Wiechmann S, Woortman J, Berner N, Müller J, Schneider A, Kramer K, Abril-Gil M, Hopf T, Reichart L, Chen L, Hansen FM, Lechner S, Samaras P, Eckert S, Lautenbacher L, Reinecke M, Hamood F, Prokofeva P, Vornholz L, Falcomata C, Dorsch M, Schröder A, Venhuizen A, Wilhelm S, Medard G, Stoehr G, Ruland J, Grüner BM, Saur D, Buchner M, Ruprecht B, Hahne H, The M, Wilhelm M, Kuster B
doi: 10.1126/science.ade3925

2023 Mar
Lebensmittelchemie
The Proteomes that Feed the World,
Piller A, Brajkovic S, Abbas Q, Andrade-Galan P, Aydin E, Corongiu G, Giordano G, Haljiti G, Hein S, Pan J, Picciani M, Ramirez V, Röhrl P, Saylan CC, Soleymaniniya A, Urzinger S, Würstl L, Avramova V, Dawid C, Frishman D, Gutjahr C, Hückelhoven R, Ludwig C, Pauling J, Schön CC, Schwechheimer C, Wilhelm M, Wilhelm S, Poppenberger B, Küster B
doi: 10.1002/lemi.202352025

2023 Feb
Jounal of Proteome Research
Toward an integrated machine learning model of a proteomics experiment,
Neely BA, Dorfer V, Martens L, Bludau I, Bouwmeester R, Degroeve S, Deutsch EW, Gessulat S, Käll L, Palczynski P, Payne SH, Rehfeldt TG, Schmidt T, Schwämmle V, Uszkoreit J, Vizcaino JA, Wilhelm M, Palmblad M
doi: 10.1021/acs.jproteome.2c00711

2022 Dec
Mol Cell Proteomics
Reanalysis of ProteomicsDB Using an Accurate, Sensitive, and Scalable False Discovery Rate Estimation Approach for Protein Groups,
The M, Samaras P, Kuster B, Wilhelm M
doi: 10.1016/j.mcpro.2022.100437

2022 Oct
Proteomics
Predicting fragment intensities and retention time of iTRAQ-and TMTPro-labeled peptides with Prosit-TMT,
Gabriel W, Giurcoiu V, Lautenbacher L, Wilhelm M
doi: 10.1002/pmic.202100257

2022 Sep
Nature Chemical Biology
Target deconvolution of HDAC pharmacopoeia reveals MBLAC2 as common off-target,
Lechner S, Malgapo MIP, Grätz C, Steimbach RR, Baron A, Rüther P, Nadal S, Stumpf C, Loos C, Ku X, Prokofeva P, Lautenbacher L, Heimburg T, Würf V, Meng C, Wilhelm M, Sippl W, Kleigrewe K, Pauling JK, Kramer K, Miller AK, Pfaffl MW, Linder ME, Kuster B, Medard G
doi: 10.1038/s41589-022-01015-5

2022 Sep ***Mol Cell Proteomics***	**SIMSI-Transfer: Software-assisted reduction of missing values in phosphoproteomic and proteomic isobaric labeling data using tandem mass spectrum clustering**, *Hamood F, Bayer FP, Wilhelm M, Kuster B* doi: 10.1016/j.mcpro.2022.100238
2022 Jul **Nature Methods**	**Mass spectrometry-based draft of the mouse proteome**, *Giansanti P, Samaras P, Bian Y, Meng C, Coluccio A, Frejno M, Jakubowsky H, Dobiasch S, Hazarika RR, Rechenberger J, Calzada-Wack J, Krumm J, Mueller S, Lee CY, Wimberger N, Lautenbacher L, Hassan Z, Chang YZ, Falcomata C, Bayer FP, Bärthel S, Schmidt T, Rad R, Combs SE, The M, Johannes F, Saur D, Hrabe de Angelis M, Wilhelm M, Schneider G, Kuster B* doi: 10.1038/s41592-022-01526-y
2022 May ***Analytical Chemistry***	**Prosit-TMT: deep learning boosts identification of TMT-labeled peptides**, *Gabriel W, The M, Zolg DP, Bayer FP, Shouman O, Lautenbacher L, Schnatbaum K, Zerweck J, Knaute T, Delanghe B, Huhmer A, Wenschuh H, Reimer U, Medard G, Kuster B, Wilhelm M* doi: 10.1021/acs.analchem.1c05435
2022 Apr ***Journal of Proteome Research***	**Prosit Transformer: A transformer for Prediction of MS2 Spectrum Intensities**, *Ekvall M, Truong P, Gabriel W, Wilhelm M, Käll L* doi: 10.1021/acs.jproteome.1c00870
2022 Mar ***Cell Reports***	**High temporal resolution proteome and phosphoproteome profiling of stem cell-derived hepatocyte development**, *Krumm J, Sekine K, Samaras P, Brazovskaja A, Breunig M, Yasui R, Kleger A, Taniguchi H, Wilhelm M, Treutlein B, Camp JG, Kuster B* doi: 10.1016/j.celrep.2022.110604
2022 Feb ***Journal of Proteome Research***	**Interpretation of the DOME Recommendations for Machine Learning in Proteomics and Metabolomics**, *Palmblad[#] M, Böcker S, Degroeve S, Kohlbacher O, Käll L, Noble WS, Wilhelm M* doi: 10.1021/acs.jproteome.1c00900
2022 Jan ***Nature communications***	**Linking post-translational modifications and protein turnover by site-resolved protein turnover profiling**, *Zecha J, Gabriel W, Spallek R, Chang YC, Mergner J, Wilhelm M, Bassermann F, Kuster B* doi: 10.1038/s41467-021-27639-0
2020 Jan ***Nucleic Acids Research***	**ProteomicsDB: toward a FAIR open-source resource for life-science research**, *Lautenbacher L, Samaras P, Muller J, Grafberger A, Shraideh M, Rank J, Fuchs ST, Schmidt TK, The M, Dallago C, Wittges H, Rost B, Krcmar H, Kuster B, Wilhelm M* doi: 10.1093/nar/gkab1026
2022 Sep ***NeurIPS***	**PROSPECT: Labeled Tandem Mass Spectrometry Dataset for Machine Learning in Proteomics**, *Shouman O, Gabriel W, Giurcoiu VG, Sternlicht V, Wilhelm M* doi: TBA
2021 Oct ***Nature Communications***	**A proteomics sample metadata representation for multiomics integration and big data analysis**, *Dai C, Füllgrabe A, Pfeuffer J, Solovyeva EM, Deng J, Moreno P, Kamatchinathan S, Kundu DJ, George N, Fexova S, Grüning B, Christine Föll M, Griss J, Vaudel M, Audain E, Locard-Paulet M, Turewicz M, Eisenacher M, Uszkoreit J, Van Den Bossche T, Schwämmle V, Webel H, Schulze S, Bouyssie D, Jayaram S, Duggineni VK, Samaras P, Wilhelm M, Choi M, Wang M, Kohlbacher O, Brazma A, Papatheodorou I, Bandeira N, Deutsch EW, Vizcaíno JA, Bai M, Sachsenberg T, Levitsky LI, Perez-Riverol Y* doi: 10.1038/s41467-021-26111-3
2021 Jun ***Analytical Chemistry***	**Identification of 7 000–9 000 Proteins from Cell Lines and Tissues by Single-Shot Microflow LC–MS/MS**, *Bian Y, The M, Giansanti P, Mergner J, Zheng R, Wilhelm M, Boychenko A, Kuster B* doi: 10.1021/acs.analchem.1c00738
2021 Jun ***Nature communications***	**Deep learning boosts sensitivity of mass spectrometry-based immunopeptidomics**, *Wilhelm[*#] M, Zolg DP[*], Graber M, GessulatS, Schmidt T, Schnatbaum K, Schwencke-Westphal C, Seifert P, de Andrade Krätzig N, Zerweck J, Knaute T, Bräunlein E, Samaras P, Lautenbacher L, Klaeger S, Wenschuh H, Rad R, Delanghe B, Huhmer A, Carr SA, Clauser KR, Krackhardt AM, Reimer U, Kuster B* doi: 10.1038/s41467-021-23713-9

2021 Jun
Nature methods
The emerging landscape of single-molecule protein sequencing technologies,
Alfaro JA, Bohländer P, Dai M, Filius M, Howard CJ, Van Kooten XF, Ohayon S, Pomorski A, Schmid S, Aksimentiev A, Anslyn EV, Bedran G, Cao C, Chinappi M, Coyaud E, Dekker C, Dittmar G, Drachman N, Eelkema R, Goodlett D, Hentz S, Kalathiya U, Kelleher NL, Kelly RT, Kelman Z, Kim SH, Kuster B, Rodriguez-Larrea D, Lindsay S, Maglia G, Marcotte EM, Marino JP, Masselon C, Mayer M, Samaras P, Sarthak K, Sepiashvili L, Stein D, Wanunu M, Wilhelm M, Yin P, MellerA, Joo C
doi: 10.1038/s41592-021-01143-1

2021 May
Journal of proteome research
Universal spectrum explorer: a standalone (web-) application for cross-resource spectrum comparison,
Schmidt T, Samaras P, Dorfer V, Panse C, Kockmann T, Bichmann L, Puyvelde BV, Perez-Riverol Y, Deutsch EW, Kuster B, Wilhelm M
doi: 10.1021/acs.jproteome.1c00096

2021 Jan
Molecular and Cellular Proteomics
Spectral prediction features as a solution for the search space size problem in proteogenomics,
Verbruggen S, Gessulat S, Gabriels R, Matsaroki A, Van de Voorde H, Kuster B, Degroeve S, Martens L, Criekinge WV, Wilhelm M, Menschaert G
doi: 10.1016/j.mcpro.2021.100076

2020 Oct
Scientific Data
Proteomic and transcriptomic profiling of aerial organ development in Arabidopsis,
Mergner J, Frejno M, Messerer M, Lang D, Samaras P, Wilhelm M, Mayer KFX, Schwechheimer C, Kuster B
doi: 10.1038/s41597-020-00678-w

2020 July
Nat Commun
Proteome activity landscapes of tumor cell lines determine drug responses,
Frejno M, Meng C*, Ruprecht B*, Oellerich T, Scheich S, Kleigrewe K, Samaras P, Helm D, Hogrebe A, Mergner J, Zecha J, Heinzlmeir S, Wilhelm M, Dorn J, Hans-Kvasnicka HM, Serve H, Weichert W, Kuster B*
doi: 10.1038/s41467-020-17336-9

2020 May
Nat Methods
Meltome Atlas - thermal proteome stability across the tree of life,
Jarzab A, Kurzawa N*, Hopf T*, Moerch M, Zecha J, Leijten N, Musiol E, Stoehr G, Daly C, Schmidt T, Mergner J, Spanier B, Angelov A, Werner T, Bantscheff M, Wilhelm M, Klingenspor M, Lemeer S, Liebl W, Hahne H#, Savitski MM#, Kuster B#*
doi: 10.1038/s41592-020-0801-4

2020 Mar
Nat Commun
Generating high-quality libraries for DIA-MS with empirically-corrected peptide predictions,
Searle BC#, Swearingen KE, Barnes CA, Schmidt T, Gessulat S, Kuster B, Wilhelm M
doi: 10.1038/s41467-020-15346-1

2020 Mar
Nature
Mass-spectrometry-based draft of the Arabidopsis proteome,
Mergner J, Frejno M, List M, Papacek M, Chaudhary A, Chen X, Samaras P, Richter S, Shikata H, Messerer M, Lang D, Altmann A, Cyprys P, Zolg DP, Mathieson T, Bantscheff M, Dawid C, Dunkel A, Hofmann T, Sprunck S, Falter-Braun P, Mayer K, Jurgens G, Wilhelm M, Baumbach J, Schneitz K, Grill E, Schwechheimer C and Kuster B
doi: 10.1038/s41586-020-2094-2

2019 Dec
Book: Target Discovery and Validation
Kinobeads: A Chemical Proteomic Approach for Kinase Inhibitor Selectivity Profiling and Target Discovery,
Reinecke M, Heinzlmeir S, Wilhelm M, Medard G, Klaeger S, Kuster B
doi: 10.1002/9783527818242.ch4

2019 Oct
Nucleic Acids Res
ProteomicsDB: A multi-omics and multi-organism resource for life science research,
Samaras P, Schmidt T, Martin F, Gessulat S, Reinecke M, Jarzab A, Zecha J, Mergner J, Giansanti P, Ehrlich HC, Aiche S, Rank J, Kienegger H, Krcmar H, Kuster B#, Wilhelm M#
doi: 10.1093/nar/gkz974

2019 May
Nat Methods
PROSIT: Proteome-wide prediction of peptide tandem mass spectra by deep learning,
Gessulat S, Schmidt T*, Zolg DP, Samaras P, Schnatbaum K, Zerweck J, Knaute T, Rechenberger J, Delanghe B, Huhmer A, Reimer U, Ehrlich HC, Aiche S, Kuster B#, Wilhelm M#*
doi: 10.1038/s41592-019-0426-7

2019 Apr
Mol Cell Proteomics
PROTEOFORMER 2.0: further developments in the ribosome profiling-assisted proteogenomic hunt for new proteoforms,
Verbruggen S, Ndah E, Criekinge WV, Gessulat S, Kuster B, Wilhelm M, Damme PV, and Menschaert G
Journal Impact Factor: 6.5 – doi: 10.1074/mcp.RA118.001218

2019 Mar
ACS Chem Biol
Chemoproteomic selectivity profiling of PIKK and PI3K kinase inhibitors,
Reinecke M*, Ruprecht B*, Poser S, Petzoldt S, Wilhelm M, Heinzlmeir S, Kuster B#, Médard G#
doi: 10.1021/acschembio.8b01020

2019 Feb
J Proteome Res
CiRCus: A framework to enable classification of complex high-throughput experiments,
Seefried F, Schmidt T, Reinecke M, Heinzlmeir S, Kuster B, Wilhelm M
doi: 10.1021/acs.jproteome.8b00724

2019 Feb
Mol Syst Biol
A deep proteome and transcriptome abundance atlas of 29 healthy human tissues,
Wang D*, Eraslan B*, Wieland T, Hallström BM, Hopf T, Zolg DP, Zecha J, Asplund A, Li L, Meng C, Frejno M, Schmidt T, Schnatbaum K, Wilhelm M, Pontén F, Uhlén M, Gagneur J, Hahne H, Kuster B
doi: 10.15252/msb.20188503

2019 Jan
Proteomes
Challenges in Clinical Metaproteomics Highlighted by the Analysis of Acute Leukemia Patients with Gut Colonization by Multidrug-Resistant Enterobacteriaceae,
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