

# Lukas Reiter

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

7,898  
citations

201674

27  
h-index

330143

37  
g-index

42  
all docs

42  
docs citations

42  
times ranked

9387  
citing authors

#	ARTICLE	IF	CITATIONS
1	MhcVizPipe: A Quality Control Software for Rapid Assessment of Small- to Large-Scale Immunopeptidome Datasets. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100178.	3.8	9
2	Different syngeneic tumors show distinctive intrinsic tumor-immunity and mechanisms of actions (MOA) of anti-PD-1 treatment. <i>Scientific Reports</i> , 2022, 12, 3278.	3.3	25
3	Mechanistic Insights into a CDK9 Inhibitor Via Orthogonal Proteomics Methods. <i>ACS Chemical Biology</i> , 2022, 17, 54-67.	3.4	6
4	Biomarker Candidates for Tumors Identified from Deep-Profiled Plasma Stem Predominantly from the Low Abundant Area. <i>Journal of Proteome Research</i> , 2022, 21, 1718-1735.	3.7	21
5	Compounds activating VCP D1 ATPase enhance both autophagic and proteasomal neurotoxic protein clearance. <i>Nature Communications</i> , 2022, 13, .	12.8	11
6	Systematic Comparison of Strategies for the Enrichment of Lysosomes by Data Independent Acquisition. <i>Journal of Proteome Research</i> , 2020, 19, 371-381.	3.7	25
7	A machine learning-based chemoproteomic approach to identify drug targets and binding sites in complex proteomes. <i>Nature Communications</i> , 2020, 11, 4200.	12.8	78
8	MassIVE.quant: a community resource of quantitative mass spectrometry-based proteomics datasets. <i>Nature Methods</i> , 2020, 17, 981-984.	19.0	66
9	Isoform-resolved correlation analysis between $\langle \text{scp} \rangle \text{mRNA} \langle / \text{scp} \rangle$ abundance regulation and protein level degradation. <i>Molecular Systems Biology</i> , 2020, 16, e9170.	7.2	42
10	Rapid and site-specific deep phosphoproteome profiling by data-independent acquisition without the need for spectral libraries. <i>Nature Communications</i> , 2020, 11, 787.	12.8	251
11	Revealing Dynamic Protein Acetylation across Subcellular Compartments. <i>Journal of Proteome Research</i> , 2020, 19, 2404-2418.	3.7	26
12	Combining Precursor and Fragment Information for Improved Detection of Differential Abundance in Data Independent Acquisition. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 421-430.	3.8	40
13	Surpassing 10 <sup>6</sup> identified and quantified proteins in a single run by optimizing current LC-MS instrumentation and data analysis strategy. <i>Molecular Omics</i> , 2019, 15, 348-360.	2.8	137
14	Analysis of 1508 Plasma Samples by Capillary-Flow Data-Independent Acquisition Profiles Proteomics of Weight Loss and Maintenance. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1242-1254.	3.8	162
15	Comparison of Protein Quantification in a Complex Background by DIA and TMT Workflows with Fixed Instrument Time. <i>Journal of Proteome Research</i> , 2019, 18, 1340-1351.	3.7	107
16	Classification of mouse B cell types using surfaceome proteotype maps. <i>Nature Communications</i> , 2019, 10, 5734.	12.8	31
17	Data-independent Acquisition Improves Quantitative Cross-linking Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 786-795.	3.8	31
18	Cost-effective generation of precise label-free quantitative proteomes in high-throughput by microLC and data-independent acquisition. <i>Scientific Reports</i> , 2018, 8, 4346.	3.3	66

#	ARTICLE	IF	CITATIONS
19	New targeted approaches for the quantification of data-independent acquisition mass spectrometry. <i>Proteomics</i> , 2017, 17, 1700021.	2.2	49
20	Optimization of Experimental Parameters in Data-Independent Mass Spectrometry Significantly Increases Depth and Reproducibility of Results. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2296-2309.	3.8	349
21	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. <i>Nature Methods</i> , 2017, 14, 921-927.	19.0	189
22	A multicenter study benchmarks software tools for label-free proteome quantification. <i>Nature Biotechnology</i> , 2016, 34, 1130-1136.	17.5	321
23	High-precision iRT prediction in the targeted analysis of data-independent acquisition and its impact on identification and quantitation. <i>Proteomics</i> , 2016, 16, 2246-2256.	2.2	114
24	Reproducible and Consistent Quantification of the <i>Saccharomyces cerevisiae</i> Proteome by SWATH-mass spectrometry *. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 739-749.	3.8	158
25	Quantification of SAHA-Dependent Changes in Histone Modifications Using Data-Independent Acquisition Mass Spectrometry. <i>Journal of Proteome Research</i> , 2015, 14, 3252-3262.	3.7	45
26	Extending the Limits of Quantitative Proteome Profiling with Data-Independent Acquisition and Application to Acetaminophen-Treated Three-Dimensional Liver Microtissues. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1400-1410.	3.8	873
27	Advancing Urinary Protein Biomarker Discovery by Data-Independent Acquisition on a Quadrupole-Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2015, 14, 4752-4762.	3.7	109
28	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. <i>Nature</i> , 2013, 494, 266-270.	27.8	307
29	RIP-chip-SRM—a new combinatorial large-scale approach identifies a set of translationally regulated bantam/miR-58 targets in <i>C. elegans</i> . <i>Genome Research</i> , 2012, 22, 1360-1371.	5.5	18
30	Using $\langle RT \rangle$ , a normalized retention time for more targeted measurement of peptides. <i>Proteomics</i> , 2012, 12, 1111-1121.	2.2	517
31	Targeted Data Extraction of the MS/MS Spectra Generated by Data-independent Acquisition: A New Concept for Consistent and Accurate Proteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.016717.	3.8	2,285
32	Comprehensive quantitative analysis of central carbon and amino acid metabolism in <i>Saccharomyces cerevisiae</i> under multiple conditions by targeted proteomics. <i>Molecular Systems Biology</i> , 2011, 7, 464.	7.2	105
33	mProphet: automated data processing and statistical validation for large-scale SRM experiments. <i>Nature Methods</i> , 2011, 8, 430-435.	19.0	481
34	A quantitative targeted proteomics approach to validate predicted microRNA targets in <i>C. elegans</i> . <i>Nature Methods</i> , 2010, 7, 837-842.	19.0	80
35	Protein Identification False Discovery Rates for Very Large Proteomics Data Sets Generated by Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2405-2417.	3.8	282