

# Lindsay K Pino

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8070607/publications.pdf>

Version: 2024-02-01

12  
papers

1,244  
citations

933447

10  
h-index

1199594

12  
g-index

15  
all docs

15  
docs citations

15  
times ranked

2028  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Skyline ecosystem: Informatics for quantitative mass spectrometry proteomics. <i>Mass Spectrometry Reviews</i> , 2020, 39, 229-244.	5.4	469
2	Chromatogram libraries improve peptide detection and quantification by data independent acquisition mass spectrometry. <i>Nature Communications</i> , 2018, 9, 5128.	12.8	337
3	Acquiring and Analyzing Data Independent Acquisition Proteomics Experiments without Spectrum Libraries. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1088-1103.	3.8	164
4	Reduced-representation Phosphosignatures Measured by Quantitative Targeted MS Capture Cellular States and Enable Large-scale Comparison of Drug-induced Phenotypes. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1622-1641.	3.8	92
5	Matrix-Matched Calibration Curves for Assessing Analytical Figures of Merit in Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 1147-1153.	3.7	41
6	Improved SILAC Quantification with Data-Independent Acquisition to Investigate Bortezomib-Induced Protein Degradation. <i>Journal of Proteome Research</i> , 2021, 20, 1918-1927.	3.7	36
7	Calibration Using a Single-Point External Reference Material Harmonizes Quantitative Mass Spectrometry Proteomics Data between Platforms and Laboratories. <i>Analytical Chemistry</i> , 2018, 90, 13112-13117.	6.5	30
8	Emerging mass spectrometry-based proteomics methodologies for novel biomedical applications. <i>Biochemical Society Transactions</i> , 2020, 48, 1953-1966.	3.4	22
9	Highly Parallel Quantification and Compartment Localization of Transcription Factors and Nuclear Proteins. <i>Cell Reports</i> , 2020, 30, 2463-2471.e5.	6.4	20
10	Nonlinear Regression Improves Accuracy of Characterization of Multiplexed Mass Spectrometric Assays. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 913-924.	3.8	18
11	2018 YPIC Challenge: A Case Study in Characterizing an Unknown Protein Sample. <i>Journal of Proteome Research</i> , 2019, 18, 3936-3943.	3.7	7
12	Proximity labeling and other novel mass spectrometric approaches for spatiotemporal protein dynamics. <i>Expert Review of Proteomics</i> , 2021, 18, 757-765.	3.0	6