

Lindsay K Pino

List of Publications by Year in descending order

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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 | 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 |
| 2 | 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 |
| 3 | The Skyline ecosystem: Informatics for quantitative mass spectrometry proteomics. <i>Mass Spectrometry Reviews</i> , 2020, 39, 229-244. | 5.4 | 469 |
| 4 | 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 |
| 5 | Highly Parallel Quantification and Compartment Localization of Transcription Factors and Nuclear Proteins. <i>Cell Reports</i> , 2020, 30, 2463-2471.e5. | 6.4 | 20 |
| 6 | Acquiring and Analyzing Data Independent Acquisition Proteomics Experiments without Spectrum Libraries. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1088-1103. | 3.8 | 164 |
| 7 | Emerging mass spectrometry-based proteomics methodologies for novel biomedical applications. <i>Biochemical Society Transactions</i> , 2020, 48, 1953-1966. | 3.4 | 22 |
| 8 | 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 |
| 9 | Nonlinear Regression Improves Accuracy of Characterization of Multiplexed Mass Spectrometric Assays. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 913-924. | 3.8 | 18 |
| 10 | Chromatogram libraries improve peptide detection and quantification by data independent acquisition mass spectrometry. <i>Nature Communications</i> , 2018, 9, 5128. | 12.8 | 337 |
| 11 | 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 |
| 12 | 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 |