

Lin Lin

List of Publications by Year in descending order

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16
papers

619
citations

840776

11
h-index

996975

15
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16
docs citations

16
times ranked

1075
citing authors

#	ARTICLE	IF	CITATIONS
1	Advancing serum peptidomic profiling by data-independent acquisition for clear-cell renal cell carcinoma detection and biomarker discovery. <i>Journal of Proteomics</i> , 2020, 215, 103671.	2.4	15
2	Application of a Pseudotargeted MS Method for the Quantification of Glycated Hemoglobin for the Improved Diagnosis of Diabetes Mellitus. <i>Analytical Chemistry</i> , 2020, 92, 3237-3245.	6.5	8
3	Spatial-Resolution Cell Type Proteome Profiling of Cancer Tissue by Fully Integrated Proteomics Technology. <i>Analytical Chemistry</i> , 2018, 90, 5879-5886.	6.5	35
4	High throughput and accurate serum proteome profiling by integrated sample preparation technology and single-run data independent mass spectrometry analysis. <i>Journal of Proteomics</i> , 2018, 174, 9-16.	2.4	66
5	Fast quantitative urinary proteomic profiling workflow for biomarker discovery in kidney cancer. <i>Clinical Proteomics</i> , 2018, 15, 42.	2.1	16
6	Mixed-mode ion exchange-based integrated proteomics technology for fast and deep plasma proteome profiling. <i>Journal of Chromatography A</i> , 2018, 1564, 76-84.	3.7	28
7	SH2 Domains as Affinity Reagents for Phosphotyrosine Protein Enrichment and Proteomic Analysis. <i>Methods in Molecular Biology</i> , 2017, 1555, 395-406.	0.9	3
8	3D-SISPROT: A simple and integrated spintip-based protein digestion and three-dimensional peptide fractionation technology for deep proteome profiling. <i>Journal of Chromatography A</i> , 2017, 1498, 207-214.	3.7	26
9	Identification, Quantification, and Site Localization of Protein Posttranslational Modifications via Mass Spectrometry-Based Proteomics. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 345-382.	1.6	51
10	Holistic metabonomic profiling of urine affords potential early diagnosis for bladder and kidney cancers. <i>Metabolomics</i> , 2013, 9, 119-129.	3.0	23
11	LC-MS based serum metabolic profiling for genitourinary cancer classification and cancer type-specific biomarker discovery. <i>Proteomics</i> , 2012, 12, 2238-2246.	2.2	67
12	Peptidome workflow of serum and urine samples for biomarker discovery. <i>Analytical Methods</i> , 2011, 3, 773.	2.7	11
13	LC-MS based serum metabonomic analysis for renal cell carcinoma diagnosis, staging, and biomarker discovery. <i>Journal of Proteome Research</i> , 2011, 10, 1396-1405.	3.7	135
14	A Comparative Study of Elution Gradients in UPLC-TOF-MS-Based Metabonomics Research. <i>Chromatographia</i> , 2010, 72, 807-813.	1.3	2
15	Direct infusion mass spectrometry or liquid chromatography mass spectrometry for human metabonomics? A serum metabonomic study of kidney cancer. <i>Analyst</i> , 2010, 135, 2970.	3.5	133
16	Improved profiling of low molecular weight serum proteome for gastric carcinoma by data-independent acquisition. <i>Analytical and Bioanalytical Chemistry</i> , 0, , .	3.7	0