

Chang-Cai Liu

List of Publications by Year in descending order

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16
papers

189
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1163117

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1058476

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331
citing authors

#	ARTICLE	IF	CITATIONS
1	Simultaneous solvent extraction and quantification of eleven amine compounds related to Chemical Weapon Convention in soils via hydrophilic interaction liquid chromatography-tandem mass spectrometry. <i>Journal of Chromatography A</i> , 2022, 1671, 462990.	3.7	2
2	Quantitative detection of ricin in beverages using trypsin/Glu-C tandem digestion coupled with ultra-high-pressure liquid chromatography-tandem mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 585-597.	3.7	7
3	Direct Acetonitrile-Assisted Trypsin Digestion Method Combined with LC-MS/MS-Targeted Peptide Analysis for Unambiguous Identification of Intact Ricin. <i>Journal of Proteome Research</i> , 2021, 20, 369-380.	3.7	9
4	Rapid Differential Detection of Abrin Isoforms by an Acetonitrile- and Ultrasound-Assisted On-Bead Trypsin Digestion Coupled with LC-MS/MS Analysis. <i>Toxins</i> , 2021, 13, 358.	3.4	2
5	LC-HRMS Screening and Identification of Novel Peptide Markers of Ricin Based on Multiple Protease Digestion Strategies. <i>Toxins</i> , 2019, 11, 393.	3.4	5
6	A sensitive quantification approach for detection of HETE-CP adduct after benzyl chloroformate derivatization using ultra-high-pressure liquid chromatography tandem mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 3405-3415.	3.7	11
7	Simultaneous quantification of four metabolites of sulfur mustard in urine samples by ultra-high performance liquid chromatography-tandem mass spectrometry after solid phase extraction. <i>Journal of Chromatography A</i> , 2017, 1492, 41-48.	3.7	18
8	Simultaneous quantification of soman and VX adducts to butyrylcholinesterase, their aged methylphosphonic acid adduct and butyrylcholinesterase in plasma using an off-column procainamide-gel separation method combined with UHPLC-MS/MS. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016, 1036-1037, 57-65.	2.3	16
9	Large-scale comparative phosphoprotein analysis of maize seedling leaves during greening. <i>Planta</i> , 2016, 243, 501-517.	3.2	15
10	In Silico Identification and Characterization of N-Terminal Acetyltransferase Genes of Poplar (<i>Populus trichocarpa</i>). <i>International Journal of Molecular Sciences</i> , 2014, 15, 1852-1864.	4.1	8
11	Label-free quantitative proteomics analysis of dormant terminal buds of poplar. <i>Molecular Biology Reports</i> , 2013, 40, 4529-4542.	2.3	12
12	Identification and Analysis of the Acetylated Status of Poplar Proteins Reveals Analogous N-Terminal Protein Processing Mechanisms with Other Eukaryotes. <i>PLoS ONE</i> , 2013, 8, e58681.	2.5	7
13	Genome-Wide Identification and in Silico Analysis of Poplar Peptide Deformylases. <i>International Journal of Molecular Sciences</i> , 2012, 13, 5112-5124.	4.1	4
14	Genome-wide Identification and Characterization of a Dehydrin Gene Family in Poplar (<i>Populus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	1.8	34
15	Identification and analysis of phosphorylation status of proteins in dormant terminal buds of poplar. <i>BMC Plant Biology</i> , 2011, 11, 158.	3.6	22
16	Phosphoproteomic identification and phylogenetic analysis of ribosomal P-proteins in <i>Populus</i> dormant terminal buds. <i>Planta</i> , 2010, 231, 571-581.	3.2	17