

Zheng-Jiang Zhu

List of Publications by Year in descending order

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75
papers

7,170
citations

66234

42
h-index

74018

75
g-index

81
all docs

81
docs citations

81
times ranked

12811
citing authors

#	ARTICLE	IF	CITATIONS
1	An accelerated workflow for untargeted metabolomics using the METLIN database. <i>Nature Biotechnology</i> , 2012, 30, 826-828.	9.4	472
2	A lipidome atlas in MS-DIAL 4. <i>Nature Biotechnology</i> , 2020, 38, 1159-1163.	9.4	424
3	Liquid chromatography quadrupole time-of-flight mass spectrometry characterization of metabolites guided by the METLIN database. <i>Nature Protocols</i> , 2013, 8, 451-460.	5.5	379
4	Effect of Surface Charge on the Uptake and Distribution of Gold Nanoparticles in Four Plant Species. <i>Environmental Science & Technology</i> , 2012, 46, 12391-12398.	4.6	332
5	Colorimetric Bacteria Sensing Using a Supramolecular Enzymeâ€“Nanoparticle Biosensor. <i>Journal of the American Chemical Society</i> , 2011, 133, 9650-9653.	6.6	317
6	Entrapment of Hydrophobic Drugs in Nanoparticle Monolayers with Efficient Release into Cancer Cells. <i>Journal of the American Chemical Society</i> , 2009, 131, 1360-1361.	6.6	305
7	Recognition-mediated activation of therapeutic gold nanoparticles inside living cells. <i>Nature Chemistry</i> , 2010, 2, 962-966.	6.6	295
8	Toward â€“Omic Scale Metabolite Profiling: A Dual Separationâ€“Mass Spectrometry Approach for Coverage of Lipid and Central Carbon Metabolism. <i>Analytical Chemistry</i> , 2013, 85, 6876-6884.	3.2	242
9	The Role of Surface Functionality on Acute Cytotoxicity, ROS Generation and DNA Damage by Cationic Gold Nanoparticles. <i>Small</i> , 2010, 6, 2246-2249.	5.2	232
10	Metabolic reaction network-based recursive metabolite annotation for untargeted metabolomics. <i>Nature Communications</i> , 2019, 10, 1516.	5.8	218
11	Ion mobility collision cross-section atlas for known and unknown metabolite annotation in untargeted metabolomics. <i>Nature Communications</i> , 2020, 11, 4334.	5.8	194
12	Intracellular Delivery of a Membrane-Impermeable Enzyme in Active Form Using Functionalized Gold Nanoparticles. <i>Journal of the American Chemical Society</i> , 2010, 132, 2642-2645.	6.6	176
13	Direct Delivery of Functional Proteins and Enzymes to the Cytosol Using Nanoparticle-Stabilized Nanocapsules. <i>ACS Nano</i> , 2013, 7, 6667-6673.	7.3	176
14	Large-Scale Prediction of Collision Cross-Section Values for Metabolites in Ion Mobility-Mass Spectrometry. <i>Analytical Chemistry</i> , 2016, 88, 11084-11091.	3.2	173
15	LipidCCS: Prediction of Collision Cross-Section Values for Lipids with High Precision To Support Ion Mobilityâ€“Mass Spectrometry-Based Lipidomics. <i>Analytical Chemistry</i> , 2017, 89, 9559-9566.	3.2	171
16	Serum metabolomics for early diagnosis of esophageal squamous cell carcinoma by UHPLC-QTOF/MS. <i>Metabolomics</i> , 2016, 12, 1.	1.4	141
17	Normalization and integration of large-scale metabolomics data using support vector regression. <i>Metabolomics</i> , 2016, 12, 1.	1.4	134
18	Multiplexed Screening of Cellular Uptake of Gold Nanoparticles Using Laser Desorption/Ionization Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2008, 130, 14139-14143.	6.6	126

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19	Stability of quantum dots in live cells. <i>Nature Chemistry</i> , 2011, 3, 963-968.	6.6	121
20	Drug Delivery Using Nanoparticle-Stabilized Nanocapsules. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 477-481.	7.2	114
21	Surface Properties Dictate Uptake, Distribution, Excretion, and Toxicity of Nanoparticles in Fish. <i>Small</i> , 2010, 6, 2261-2265.	5.2	113
22	Epigenetic drift of H3K27me3 in aging links glycolysis to healthy longevity in <i>Drosophila</i> . <i>ELife</i> , 2018, 7, .	2.8	113
23	An integrated targeted metabolomic platform for high-throughput metabolite profiling and automated data processing. <i>Metabolomics</i> , 2015, 11, 1575-1586.	1.4	112
24	One-Step Immobilization of Glucose Oxidase in a Silica Matrix on a Pt Electrode by an Electrochemically Induced Sol-Gel Process. <i>Langmuir</i> , 2007, 23, 11896-11900.	1.6	106
25	Advancing untargeted metabolomics using data-independent acquisition mass spectrometry technology. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 4349-4357.	1.9	102
26	SWATHtoMRM: Development of High-Coverage Targeted Metabolomics Method Using SWATH Technology for Biomarker Discovery. <i>Analytical Chemistry</i> , 2018, 90, 4062-4070.	3.2	99
27	Degradation of HK2 by chaperone-mediated autophagy promotes metabolic catastrophe and cell death. <i>Journal of Cell Biology</i> , 2015, 210, 705-716.	2.3	95
28	Daily Oscillation of the Excitation-Inhibition Balance in Visual Cortical Circuits. <i>Neuron</i> , 2020, 105, 621-629.e4.	3.8	94
29	MetDIA: Targeted Metabolite Extraction of Multiplexed MS/MS Spectra Generated by Data-Independent Acquisition. <i>Analytical Chemistry</i> , 2016, 88, 8757-8764.	3.2	93
30	A vitamin-C-derived DNA modification catalysed by an algal TET homologue. <i>Nature</i> , 2019, 569, 581-585.	13.7	72
31	The Interplay of Monolayer Structure and Serum Protein Interactions on the Cellular Uptake of Gold Nanoparticles. <i>Small</i> , 2012, 8, 2659-2663.	5.2	71
32	MetCCS predictor: a web server for predicting collision cross-section values of metabolites in ion mobility-mass spectrometry based metabolomics. <i>Bioinformatics</i> , 2017, 33, 2235-2237.	1.8	67
33	Absolute quantitative lipidomics reveals lipidome-wide alterations in aging brain. <i>Metabolomics</i> , 2018, 14, 5.	1.4	66
34	Advancing the large-scale CCS database for metabolomics and lipidomics at the machine-learning era. <i>Current Opinion in Chemical Biology</i> , 2018, 42, 34-41.	2.8	64
35	Laser desorption/ionization mass spectrometry analysis of monolayer-protected gold nanoparticles. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 396, 1025-1035.	1.9	62
36	Arteriovenous Blood Metabolomics: A Readout of Intra-Tissue Metabostasis. <i>Scientific Reports</i> , 2015, 5, 12757.	1.6	62

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37	Comprehensive metabolomics identified lipid peroxidation as a prominent feature in human plasma of patients with coronary heart diseases. <i>Redox Biology</i> , 2017, 12, 899-907.	3.9	59
38	LipidIMMS Analyzer: integrating multi-dimensional information to support lipid identification in ion mobility-mass spectrometry based lipidomics. <i>Bioinformatics</i> , 2019, 35, 698-700.	1.8	55
39	CLOCK Acetylates ASS1 to Drive Circadian Rhythm of Ureagenesis. <i>Molecular Cell</i> , 2017, 68, 198-209.e6.	4.5	53
40	The emerging role of ion mobility-mass spectrometry in lipidomics to facilitate lipid separation and identification. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 116, 332-339.	5.8	53
41	Engineered nanoparticle surfaces for improved mass spectrometric analyses. <i>Analyst</i> , 2009, 134, 2183.	1.7	52
42	Comprehensive bioimaging with fluorinated nanoparticles using breathable liquids. <i>Nature Communications</i> , 2015, 6, 5998.	5.8	50
43	Serum Metabolomics Identifies Dysregulated Pathways and Potential Metabolic Biomarkers for Hyperuricemia and Gout. <i>Arthritis and Rheumatology</i> , 2021, 73, 1738-1748.	2.9	49
44	DecoMetDIA: Deconvolution of Multiplexed MS/MS Spectra for Metabolite Identification in SWATH-MS-Based Untargeted Metabolomics. <i>Analytical Chemistry</i> , 2019, 91, 11897-11904.	3.2	43
45	Predicting the pathological response to neoadjuvant chemoradiation using untargeted metabolomics in locally advanced rectal cancer. <i>Radiotherapy and Oncology</i> , 2018, 128, 548-556.	0.3	42
46	Determination of the Intracellular Stability of Gold Nanoparticle Monolayers Using Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 4321-4326.	3.2	40
47	Regulating exocytosis of nanoparticles via host-guest chemistry. <i>Organic and Biomolecular Chemistry</i> , 2015, 13, 2474-2479.	1.5	40
48	WaveICA: A novel algorithm to remove batch effects for large-scale untargeted metabolomics data based on wavelet analysis. <i>Analytica Chimica Acta</i> , 2019, 1061, 60-69.	2.6	40
49	Development of a Correlative Strategy To Discover Colorectal Tumor Tissue Derived Metabolite Biomarkers in Plasma Using Untargeted Metabolomics. <i>Analytical Chemistry</i> , 2019, 91, 2401-2408.	3.2	36
50	NormAE: Deep Adversarial Learning Model to Remove Batch Effects in Liquid Chromatography Mass Spectrometry-Based Metabolomics Data. <i>Analytical Chemistry</i> , 2020, 92, 5082-5090.	3.2	32
51	The Application of Ion Mobility-Mass Spectrometry in Untargeted Metabolomics: from Separation to Identification. <i>Journal of Analysis and Testing</i> , 2020, 4, 163-174.	2.5	31
52	Ion mobility-based sterolomics reveals spatially and temporally distinctive sterol lipids in the mouse brain. <i>Nature Communications</i> , 2021, 12, 4343.	5.8	31
53	Different regions of synaptic vesicle membrane regulate VAMP2 conformation for the SNARE assembly. <i>Nature Communications</i> , 2020, 11, 1531.	5.8	30
54	MetFlow: an interactive and integrated workflow for metabolomics data cleaning and differential metabolite discovery. <i>Bioinformatics</i> , 2019, 35, 2870-2872.	1.8	29

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55	Characterization of surface ligands on functionalized magnetic nanoparticles using laser desorption/ionization mass spectrometry (LDI-MS). <i>Nanoscale</i> , 2013, 5, 5063.	2.8	25
56	Development of a combined strategy for accurate lipid structural identification and quantification in ion-mobility mass spectrometry based untargeted lipidomics. <i>Analytica Chimica Acta</i> , 2020, 1136, 115-124.	2.6	23
57	NEK1-mediated retromer trafficking promotes blood-brain barrier integrity by regulating glucose metabolism and RIPK1 activation. <i>Nature Communications</i> , 2021, 12, 4826.	5.8	20
58	Metabolomics approach for predicting response to neoadjuvant chemotherapy for colorectal cancer. <i>Metabolomics</i> , 2018, 14, 110.	1.4	19
59	Exploring the protective effects of Danqi Tongmai tablet on acute myocardial ischemia rats by comprehensive metabolomics profiling. <i>Phytomedicine</i> , 2020, 74, 152918.	2.3	17
60	Proteome-Wide Analysis of N-Glycosylation Stoichiometry Using SWATH Technology. <i>Journal of Proteome Research</i> , 2017, 16, 3830-3840.	1.8	15
61	metID: an R package for automatable compound annotation for LC-MS-based data. <i>Bioinformatics</i> , 2022, 38, 568-569.	1.8	15
62	A High-Throughput Targeted Metabolomics Workflow for the Detection of 200 Polar Metabolites in Central Carbon Metabolism. <i>Methods in Molecular Biology</i> , 2019, 1859, 263-274.	0.4	13
63	Multi-dimensional characterization and identification of sterols in untargeted LC-MS analysis using all ion fragmentation technology. <i>Analytica Chimica Acta</i> , 2021, 1142, 108-117.	2.6	12
64	Trapped ion mobility spectrometry-mass spectrometry improves the coverage and accuracy of four-dimensional untargeted lipidomics. <i>Analytica Chimica Acta</i> , 2022, 1210, 339886.	2.6	10
65	WaveICA 2.0: a novel batch effect removal method for untargeted metabolomics data without using batch information. <i>Metabolomics</i> , 2021, 17, 87.	1.4	9
66	Global stable-isotope tracing metabolomics reveals system-wide metabolic alternations in aging <i>Drosophila</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	9
67	Discovery of novel 1,2,3,4-tetrahydrobenzo[4, 5]thieno[2, 3- c]pyridine derivatives as potent and selective CYP17 inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2017, 132, 157-172.	2.6	8
68	A serum metabolomics analysis reveals a panel of screening metabolic biomarkers for esophageal squamous cell carcinoma. <i>Clinical and Translational Medicine</i> , 2021, 11, e419.	1.7	7
69	Subacute Toxicity Study of Nicotinamide Mononucleotide via Oral Administration. <i>Frontiers in Pharmacology</i> , 2020, 11, 604404.	1.6	7
70	RIPK1 regulates starvation resistance by modulating aspartate catabolism. <i>Nature Communications</i> , 2021, 12, 6144.	5.8	6
71	Overview of Tandem Mass Spectral and Metabolite Databases for Metabolite Identification in Metabolomics. <i>Methods in Molecular Biology</i> , 2020, 2104, 139-148.	0.4	5
72	The Use of LipidIMMS Analyzer for Lipid Identification in Ion Mobility-Mass Spectrometry-Based Untargeted Lipidomics. <i>Methods in Molecular Biology</i> , 2020, 2084, 269-282.	0.4	4

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73	Aspirin Reshapes Acetylomes in Inflammatory and Cancer Cells via CoA-Dependent and CoA-Independent Pathways. <i>Journal of Proteome Research</i> , 2020, 19, 962-972.	1.8	2
74	Stable-isotope Labeled Metabolic Analysis in <i>Drosophila melanogaster</i> : from Experimental Setup to Data Analysis. <i>Bio-protocol</i> , 2018, 8, e3015.	0.2	2
75	Degradation of HK2 by chaperone-mediated autophagy promotes metabolic catastrophe and cell death. <i>Journal of Experimental Medicine</i> , 2015, 212, 212100IA79.	4.2	0