Zheng-Jiang Zhu

List of Publications by Year
in descending order

75	7,170	66343	74163
papers	citations	42 h-index	75 g-index

81	81	81	12811
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	metID: an R package for automatable compound annotation for LCâ^'MS-based data. Bioinformatics, 2022, 38, 568-569.	4.1	15
2	Trapped ion mobility spectrometry-mass spectrometry improves the coverage and accuracy of four-dimensional untargeted lipidomics. Analytica Chimica Acta, 2022, 1210, 339886.	5.4	10
3	Global stable-isotope tracing metabolomics reveals system-wide metabolic alternations in aging Drosophila. Nature Communications, 2022, 13, .	12.8	9
4	Multi-dimensional characterization and identification of sterols in untargeted LC-MS analysis using all ion fragmentation technology. Analytica Chimica Acta, 2021, 1142, 108-117.	5.4	12
5	A serum metabolomics analysis reveals a panel of screening metabolic biomarkers for esophageal squamous cell carcinoma. Clinical and Translational Medicine, 2021, 11, e419.	4.0	7
6	Ion mobility-based sterolomics reveals spatially and temporally distinctive sterol lipids in the mouse brain. Nature Communications, 2021, 12, 4343.	12.8	31
7	NEK1-mediated retromer trafficking promotes bloodâ€"brain barrier integrity by regulating glucose metabolism and RIPK1 activation. Nature Communications, 2021, 12, 4826.	12.8	20
8	Serum Metabolomics Identifies Dysregulated Pathways and Potential Metabolic Biomarkers for Hyperuricemia and Gout. Arthritis and Rheumatology, 2021, 73, 1738-1748.	5.6	49
9	WaveICA 2.0: a novel batch effect removal method for untargeted metabolomics data without using batch information. Metabolomics, 2021, 17, 87.	3.0	9
10	RIPK1 regulates starvation resistance by modulating aspartate catabolism. Nature Communications, 2021, 12, 6144.	12.8	6
11	Exploring the protective effects of Danqi Tongmai tablet on acute myocardial ischemia rats by comprehensive metabolomics profiling. Phytomedicine, 2020, 74, 152918.	5.3	17
12	Aspirin Reshapes Acetylomes in Inflammatory and Cancer Cells via CoA-Dependent and CoA-Independent Pathways. Journal of Proteome Research, 2020, 19, 962-972.	3.7	2
13	Daily Oscillation of the Excitation-Inhibition Balance in Visual Cortical Circuits. Neuron, 2020, 105, 621-629.e4.	8.1	94
14	Development of a combined strategy for accurate lipid structural identification and quantification in ion-mobility mass spectrometry based untargeted lipidomics. Analytica Chimica Acta, 2020, 1136, 115-124.	5.4	23
15	Ion mobility collision cross-section atlas for known and unknown metabolite annotation in untargeted metabolomics. Nature Communications, 2020, 11, 4334.	12.8	194
16	The Application of Ion Mobility-Mass Spectrometry in Untargeted Metabolomics: from Separation to Identification. Journal of Analysis and Testing, 2020, 4, 163-174.	5.1	31
17	A lipidome atlas in MS-DIAL 4. Nature Biotechnology, 2020, 38, 1159-1163.	17.5	424
18	Different regions of synaptic vesicle membrane regulate VAMP2 conformation for the SNARE assembly. Nature Communications, 2020, 11, 1531.	12.8	30

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19	NormAE: Deep Adversarial Learning Model to Remove Batch Effects in Liquid Chromatography Mass Spectrometry-Based Metabolomics Data. Analytical Chemistry, 2020, 92, 5082-5090.	6.5	32
20	The Use of LipidIMMS Analyzer for Lipid Identification in Ion Mobility-Mass Spectrometry-Based Untargeted Lipidomics. Methods in Molecular Biology, 2020, 2084, 269-282.	0.9	4
21	Subacute Toxicity Study of Nicotinamide Mononucleotide via Oral Administration. Frontiers in Pharmacology, 2020, 11, 604404.	3.5	7
22	Overview of Tandem Mass Spectral and Metabolite Databases for Metabolite Identification in Metabolomics. Methods in Molecular Biology, 2020, 2104, 139-148.	0.9	5
23	LipidIMMS Analyzer: integrating multi-dimensional information to support lipid identification in ion mobilityâ€”mass spectrometry based lipidomics. Bioinformatics, 2019, 35, 698-700.	4.1	55
24	DecoMetDIA: Deconvolution of Multiplexed MS/MS Spectra for Metabolite Identification in SWATH-MS-Based Untargeted Metabolomics. Analytical Chemistry, 2019, 91, 11897-11904.	6.5	43
25	A vitamin-C-derived DNA modification catalysed by an algal TET homologue. Nature, 2019, 569, 581-585.	27.8	72
26	The emerging role of ion mobility-mass spectrometry in lipidomics to facilitate lipid separation and identification. TrAC - Trends in Analytical Chemistry, 2019, 116, 332-339.	11.4	53
27	Advancing untargeted metabolomics using data-independent acquisition mass spectrometry technology. Analytical and Bioanalytical Chemistry, 2019, 411, 4349-4357.	3.7	102
28	Metabolic reaction network-based recursive metabolite annotation for untargeted metabolomics. Nature Communications, 2019, 10, 1516.	12.8	218
29	WaveICA: A novel algorithm to remove batch effects for large-scale untargeted metabolomics data based on wavelet analysis. Analytica Chimica Acta, 2019, 1061, 60-69.	5.4	40
30	Development of a Correlative Strategy To Discover Colorectal Tumor Tissue Derived Metabolite Biomarkers in Plasma Using Untargeted Metabolomics. Analytical Chemistry, 2019, 91, 2401-2408.	6.5	36
31	MetFlow: an interactive and integrated workflow for metabolomics data cleaning and differential metabolite discovery. Bioinformatics, 2019, 35, 2870-2872.	4.1	29
32	A High-Throughput Targeted Metabolomics Workflow for the Detection of 200 Polar Metabolites in Central Carbon Metabolism. Methods in Molecular Biology, 2019, 1859, 263-274.	0.9	13
33	SWATHtoMRM: Development of High-Coverage Targeted Metabolomics Method Using SWATH Technology for Biomarker Discovery. Analytical Chemistry, 2018, 90, 4062-4070.	6.5	99
34	Absolute quantitative lipidomics reveals lipidome-wide alterations in aging brain. Metabolomics, 2018, 14, 5.	3.0	66
35	Advancing the large-scale CCS database for metabolomics and lipidomics at the machine-learning era. Current Opinion in Chemical Biology, 2018, 42, 34-41.	6.1	64
36	Predicting the pathological response to neoadjuvant chemoradiation using untargeted metabolomics in locally advanced rectal cancer. Radiotherapy and Oncology, 2018, 128, 548-556.	0.6	42

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37	Epigenetic drift of H3K27me3 in aging links glycolysis to healthy longevity in Drosophila. ELife, 2018, 7, .	6.0	113
38	Metabolomics approach for predicting response to neoadjuvant chemotherapy for colorectal cancer. Metabolomics, 2018, 14, 110.	3.0	19
39	Stable-isotope Labeled Metabolic Analysis in Drosophila melanogaster: from Experimental Setup to Data Analysis. Bio-protocol, 2018, 8, e3015.	0.4	2
40	Comprehensive metabolomics identified lipid peroxidation as a prominent feature in human plasma of patients with coronary heart diseases. Redox Biology, 2017, 12, 899-907.	9.0	59
41	MetCCS predictor: a web server for predicting collision cross-section values of metabolites in ion mobility-mass spectrometry based metabolomics. Bioinformatics, 2017, 33, 2235-2237.	4.1	67
42	Discovery of novel 1,2,3,4-tetrahydrobenzo[4, 5]thieno[2, 3- c]pyridine derivatives as potent and selective CYP17 inhibitors. European Journal of Medicinal Chemistry, 2017, 132, 157-172.	5.5	8
43	CLOCK Acetylates ASS1 to Drive Circadian Rhythm of Ureagenesis. Molecular Cell, 2017, 68, 198-209.e6.	9.7	53
44	Proteome-Wide Analysis of N-Glycosylation Stoichiometry Using SWATH Technology. Journal of Proteome Research, 2017, 16, 3830-3840.	3.7	15
45	LipidCCS: Prediction of Collision Cross-Section Values for Lipids with High Precision To Support Ion Mobilityâ€“Mass Spectrometry-Based Lipidomics. Analytical Chemistry, 2017, 89, 9559-9566.	6.5	171
46	MetDIA: Targeted Metabolite Extraction of Multiplexed MS/MS Spectra Generated by Data-Independent Acquisition. Analytical Chemistry, 2016, 88, 8757-8764.	6.5	93
47	Large-Scale Prediction of Collision Cross-Section Values for Metabolites in Ion Mobility-Mass Spectrometry. Analytical Chemistry, 2016, 88, 11084-11091.	6.5	173
48	Serum metabolomics for early diagnosis of esophageal squamous cell carcinoma by UHPLC-QTOF/MS. Metabolomics, 2016, 12, 1.	3.0	141
49	Normalization and integration of large-scale metabolomics data using support vector regression. Metabolomics, 2016, 12, 1.	3.0	134
50	Arteriovenous Blood Metabolomics: A Readout of Intra-Tissue Metabostasis. Scientific Reports, 2015, 5, 12757.	3.3	62
51	Comprehensive bioimaging with fluorinated nanoparticles using breathable liquids. Nature Communications, 2015, 6, 5998.	12.8	50
52	An integrated targeted metabolomic platform for high-throughput metabolite profiling and automated data processing. Metabolomics, 2015, 11, 1575-1586.	3.0	112
53	Degradation of HK2 by chaperone-mediated autophagy promotes metabolic catastrophe and cell death. Journal of Cell Biology, 2015, 210, 705-716.	5.2	95
54	Regulating exocytosis of nanoparticles via hostâ€“guest chemistry. Organic and Biomolecular Chemistry, 2015, 13, 2474-2479.	2.8	40

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55	Degradation of HK2 by chaperone-mediated autophagy promotes metabolic catastrophe and cell death. Journal of Experimental Medicine, 2015, 212, 21210OlA79.	8.5	0
56	Toward â€˜Omic Scale Metabolite Profiling: A Dual Separationâ€“Mass Spectrometry Approach for Coverage of Lipid and Central Carbon Metabolism. Analytical Chemistry, 2013, 85, 6876-6884.	6.5	242
57	Direct Delivery of Functional Proteins and Enzymes to the Cytosol Using Nanoparticle-Stabilized Nanocapsules. ACS Nano, 2013, 7, 6667-6673.	14.6	176
58	Liquid chromatography quadrupole time-of-flight mass spectrometry characterization of metabolites guided by the METLIN database. Nature Protocols, 2013, 8, 451-460.	12.0	379
59	Characterization of surface ligands on functionalized magnetic nanoparticles using laser desorption/ionization mass spectrometry (LDI-MS). Nanoscale, 2013, 5, 5063.	5.6	25
60	Effect of Surface Charge on the Uptake and Distribution of Gold Nanoparticles in Four Plant Species. Environmental Science & Technology, 2012, 46, 12391-12398.	10.0	332
61	Determination of the Intracellular Stability of Gold Nanoparticle Monolayers Using Mass Spectrometry. Analytical Chemistry, 2012, 84, 4321-4326.	6.5	40
62	An accelerated workflow for untargeted metabolomics using the METLIN database. Nature Biotechnology, 2012, 30, 826-828.	17.5	472
63	The Interplay of Monolayer Structure and Serum Protein Interactions on the Cellular Uptake of Gold Nanoparticles. Small, 2012, 8, 2659-2663.	10.0	71
64	Stability of quantum dots in live cells. Nature Chemistry, 2011, 3, 963-968.	13.6	121
65	Colorimetric Bacteria Sensing Using a Supramolecular Enzymeâ€“Nanoparticle Biosensor. Journal of the American Chemical Society, 2011, 133, 9650-9653.	13.7	317
66	Drug Delivery Using Nanoparticleâ€Stabilized Nanocapsules. Angewandte Chemie - International Edition, 2011, 50, 477-481.	13.8	114
67	Laser desorption/ionization mass spectrometry analysis of monolayer-protected gold nanoparticles. Analytical and Bioanalytical Chemistry, 2010, 396, 1025-1035.	3.7	62
68	The Role of Surface Functionality on Acute Cytotoxicity, ROS Generation and DNA Damage by Cationic Gold Nanoparticles. Small, 2010, 6, 2246-2249.	10.0	232
69	Surface Properties Dictate Uptake, Distribution, Excretion, and Toxicity of Nanoparticles in Fish. Small, 2010, 6, 2261-2265.	10.0	113
70	Recognition-mediated activation of therapeutic gold nanoparticles inside living cells. Nature Chemistry, 2010, 2, 962-966.	13.6	295
71	Intracellular Delivery of a Membrane-Impermeable Enzyme in Active Form Using Functionalized Gold Nanoparticles. Journal of the American Chemical Society, 2010, 132, 2642-2645.	13.7	176
72	Entrapment of Hydrophobic Drugs in Nanoparticle Monolayers with Efficient Release into Cancer Cells. Journal of the American Chemical Society, 2009, 131, 1360-1361.	13.7	305

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73	Engineered nanoparticle surfaces for improved mass spectrometric analyses. Analyst, The, 2009, 134, 2183.	3.5	52
74	Multiplexed Screening of Cellular Uptake of Gold Nanoparticles Using Laser Desorption/Ionization Mass Spectrometry. Journal of the American Chemical Society, 2008, 130, 14139-14143.	13.7	126
75	One-Step Immobilization of Glucose Oxidase in a Silica Matrix on a Pt Electrode by an Electrochemically Induced Solâ^'Gel Process. Langmuir, 2007, 23, 11896-11900.	3.5	106