

Xiang Zhang

List of Publications by Year in descending order

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73
papers

3,004
citations

136950

32
h-index

175258

52
g-index

74
all docs

74
docs citations

74
times ranked

3880
citing authors

#	ARTICLE	IF	CITATIONS
1	Chronic Alcohol Exposure Stimulates Adipose Tissue Lipolysis in Mice. <i>American Journal of Pathology</i> , 2012, 180, 998-1007.	3.8	183
2	Strategy for qualitative and quantitative analysis in proteomics based on signature peptides. <i>Biomedical Applications</i> , 2000, 745, 197-210.	1.7	173
3	Intestinal HIF-1 α deletion exacerbates alcoholic liver disease by inducing intestinal dysbiosis and barrier dysfunction. <i>Journal of Hepatology</i> , 2018, 69, 886-895.	3.7	160
4	Multi-dimensional liquid chromatography in proteomics—A review. <i>Analytica Chimica Acta</i> , 2010, 664, 101-113.	5.4	158
5	Transcription factor c-Maf is a checkpoint that programs macrophages in lung cancer. <i>Journal of Clinical Investigation</i> , 2020, 130, 2081-2096.	8.2	108
6	Quantitative proteomics strategy involving the selection of peptides containing both cysteine and histidine from tryptic digests of cell lysates. <i>Journal of Chromatography A</i> , 2002, 949, 153-162.	3.7	107
7	Detection of an Extended Human Volatome with Comprehensive Two-Dimensional Gas Chromatography Time-of-Flight Mass Spectrometry. <i>PLoS ONE</i> , 2013, 8, e75274.	2.5	102
8	DISCO: Distance and Spectrum Correlation Optimization Alignment for Two-Dimensional Gas Chromatography Time-of-Flight Mass Spectrometry-Based Metabolomics. <i>Analytical Chemistry</i> , 2010, 82, 5069-5081.	6.5	84
9	Comparative analysis of mass spectral matching-based compound identification in gas chromatography—mass spectrometry. <i>Journal of Chromatography A</i> , 2013, 1298, 132-138.	3.7	80
10	Saturated and Unsaturated Dietary Fats Differentially Modulate Ethanol-Induced Changes in Gut Microbiome and Metabolome in a Mouse Model of Alcoholic Liver Disease. <i>American Journal of Pathology</i> , 2016, 186, 765-776.	3.8	80
11	Hepatic and Fecal Metabolomic Analysis of the Effects of <i>Lactobacillus rhamnosus</i> GG on Alcoholic Fatty Liver Disease in Mice. <i>Journal of Proteome Research</i> , 2015, 14, 1174-1182.	3.7	77
12	Wavelet- and Fourier-Transform-Based Spectrum Similarity Approaches to Compound Identification in Gas Chromatography/Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 5631-5638.	6.5	73
13	MetSign: A Computational Platform for High-Resolution Mass Spectrometry-Based Metabolomics. <i>Analytical Chemistry</i> , 2011, 83, 7668-7675.	6.5	72
14	Chronic Alcohol Exposure Disturbs Lipid Homeostasis at the Adipose Tissue-Liver Axis in Mice: Analysis of Triacylglycerols Using High-Resolution Mass Spectrometry in Combination with In Vivo Metabolite Deuterium Labeling. <i>PLoS ONE</i> , 2013, 8, e55382.	2.5	66
15	Comparison of GC-MS and GC—GC-MS in the Analysis of Human Serum Samples for Biomarker Discovery. <i>Journal of Proteome Research</i> , 2015, 14, 1810-1817.	3.7	64
16	Data Preprocessing Method for Liquid Chromatography—Mass Spectrometry Based Metabolomics. <i>Analytical Chemistry</i> , 2012, 84, 7963-7971.	6.5	63
17	Metabolomic Analysis of the Effects of Chronic Arsenic Exposure in a Mouse Model of Diet-Induced Fatty Liver Disease. <i>Journal of Proteome Research</i> , 2014, 13, 547-554.	3.7	60
18	MetPP: a computational platform for comprehensive two-dimensional gas chromatography time-of-flight mass spectrometry-based metabolomics. <i>Bioinformatics</i> , 2013, 29, 1786-1792.	4.1	56

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19	Compound identification in GC-MS by simultaneously evaluating the mass spectrum and retention index. <i>Analyst</i> , 2014, 139, 2507-2514.	3.5	56
20	Comprehensive two-dimensional gas chromatography/time-of-flight mass spectrometry peak sorting algorithm. <i>Journal of Chromatography A</i> , 2008, 1179, 205-215.	3.7	55
21	Metabolomic Analysis of the Effects of Polychlorinated Biphenyls in Nonalcoholic Fatty Liver Disease. <i>Journal of Proteome Research</i> , 2012, 11, 3805-3815.	3.7	54
22	A method of finding optimal weight factors for compound identification in gas chromatography-mass spectrometry. <i>Bioinformatics</i> , 2012, 28, 1158-1163.	4.1	53
23	Compound Identification Using Partial and Semipartial Correlations for Gas Chromatography-mass Spectrometry Data. <i>Analytical Chemistry</i> , 2012, 84, 6477-6487.	6.5	51
24	Simultaneous quantification of straight-chain and branched-chain short chain fatty acids by gas chromatography mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2018, 1092, 359-367.	2.3	51
25	Olanzapine Activates Hepatic Mammalian Target of Rapamycin: New Mechanistic Insight into Metabolic Dysregulation with Atypical Antipsychotic Drugs. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2013, 347, 126-135.	2.5	50
26	An optimal peak alignment for comprehensive two-dimensional gas chromatography mass spectrometry using mixture similarity measure. <i>Bioinformatics</i> , 2011, 27, 1660-1666.	4.1	49
27	Discovery of a Broad-Spectrum Antiviral Compound That Inhibits Pyrimidine Biosynthesis and Establishes a Type 1 Interferon-Independent Antiviral State. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 4552-4562.	3.2	46
28	Simultaneous Quantification of Nucleosides and Nucleotides from Biological Samples. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 987-1000.	2.8	43
29	iMatch: A retention index tool for analysis of gas chromatography-mass spectrometry data. <i>Journal of Chromatography A</i> , 2011, 1218, 6522-6530.	3.7	41
30	iMatch2: Compound identification using retention index for analysis of gas chromatography-mass spectrometry data. <i>Journal of Chromatography A</i> , 2014, 1337, 202-210.	3.7	41
31	Dietary copper-fructose interactions alter gut microbial activity in male rats. <i>American Journal of Physiology - Renal Physiology</i> , 2018, 314, G119-G130.	3.4	37
32	Data Dependent Peak Model Based Spectrum Deconvolution for Analysis of High Resolution LC-MS Data. <i>Analytical Chemistry</i> , 2014, 86, 2156-2165.	6.5	33
33	In-Gel Stable-Isotope Labeling (ISIL): A Strategy for Mass Spectrometry-Based Relative Quantification. <i>Journal of Proteome Research</i> , 2006, 5, 155-163.	3.7	32
34	Cadmium and High-Fat Diet Disrupt Renal, Cardiac and Hepatic Essential Metals. <i>Scientific Reports</i> , 2019, 9, 14675.	3.3	32
35	Effects of Dietary Different Doses of Copper and High Fructose Feeding on Rat Fecal Metabolome. <i>Journal of Proteome Research</i> , 2015, 14, 4050-4058.	3.7	30
36	Smith-Waterman peak alignment for comprehensive two-dimensional gas chromatography-mass spectrometry. <i>BMC Bioinformatics</i> , 2011, 12, 235.	2.6	29

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37	Detection of volatile biomarkers of therapeutic radiation in breath. <i>Journal of Breath Research</i> , 2013, 7, 036002.	3.0	28
38	Model-based peak alignment of metabolomic profiling from comprehensive two-dimensional gas chromatography mass spectrometry. <i>BMC Bioinformatics</i> , 2012, 13, 27.	2.6	26
39	Ethanol and unsaturated dietary fat induce unique patterns of hepatic δ^6 and δ^3 PUFA oxylipins in a mouse model of alcoholic liver disease. <i>PLoS ONE</i> , 2018, 13, e0204119.	2.5	25
40	A method of calculating the second dimension retention index in comprehensive two-dimensional gas chromatography time-of-flight mass spectrometry. <i>Journal of Chromatography A</i> , 2011, 1218, 2577-2583.	3.7	24
41	Untargeted polar metabolomics of transformed MDA-MB-231 breast cancer cells expressing varying levels of human arylamine N-acetyltransferase 1. <i>Metabolomics</i> , 2016, 12, 1.	3.0	23
42	A method for the identification of glycoproteins from human serum by a combination of lectin affinity chromatography along with anion exchange and Cu-IMAC selection of tryptic peptides. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2007, 845, 143-150.	2.3	22
43	Comparative Analysis of Mass Spectral Similarity Measures on Peak Alignment for Comprehensive Two-Dimensional Gas Chromatography Mass Spectrometry. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-12.	1.3	22
44	A large scale test dataset to determine optimal retention index threshold based on three mass spectral similarity measures. <i>Journal of Chromatography A</i> , 2012, 1251, 188-193.	3.7	20
45	Kupffer cell depletion protects against the steatosis, but not the liver damage, induced by marginal-copper, high-fructose diet in male rats. <i>American Journal of Physiology - Renal Physiology</i> , 2015, 308, G934-G945.	3.4	20
46	Profiling of Polar Metabolites in Mouse Feces Using Four Analytical Platforms to Study the Effects Of Cathelicidin-Related Antimicrobial Peptide in Alcoholic Liver Disease. <i>Journal of Proteome Research</i> , 2019, 18, 2875-2884.	3.7	19
47	Analysis of stable isotope assisted metabolomics data acquired by GC-MS. <i>Analytica Chimica Acta</i> , 2017, 980, 25-32.	5.4	16
48	Sestrin2 maintains OXPHOS integrity to modulate cardiac substrate metabolism during ischemia and reperfusion. <i>Redox Biology</i> , 2021, 38, 101824.	9.0	15
49	In-gel stable isotope labeling for relative quantification using mass spectrometry. <i>Nature Protocols</i> , 2006, 1, 46-51.	12.0	14
50	Integrating comprehensive two-dimensional gas chromatography mass spectrometry and parallel two-dimensional liquid chromatography mass spectrometry for untargeted metabolomics. <i>Analyst</i> , 2019, 144, 4331-4341.	3.5	14
51	Breath Biomarkers of Whole-body Gamma Irradiation in the Göttingen Minipig. <i>Health Physics</i> , 2015, 108, 538-546.	0.5	13
52	A large, consistent plasma proteomics data set from prospectively collected breast cancer patient and healthy volunteer samples. <i>Journal of Translational Medicine</i> , 2011, 9, 80.	4.4	12
53	Global Plasma Profiling for Colorectal Cancer-Associated Volatile Organic Compounds: a Proof-of-Principle Study. <i>Journal of Chromatographic Science</i> , 2019, 57, 385-396.	1.4	12
54	An efficient post-hoc integration method improving peak alignment of metabolomics data from GCxGC/TOF-MS. <i>BMC Bioinformatics</i> , 2013, 14, 123.	2.6	11

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55	Probioticâ€derived nanoparticles inhibit ALD through intestinal miR194 suppression and subsequent FXR activation. <i>Hepatology</i> , 2023, 77, 1164-1180.	7.3	10
56	Discovery of false identification using similarity difference in GCâ€MSâ€based metabolomics. <i>Journal of Chemometrics</i> , 2015, 29, 80-86.	1.3	9
57	Elder: A compound identification tool for gas chromatography mass spectrometry data. <i>Journal of Chromatography A</i> , 2016, 1448, 107-114.	3.7	9
58	Surface fitting for calculating the second dimension retention index in comprehensive two-dimensional gas chromatography mass spectrometry. <i>Journal of Chromatography A</i> , 2018, 1539, 62-70.	3.7	9
59	Integrating Two-Dimensional Gas and Liquid Chromatography-Mass Spectrometry for Untargeted Colorectal Cancer Metabolomics: A Proof-of-Principle Study. <i>Metabolites</i> , 2020, 10, 343.	2.9	9
60	Analysis of Metabolomic Profiling Data Acquired on GCâ€MS. <i>Methods in Enzymology</i> , 2014, 543, 315-324.	1.0	8
61	Using Multiple Analytical Platforms to Investigate the Androgen Depletion Effects on Fecal Metabolites in a Mouse Model of Systemic Lupus Erythematosus. <i>Journal of Proteome Research</i> , 2020, 19, 667-676.	3.7	8
62	Metabolic Profiling of Bile Acids in the Urine of Patients with Alcoholâ€Associated Liver Disease. <i>Hepatology Communications</i> , 2021, 5, 798-811.	4.3	8
63	Analysis of sex differences in dietary copper-fructose interaction-induced alterations of gut microbial activity in relation to hepatic steatosis. <i>Biology of Sex Differences</i> , 2021, 12, 3.	4.1	7
64	Fat-1 Transgenic Mice With Augmented n3-Polyunsaturated Fatty Acids Are Protected From Liver Injury Caused by Acute-On-Chronic Ethanol Administration. <i>Frontiers in Pharmacology</i> , 2021, 12, 711590.	3.5	7
65	Differential metabolic requirement governed by transcription factor c-Maf dictates innate Î³Î³T17 effector functionality in mice and humans. <i>Science Advances</i> , 2022, 8, .	10.3	7
66	Coherent point drift peak alignment algorithms using distance and similarity measures for twoâ€dimensional gas chromatography mass spectrometry data. <i>Journal of Chemometrics</i> , 2020, 34, e3236.	1.3	6
67	A method of calculating the second dimension hold-up time for comprehensive two-dimensional gas chromatography. <i>Journal of Chromatography A</i> , 2012, 1260, 193-199.	3.7	5
68	Comprehensive Two-Dimensional Gas Chromatography Mass Spectrometry-Based Metabolomics. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1280, 57-67.	1.6	4
69	Constructing metabolic association networks using high-dimensional mass spectrometry data. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2014, 138, 193-202.	3.5	3
70	Combine multiple mass spectral similarity measures for compound identification. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 15, 84.	0.1	3
71	Generalization of Reference System for Calculating the Second Dimension Retention Index in GCâ€MS. <i>Journal of Analysis and Testing</i> , 2018, 2, 263-273.	5.1	3
72	Integrated Multilayer Omics Reveals the Genomic, Proteomic, and Metabolic Influences of Histidyl Dipeptides on the Heart. <i>Journal of the American Heart Association</i> , 2022, 11, .	3.7	3

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73	Compound Identification Using Penalized Linear Regression on Metabolomics. Journal of Modern Applied Statistical Methods, 2016, 15, 373-388.	0.2	0