Xiang Zhang

List of Publications by Year
in descending order

73	3,004	136950	175258
papers	citations	32	52
		h-index	g-index

74	74	74	3880
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Probioticâ€derived nanoparticles inhibit ALD through intestinal miR194 suppression and subsequent FXR activation. Hepatology, 2023, 77, 1164-1180.	7.3	10
2	Differential metabolic requirement governed by transcription factor c-Maf dictates innate Î³Î´T17 effector functionality in mice and humans. Science Advances, 2022, 8, .	10.3	7
3	Integrated Multilayer Omics Reveals the Genomic, Proteomic, and Metabolic Influences of Histidyl Dipeptides on theÂHeart. Journal of the American Heart Association, 2022, 11, .	3.7	3
4	Sestrin2 maintains OXPHOS integrity to modulate cardiac substrate metabolism during ischemia and reperfusion. Redox Biology, 2021, 38, 101824.	9.0	15
5	Analysis of sex differences in dietary copper-fructose interaction-induced alterations of gut microbial activity in relation to hepatic steatosis. Biology of Sex Differences, 2021, 12, 3.	4.1	7
6	Metabolic Profiling of Bile Acids in the Urine of Patients with Alcoholâ€Associated Liver Disease. Hepatology Communications, 2021, 5, 798-811.	4.3	8
7	Comprehensive Two-Dimensional Gas Chromatography Mass Spectrometry-Based Metabolomics. Advances in Experimental Medicine and Biology, 2021, 1280, 57-67.	1.6	4
8	Fat-1 Transgenic Mice With Augmented n3-Polyunsaturated Fatty Acids Are Protected From Liver Injury Caused by Acute-On-Chronic Ethanol Administration. Frontiers in Pharmacology, 2021, 12, 711590.	3.5	7
9	Using Multiple Analytical Platforms to Investigate the Androgen Depletion Effects on Fecal Metabolites in a Mouse Model of Systemic Lupus Erythematosus. Journal of Proteome Research, 2020, 19, 667-676.	3.7	8
10	Integrating Two-Dimensional Gas and Liquid Chromatography-Mass Spectrometry for Untargeted Colorectal Cancer Metabolomics: A Proof-of-Principle Study. Metabolites, 2020, 10, 343.	2.9	9
11	Coherent point drift peak alignment algorithms using distance and similarity measures for twoâ€dimensional gas chromatography mass spectrometry data. Journal of Chemometrics, 2020, 34, e3236.	1.3	6
12	Transcription factor c-Maf is a checkpoint that programs macrophages in lung cancer. Journal of Clinical Investigation, 2020, 130, 2081-2096.	8.2	108
13	Cadmium and High-Fat Diet Disrupt Renal, Cardiac and Hepatic Essential Metals. Scientific Reports, 2019, 9, 14675.	3.3	32
14	Integrating comprehensive two-dimensional gas chromatography mass spectrometry and parallel two-dimensional liquid chromatography mass spectrometry for untargeted metabolomics. Analyst, The, 2019, 144, 4331-4341.	3.5	14
15	Profiling of Polar Metabolites in Mouse Feces Using Four Analytical Platforms to Study the Effects Of Cathelicidin-Related Antimicrobial Peptide in Alcoholic Liver Disease. Journal of Proteome Research, 2019, 18, 2875-2884.	3.7	19
16	Simultaneous Quantification of Nucleosides and Nucleotides from Biological Samples. Journal of the American Society for Mass Spectrometry, 2019, 30, 987-1000.	2.8	43
17	Global Plasma Profiling for Colorectal Cancer-Associated Volatile Organic Compounds: a Proof-of-Principle Study. Journal of Chromatographic Science, 2019, 57, 385-396.	1.4	12
18	Surface fitting for calculating the second dimension retention index in comprehensive two-dimensional gas chromatography mass spectrometry. Journal of Chromatography A, 2018, 1539, 62-70.	3.7	9

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19	Dietary copper-fructose interactions alter gut microbial activity in male rats. American Journal of Physiology - Renal Physiology, 2018, 314, G119-G130.	3.4	37
20	Generalization of Reference System for Calculating the Second Dimension Retention Index in GCâ€‰Ã—â€‰GCâ€“MS. Journal of Analysis and Testing, 2018, 2, 263-273.	5.1	3
21	Ethanol and unsaturated dietary fat induce unique patterns of hepatic Ï‰-6 and Ï‰-3 PUFA oxylipins in a mouse model of alcoholic liver disease. PLoS ONE, 2018, 13, e0204119.	2.5	25
22	Intestinal HIF-1Î± deletion exacerbates alcoholic liver disease by inducing intestinal dysbiosis and barrier dysfunction. Journal of Hepatology, 2018, 69, 886-895.	3.7	160
23	Simultaneous quantification of straight-chain and branched-chain short chain fatty acids by gas chromatography mass spectrometry. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2018, 1092, 359-367.	2.3	51
24	Analysis of stable isotope assisted metabolomics data acquired by GC-MS. Analytica Chimica Acta, 2017, 980, 25-32.	5.4	16
25	Combine multiple mass spectral similarity measures for compound identification. International Journal of Data Mining and Bioinformatics, 2016, 15, 84.	0.1	3
26	Discovery of a Broad-Spectrum Antiviral Compound That Inhibits Pyrimidine Biosynthesis and Establishes a Type 1 Interferon-Independent Antiviral State. Antimicrobial Agents and Chemotherapy, 2016, 60, 4552-4562.	3.2	46
27	EIder: A compound identification tool for gas chromatography mass spectrometry data. Journal of Chromatography A, 2016, 1448, 107-114.	3.7	9
28	Untargeted polar metabolomics of transformed MDA-MB-231 breast cancer cells expressing varying levels of human arylamine N-acetyltransferase 1. Metabolomics, 2016, 12, 1.	3.0	23
29	Saturated and Unsaturated Dietary Fats Differentially Modulate Ethanol-Induced ChangesÂin Gut Microbiome and Metabolome in a Mouse Model of Alcoholic Liver Disease. American Journal of Pathology, 2016, 186, 765-776.	3.8	80
30	Compound Identification Using Penalized Linear Regression on Metabolomics. Journal of Modern Applied Statistical Methods, 2016, 15, 373-388.	0.2	0
31	Hepatic and Fecal Metabolomic Analysis of the Effects of <i>Lactobacillus rhamnosus</i> GG on Alcoholic Fatty Liver Disease in Mice. Journal of Proteome Research, 2015, 14, 1174-1182.	3.7	77
32	Effects of Dietary Different Doses of Copper and High Fructose Feeding on Rat Fecal Metabolome. Journal of Proteome Research, 2015, 14, 4050-4058.	3.7	30
33	Kupffer cell depletion protects against the steatosis, but not the liver damage, induced by marginal-copper, high-fructose diet in male rats. American Journal of Physiology - Renal Physiology, 2015, 308, G934-G945.	3.4	20
34	Breath Biomarkers of Whole-body Gamma Irradiation in the GÃ¶ttingen Minipig. Health Physics, 2015, 108, 538-546.	0.5	13
35	Comparison of GC-MS and GCÃ—GC-MS in the Analysis of Human Serum Samples for Biomarker Discovery. Journal of Proteome Research, 2015, 14, 1810-1817.	3.7	64
36	Discovery of false identification using similarity difference in GCâ€“MSâ€‘based metabolomics. Journal of Chemometrics, 2015, 29, 80-86.	1.3	9

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37	Constructing metabolic association networks using high-dimensional mass spectrometry data. Chemometrics and Intelligent Laboratory Systems, 2014, 138, 193-202.	3.5	3
38	iMatch2: Compound identification using retention index for analysis of gas chromatography–mass spectrometry data. Journal of Chromatography A, 2014, 1337, 202-210.	3.7	41
39	Compound identification in GC-MS by simultaneously evaluating the mass spectrum and retention index. Analyst, The, 2014, 139, 2507-2514.	3.5	56
40	Data Dependent Peak Model Based Spectrum Deconvolution for Analysis of High Resolution LC-MS Data. Analytical Chemistry, 2014, 86, 2156-2165.	6.5	33
41	Metabolomic Analysis of the Effects of Chronic Arsenic Exposure in a Mouse Model of Diet-Induced Fatty Liver Disease. Journal of Proteome Research, 2014, 13, 547-554.	3.7	60
42	Analysis of Metabolomic Profiling Data Acquired on GC–MS. Methods in Enzymology, 2014, 543, 315-324.	1.0	8
43	An efficient post-hoc integration method improving peak alignment of metabolomics data from GCxGC/TOF-MS. BMC Bioinformatics, 2013, 14, 123.	2.6	11
44	Detection of volatile biomarkers of therapeutic radiation in breath. Journal of Breath Research, 2013, 7, 036002.	3.0	28
45	Olanzapine Activates Hepatic Mammalian Target of Rapamycin: New Mechanistic Insight into Metabolic Dysregulation with Atypical Antipsychotic Drugs. Journal of Pharmacology and Experimental Therapeutics, 2013, 347, 126-135.	2.5	50
46	Comparative analysis of mass spectral matching-based compound identification in gas chromatography–mass spectrometry. Journal of Chromatography A, 2013, 1298, 132-138.	3.7	80
47	MetPP: a computational platform for comprehensive two-dimensional gas chromatography time-of-flight mass spectrometry-based metabolomics. Bioinformatics, 2013, 29, 1786-1792.	4.1	56
48	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. PLoS ONE, 2013, 8, e55382.	2.5	66
49	Comparative Analysis of Mass Spectral Similarity Measures on Peak Alignment for Comprehensive Two-Dimensional Gas Chromatography Mass Spectrometry. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-12.	1.3	22
50	Detection of an Extended Human Volatome with Comprehensive Two-Dimensional Gas Chromatography Time-of-Flight Mass Spectrometry. PLoS ONE, 2013, 8, e75274.	2.5	102
51	A method of finding optimal weight factors for compound identification in gas chromatography–mass spectrometry. Bioinformatics, 2012, 28, 1158-1163.	4.1	53
52	A method of calculating the second dimension hold-up time for comprehensive two-dimensional gas chromatography. Journal of Chromatography A, 2012, 1260, 193-199.	3.7	5
53	Compound Identification Using Partial and Semipartial Correlations for Gas Chromatography–Mass Spectrometry Data. Analytical Chemistry, 2012, 84, 6477-6487.	6.5	51
54	Metabolomic Analysis of the Effects of Polychlorinated Biphenyls in Nonalcoholic Fatty Liver Disease. Journal of Proteome Research, 2012, 11, 3805-3815.	3.7	54

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55	Chronic Alcohol Exposure Stimulates Adipose Tissue Lipolysis in Mice. American Journal of Pathology, 2012, 180, 998-1007.	3.8	183
56	A large scale test dataset to determine optimal retention index threshold based on three mass spectral similarity measures. Journal of Chromatography A, 2012, 1251, 188-193.	3.7	20
57	Data Preprocessing Method for Liquid Chromatography–Mass Spectrometry Based Metabolomics. Analytical Chemistry, 2012, 84, 7963-7971.	6.5	63
58	Model-based peak alignment of metabolomic profiling from comprehensive two-dimensional gas chromatography mass spectrometry. BMC Bioinformatics, 2012, 13, 27.	2.6	26
59	Wavelet- and Fourier-Transform-Based Spectrum Similarity Approaches to Compound Identification in Gas Chromatography/Mass Spectrometry. Analytical Chemistry, 2011, 83, 5631-5638.	6.5	73
60	MetSign: A Computational Platform for High-Resolution Mass Spectrometry-Based Metabolomics. Analytical Chemistry, 2011, 83, 7668-7675.	6.5	72
61	iMatch: A retention index tool for analysis of gas chromatography–mass spectrometry data. Journal of Chromatography A, 2011, 1218, 6522-6530.	3.7	41
62	A method of calculating the second dimension retention index in comprehensive two-dimensional gas chromatography time-of-flight mass spectrometry. Journal of Chromatography A, 2011, 1218, 2577-2583.	3.7	24
63	A large, consistent plasma proteomics data set from prospectively collected breast cancer patient and healthy volunteer samples. Journal of Translational Medicine, 2011, 9, 80.	4.4	12
64	Smith-Waterman peak alignment for comprehensive two-dimensional gas chromatography-mass spectrometry. BMC Bioinformatics, 2011, 12, 235.	2.6	29
65	An optimal peak alignment for comprehensive two-dimensional gas chromatography mass spectrometry using mixture similarity measure. Bioinformatics, 2011, 27, 1660-1666.	4.1	49
66	Multi-dimensional liquid chromatography in proteomics—A review. Analytica Chimica Acta, 2010, 664, 101-113.	5.4	158
67	DISCO: Distance and Spectrum Correlation Optimization Alignment for Two-Dimensional Gas Chromatography Time-of-Flight Mass Spectrometry-Based Metabolomics. Analytical Chemistry, 2010, 82, 5069-5081.	6.5	84
68	Comprehensive two-dimensional gas chromatography/time-of-flight mass spectrometry peak sorting algorithm. Journal of Chromatography A, 2008, 1179, 205-215.	3.7	55
69	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. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2007, 845, 143-150.	2.3	22
70	In-Gel Stable-Isotope Labeling (ISIL):‰ A Strategy for Mass Spectrometry-Based Relative Quantification. Journal of Proteome Research, 2006, 5, 155-163.	3.7	32
71	In-gel stable isotope labeling for relative quantification using mass spectrometry. Nature Protocols, 2006, 1, 46-51.	12.0	14
72	Quantitative proteomics strategy involving the selection of peptides containing both cysteine and histidine from tryptic digests of cell lysates. Journal of Chromatography A, 2002, 949, 153-162.	3.7	107

#	ARTICLE	IF	CITATIONS
73	Strategy for qualitative and quantitative analysis in proteomics based on signature peptides. Biomedical Applications, 2000, 745, 197-210.	1.7	173