

Xiuxia Du

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

1,522
citations

304743

22
h-index

434195

31
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34
all docs

34
docs citations

34
times ranked

2613
citing authors

#	ARTICLE	IF	CITATIONS
1	One Step Forward for Reducing False Positive and False Negative Compound Identifications from Mass Spectrometry Metabolomics Data: New Algorithms for Constructing Extracted Ion Chromatograms and Detecting Chromatographic Peaks. <i>Analytical Chemistry</i> , 2017, 89, 8696-8703.	6.5	275
2	Detailed Investigation and Comparison of the XCMS and MZmine 2 Chromatogram Construction and Chromatographic Peak Detection Methods for Preprocessing Mass Spectrometry Metabolomics Data. <i>Analytical Chemistry</i> , 2017, 89, 8689-8695.	6.5	146
3	Identification of Cross-Linked Peptides after Click-Based Enrichment Using Sequential Collision-Induced Dissociation and Electron Transfer Dissociation Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 5524-5532.	6.5	91
4	Auto-deconvolution and molecular networking of gas chromatography–mass spectrometry data. <i>Nature Biotechnology</i> , 2021, 39, 169-173.	17.5	78
5	Comparative Proteomics of Human Monkeypox and Vaccinia Intracellular Mature and Extracellular Enveloped Virions. <i>Journal of Proteome Research</i> , 2008, 7, 960-968.	3.7	75
6	ADAP-GC 2.0: Deconvolution of Coeluting Metabolites from GC/TOF-MS Data for Metabolomics Studies. <i>Analytical Chemistry</i> , 2012, 84, 6619-6629.	6.5	69
7	The PHD and Chromo Domains Regulate the ATPase Activity of the Human Chromatin Remodeler CHD4. <i>Journal of Molecular Biology</i> , 2012, 422, 3-17.	4.2	68
8	Training in metabolomics research. I. Designing the experiment, collecting and extracting samples and generating metabolomics data. <i>Journal of Mass Spectrometry</i> , 2016, 51, 461-475.	1.6	64
9	ADAP-GC 3.0: Improved Peak Detection and Deconvolution of Co-eluting Metabolites from GC/TOF-MS Data for Metabolomics Studies. <i>Analytical Chemistry</i> , 2016, 88, 8802-8811.	6.5	63
10	An Automated Data Analysis Pipeline for GC–TOF–MS Metabolomics Studies. <i>Journal of Proteome Research</i> , 2010, 9, 5974-5981.	3.7	59
11	Xlink-Identifier: An Automated Data Analysis Platform for Confident Identifications of Chemically Cross-Linked Peptides Using Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2011, 10, 923-931.	3.7	55
12	SPECTRAL DECONVOLUTION FOR GAS CHROMATOGRAPHY MASS SPECTROMETRY-BASED METABOLOMICS: CURRENT STATUS AND FUTURE PERSPECTIVES. <i>Computational and Structural Biotechnology Journal</i> , 2013, 4, e201301013.	4.1	55
13	Training in metabolomics research. II. Processing and statistical analysis of metabolomics data, metabolite identification, pathway analysis, applications of metabolomics and its future. <i>Journal of Mass Spectrometry</i> , 2016, 51, 535-548.	1.6	49
14	ADAP-GC 4.0: Application of Clustering-Assisted Multivariate Curve Resolution to Spectral Deconvolution of Gas Chromatography–Mass Spectrometry Metabolomics Data. <i>Analytical Chemistry</i> , 2019, 91, 9069-9077.	6.5	44
15	Linear Discriminant Analysis-Based Estimation of the False Discovery Rate for Phosphopeptide Identifications. <i>Journal of Proteome Research</i> , 2008, 7, 2195-2203.	3.7	37
16	Metabolomics Data Preprocessing Using ADAP and MZmine 2. <i>Methods in Molecular Biology</i> , 2020, 2104, 25-48.	0.9	35
17	Metabolic Reprogramming by Folate Restriction Leads to a Less Aggressive Cancer Phenotype. <i>Molecular Cancer Research</i> , 2017, 15, 189-200.	3.4	33
18	A Practical Guide to Metabolomics Software Development. <i>Analytical Chemistry</i> , 2021, 93, 1912-1923.	6.5	30

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19	A Computational Strategy to Analyze Label-Free Temporal Bottom-Up Proteomics Data. <i>Journal of Proteome Research</i> , 2008, 7, 2595-2604.	3.7	29
20	Protein Structural Analysis via Mass Spectrometry-Based Proteomics. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 397-431.	1.6	27
21	ADAP-GC 3.2: Graphical Software Tool for Efficient Spectral Deconvolution of Gas Chromatography-High-Resolution Mass Spectrometry Metabolomics Data. <i>Journal of Proteome Research</i> , 2018, 17, 470-478.	3.7	23
22	Applying a Targeted Label-Free Approach Using LC-MS AMT Tags to Evaluate Changes in Protein Phosphorylation Following Phosphatase Inhibition. <i>Journal of Proteome Research</i> , 2007, 6, 4489-4497.	3.7	22
23	Phosphoproteomics Profiling of Human Skin Fibroblast Cells Reveals Pathways and Proteins Affected by Low Doses of Ionizing Radiation. <i>PLoS ONE</i> , 2010, 5, e14152.	2.5	21
24	Encoding and Decoding Target Locations With Waves in the Turtle Visual Cortex. <i>IEEE Transactions on Biomedical Engineering</i> , 2005, 52, 566-577.	4.2	20
25	Quantitative Phosphoproteome Analysis of Lysophosphatidic Acid Induced Chemotaxis Applying Dual-Step ¹⁸ O Labeling Coupled with Immobilized Metal-Ion Affinity Chromatography. <i>Journal of Proteome Research</i> , 2008, 7, 4215-4224.	3.7	16
26	Aggregate Interactome Based on Protein Cross-linking Interfaces Predicts Drug Targets to Limit Aggregation in Neurodegenerative Diseases. <i>IScience</i> , 2019, 20, 248-264.	4.1	12
27	Encoding of Motion Targets by Waves in Turtle Visual Cortex. <i>IEEE Transactions on Biomedical Engineering</i> , 2006, 53, 1688-1695.	4.2	8
28	An integrated cross-linking-MS approach to investigate cell penetrating peptides interacting partners. <i>EuPA Open Proteomics</i> , 2014, 3, 229-238.	2.5	7
29	ADAP-KDB: A Spectral Knowledgebase for Tracking and Prioritizing Unknown GC-MS Spectra in the NIH's Metabolomics Data Repository. <i>Analytical Chemistry</i> , 2021, 93, 12213-12220.	6.5	6
30	A preparatory study of how to construct consensus mass spectra of recurrent unknown metabolites from untargeted GC-MS metabolomics data. <i>International Journal of Mass Spectrometry</i> , 2018, 427, 73-78.	1.5	3
31	Memory-Efficient Searching of Gas-Chromatography Mass Spectra Accelerated by Prescreening. <i>Metabolites</i> , 2022, 12, 491.	2.9	2
32	Aggregate Interactome Based on Protein-Crosslinking Interfaces Predicts Drug Targets to Limit Aggregation in Neurodegenerative Diseases. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0