Xiuxia Du

List of Publications by Year
in descending order

32 papers	1,522 citations	304743 22 h-index	434195 31 g-index
34 all docs	34 docs citations	34 times ranked	2613 citing authors

#	Article	IF	Citations
1	Memory-Efficient Searching of Gas-Chromatography Mass Spectra Accelerated by Prescreening. Metabolites, 2022, 12, 491.	2.9	2
2	Auto-deconvolution and molecular networking of gas chromatography–mass spectrometry data. Nature Biotechnology, 2021, 39, 169-173.	17.5	78
3	A Practical Guide to Metabolomics Software Development. Analytical Chemistry, 2021, 93, 1912-1923.	6.5	30
4	ADAP-KDB: A Spectral Knowledgebase for Tracking and Prioritizing Unknown GC–MS Spectra in the NIH's Metabolomics Data Repository. Analytical Chemistry, 2021, 93, 12213-12220.	6.5	6
5	Metabolomics Data Preprocessing Using ADAP and MZmine 2. Methods in Molecular Biology, 2020, 2104, 25-48.	0.9	35
6	Aggregate Interactome Based on Protein Cross-linking Interfaces Predicts Drug Targets to Limit Aggregation in Neurodegenerative Diseases. IScience, 2019, 20, 248-264.	4.1	12
7	ADAP-GC 4.0: Application of Clustering-Assisted Multivariate Curve Resolution to Spectral Deconvolution of Gas Chromatography–Mass Spectrometry Metabolomics Data. Analytical Chemistry, 2019, 91, 9069-9077.	6.5	44
8	ADAP-GC 3.2: Graphical Software Tool for Efficient Spectral Deconvolution of Gas Chromatography–High-Resolution Mass Spectrometry Metabolomics Data. Journal of Proteome Research, 2018, 17, 470-478.	3.7	23
9	A preparatory study of how to construct consensus mass spectra of recurrent unknown metabolites from untargeted GC–MS metabolomics data. International Journal of Mass Spectrometry, 2018, 427, 73-78.	1.5	3
10	Metabolic Reprogramming by Folate Restriction Leads to a Less Aggressive Cancer Phenotype. Molecular Cancer Research, 2017, 15, 189-200.	3.4	33
11	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. Analytical Chemistry, 2017, 89, 8696-8703.	6.5	275
12	Detailed Investigation and Comparison of the XCMS and MZmine 2 Chromatogram Construction and Chromatographic Peak Detection Methods for Preprocessing Mass Spectrometry Metabolomics Data. Analytical Chemistry, 2017, 89, 8689-8695.	6.5	146
13	Protein Structural Analysis via Mass Spectrometry-Based Proteomics. Advances in Experimental Medicine and Biology, 2016, 919, 397-431.	1.6	27
14	ADAP-GC 3.0: Improved Peak Detection and Deconvolution of Co-eluting Metabolites from GC/TOF-MS Data for Metabolomics Studies. Analytical Chemistry, 2016, 88, 8802-8811.	6.5	63
15	Training in metabolomics research. I. Designing the experiment, collecting and extracting samples and generating metabolomics data. Journal of Mass Spectrometry, 2016, 51, 461-475.	1.6	64
16	Training in metabolomics research. II. Processing and statistical analysis of metabolomics data, metabolite identification, pathway analysis, applications of metabolomics and its future. Journal of Mass Spectrometry, 2016, 51, 535-548.	1.6	49
17	An integrated cross-linking-MS approach to investigate cell penetrating peptides interacting partners. EuPA Open Proteomics, 2014, 3, 229-238.	2.5	7
18	SPECTRAL DECONVOLUTION FOR GAS CHROMATOGRAPHY MASS SPECTROMETRY-BASED METABOLOMICS: CURRENT STATUS AND FUTURE PERSPECTIVES. Computational and Structural Biotechnology Journal, 2013, 4, e201301013.	4.1	55

#	Article	IF	Citations
19	The PHD and Chromo Domains Regulate the ATPase Activity of the Human Chromatin Remodeler CHD4. Journal of Molecular Biology, 2012, 422, 3-17.	4.2	68
20	ADAP-GC 2.0: Deconvolution of Coeluting Metabolites from GC/TOF-MS Data for Metabolomics Studies. Analytical Chemistry, 2012, 84, 6619-6629.	6.5	69
21	Xlink-Identifier: An Automated Data Analysis Platform for Confident Identifications of Chemically Cross-Linked Peptides Using Tandem Mass Spectrometry. Journal of Proteome Research, 2011, 10, 923-931.	3.7	55
22	Phosphoproteomics Profiling of Human Skin Fibroblast Cells Reveals Pathways and Proteins Affected by Low Doses of Ionizing Radiation. PLoS ONE, 2010, 5, e14152.	2.5	21
23	An Automated Data Analysis Pipeline for GCâˆˆTOFâˆˆMS Metabonomics Studies. Journal of Proteome Research, 2010, 9, 5974-5981.	3.7	59
24	Identification of Cross-Linked Peptides after Click-Based Enrichment Using Sequential Collision-Induced Dissociation and Electron Transfer Dissociation Tandem Mass Spectrometry. Analytical Chemistry, 2009, 81, 5524-5532.	6.5	91
25	Linear Discriminant Analysis-Based Estimation of the False Discovery Rate for Phosphopeptide Identifications. Journal of Proteome Research, 2008, 7, 2195-2203.	3.7	37
26	A Computational Strategy to Analyze Label-Free Temporal Bottom-Up Proteomics Data. Journal of Proteome Research, 2008, 7, 2595-2604.	3.7	29
27	Quantitative Phosphoproteome Analysis of Lysophosphatidic Acid Induced Chemotaxis Applying Dual-Step ^{18}O Labeling Coupled with Immobilized Metal-Ion Affinity Chromatography. Journal of Proteome Research, 2008, 7, 4215-4224.	3.7	16
28	Comparative Proteomics of Human Monkeypox and Vaccinia Intracellular Mature and Extracellular Enveloped Virions. Journal of Proteome Research, 2008, 7, 960-968.	3.7	75
29	Applying a Targeted Label-Free Approach Using LCâˆˆMS AMT Tags to Evaluate Changes in Protein Phosphorylation Following Phosphatase Inhibition. Journal of Proteome Research, 2007, 6, 4489-4497.	3.7	22
30	Encoding of Motion Targets by Waves in Turtle Visual Cortex. IEEE Transactions on Biomedical Engineering, 2006, 53, 1688-1695.	4.2	8
31	Encoding and Decoding Target Locations With Waves in the Turtle Visual Cortex. IEEE Transactions on Biomedical Engineering, 2005, 52, 566-577.	4.2	20
32	Aggregate Interactome Based on Protein-Crosslinking Interfaces Predicts Drug Targets to Limit Aggregation in Neurodegenerative Diseases. SSRN Electronic Journal, 0, , .	0.4	0