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List of Publications by Year
in descending order

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36 papers	1,392 citations	331259 21 h-index	360668 35 g-index
39 all docs	39 docs citations	39 times ranked	1802 citing authors

#	Article	IF	Citations
1	Elucidation of xenoestrogen metabolism by non-targeted, stable isotope-assisted mass spectrometry in breast cancer cells. Environment International, 2022, 158, 106940.	4.8	9
2	A novel method combining stable isotopic labeling and high-resolution mass spectrometry to trace the quinone reaction products in wines. Food Chemistry, 2022, 383, 132448.	4.2	4
3	CPExtract, a Software Tool for the Automated Tracer-Based Pathway Specific Screening of Secondary Metabolites in LC-HRMS Data. Analytical Chemistry, 2022, 94, 3543-3552.	3.2	4
4	PeakBot: machine-learning-based chromatographic peak picking. Bioinformatics, 2022, 38, 3422-3428.	1.8	10
5	Towards a broader view of the metabolome: untargeted profiling of soluble and bound polyphenols in plants. Analytical and Bioanalytical Chemistry, 2022, 414, 7421-7433.	1.9	2
6	Trichoderma spp. volatile organic compounds protect grapevine plants by activating defenseâ€related processes against downy mildew. Physiologia Plantarum, 2021, 172, 1950-1965.	2.6	42
7	The Comprehensive and Reliable Detection of Secondary Metabolites in Trichoderma reesei: A Tool for the Discovery of Novel Substances. Methods in Molecular Biology, 2021, 2234, 271-295.	0.4	0
8	Enhanced Metabolome Coverage and Evaluation of Matrix Effects by the Use of Experimental-Condition-Matched 13C-Labeled Biological Samples in Isotope-Assisted LC-HRMS Metabolomics. Metabolites, 2020, 10, 434.	1.3	4
9	Stable Isotope-Assisted Metabolomics for Deciphering Xenobiotic Metabolism in Mammalian Cell Culture. ACS Chemical Biology, 2020, 15, 970-981.	1.6	25
10	Preparation of uniformly labelled 13C- and 15N-plants using customised growth chambers. Plant Methods, 2020, 16, 46.	1.9	13
11	Stable Isotope-Assisted Plant Metabolomics: Investigation of Phenylalanine-Related Metabolic Response in Wheat Upon Treatment With the Fusarium Virulence Factor Deoxynivalenol. Frontiers in Plant Science, 2019, 10, 1137.	1.7	35
12	Stable Isotopeâ€"Assisted Plant Metabolomics: Combination of Global and Tracer-Based Labeling for Enhanced Untargeted Profiling and Compound Annotation. Frontiers in Plant Science, 2019, 10, 1366.	1.7	23
13	Volatiles from the Mandibular Gland Reservoir Content of Colobopsis explodens Laciny and Zettel, 2018, Worker Ants (Hymenoptera: Formicidae). Molecules, 2019, 24, 3468.	1.7	5
14	Tracing oxidation reaction pathways in wine using 13C isotopolog patterns and a putative compound database. Analytica Chimica Acta, 2019, 1054, 74-83.	2.6	17
15	Untargeted LCâ€"MS based 13C labelling provides a full mass balance of deoxynivalenol and its degradation products formed during baking of crackers, biscuits and bread. Food Chemistry, 2019, 279, 303-311.	4.2	23
16	Downy mildew symptoms on grapevines can be reduced by volatile organic compounds of resistant genotypes. Scientific Reports, 2018, 8, 1618.	1.6	38
17	Partially 13C-labeled mouse tissue as reference for LC-MS based untargeted metabolomics. Analytical Biochemistry, 2018, 556, 63-69.	1.1	6
18	Methanol Generates Numerous Artifacts during Sample Extraction and Storage of Extracts in Metabolomics Research. Metabolites, 2018, 8, 1.	1.3	73

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19	Transcription factor Xpp1 is a switch between primary and secondary fungal metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E560-E569.	3.3	86
20	The Profile and Dynamics of RNA Modifications in Animals. ChemBioChem, 2017, 18, 979-984.	1.3	30
21	MetExtract II: A Software Suite for Stable Isotope-Assisted Untargeted Metabolomics. Analytical Chemistry, 2017, 89, 9518-9526.	3.2	80
22	Metabolism of HT-2 Toxin and T-2 Toxin in Oats. Toxins, 2016, 8, 364.	1.5	31
23	Stable Isotope-Assisted Evaluation of Different Extraction Solvents for Untargeted Metabolomics of Plants. International Journal of Molecular Sciences, 2016, 17, 1017.	1.8	64
24	MetMatch: A Semi-Automated Software Tool for the Comparison and Alignment of LC-HRMS Data from Different Metabolomics Experiments. Metabolites, 2016, 6, 39.	1.3	12
25	QCScreen: a software tool for data quality control in LC-HRMS based metabolomics. BMC Bioinformatics, 2015, 16, 341.	1.2	16
26	Joint Transcriptomic and Metabolomic Analyses Reveal Changes in the Primary Metabolism and Imbalances in the Subgenome Orchestration in the Bread Wheat Molecular Response toFusarium graminearum. G3: Genes, Genomes, Genetics, 2015, 5, 2579-2592.	0.8	45
27	GCâ€“MS based targeted metabolic profiling identifies changes in the wheat metabolome following deoxynivalenol treatment. Metabolomics, 2015, 11, 722-738.	1.4	117
28	Biotransformation of the Mycotoxin Deoxynivalenol in Fusarium Resistant and Susceptible Near Isogenic Wheat Lines. PLoS ONE, 2015, 10, e0119656.	1.1	93
29	Metabolism of the Fusarium Mycotoxins T-2 Toxin and HT-2 Toxin in Wheat. Journal of Agricultural and Food Chemistry, 2015, 63, 7862-7872.	2.4	78
30	Tracing the metabolism of HT-2 toxin and T-2 toxin in barley by isotope-assisted untargeted screening and quantitative LC-HRMS analysis. Analytical and Bioanalytical Chemistry, 2015, 407, 8019-8033.	1.9	56
31	Tracing flavonoid degradation in grapes by MS filtering with stable isotopes. Food Chemistry, 2015, 166, 448-455.	4.2	23
32	Untargeted Profiling of Tracer-Derived Metabolites Using Stable Isotopic Labeling and Fast Polarity-Switching LCâ€“ESI-HRMS. Analytical Chemistry, 2014, 86, 11533-11537.	3.2	52
33	A novel stable isotope labelling assisted workflow for improved untargeted LCâ€“HRMS based metabolomics research. Metabolomics, 2014, 10, 754-769.	1.4	84
34	Automated LC-HRMS(/MS) Approach for the Annotation of Fragment Ions Derived from Stable Isotope Labeling-Assisted Untargeted Metabolomics. Analytical Chemistry, 2014, 86, 7320-7327.	3.2	22
35	Stable isotopic labelling-assisted untargeted metabolic profiling reveals novel conjugates of the mycotoxin deoxynivalenol in wheat. Analytical and Bioanalytical Chemistry, 2013, 405, 5031-5036.	1.9	102
36	MetExtract: a new software tool for the automated comprehensive extraction of metabolite-derived LC/MS signals in metabolomics research. Bioinformatics, 2012, 28, 736-738.	1.8	68