Hiroshi Tsugawa

List of Publications by Year
in descending order

58	6,711	147566	168136
papers	citations	31 h-index	53 g-index

64	64	64	9681
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	MS-DIAL: data-independent MS/MS deconvolution for comprehensive metabolome analysis. Nature Methods, 2015, 12, 523-526.	9.0	1,955
2	Feature-based molecular networking in the GNPS analysis environment. Nature Methods, 2020, 17, 905-908.	9.0	650
3	Hydrogen Rearrangement Rules: Computational MS/MS Fragmentation and Structure Elucidation Using MS-FINDER Software. Analytical Chemistry, 2016, 88, 7946-7958.	3.2	441
4	A lipidome atlas in MS-DIAL 4. Nature Biotechnology, 2020, 38, 1159-1163.	9.4	424
5	Identifying metabolites by integrating metabolome databases with mass spectrometry cheminformatics. Nature Methods, 2018, 15, 53-56.	9.0	368
6	Identification of small molecules using accurate mass MS/MS search. Mass Spectrometry Reviews, 2018, 37, 513-532.	2.8	292
7	A cheminformatics approach to characterize metabolomes in stable-isotope-labeled organisms. Nature Methods, 2019, 16, 295-298.	9.0	194
8	Current metabolomics: Technological advances. Journal of Bioscience and Bioengineering, 2013, 116, 9-16.	1.1	178
9	GC/MS based metabolomics: development of a data mining system for metabolite identification by using soft independent modeling of class analogy (SIMCA). BMC Bioinformatics, 2011, 12, 131.	1.2	171
10	Retip: Retention Time Prediction for Compound Annotation in Untargeted Metabolomics. Analytical Chemistry, 2020, 92, 7515-7522.	3.2	128
11	Critical Assessment of Small Molecule Identification 2016: automated methods. Journal of Cheminformatics, 2017, 9, 22.	2.8	122
12	Ion identity molecular networking for mass spectrometry-based metabolomics in the GNPS environment. Nature Communications, 2021, 12, 3832.	5.8	119
13	Bulk <scp>RNA</scp> degradation by nitrogen starvationâ€induced autophagy in yeast. EMBO Journal, 2015, 34, 154-168.	3.5	114
14	Practical non-targeted gas chromatography/mass spectrometry-based metabolomics platform for metabolic phenotype analysis. Journal of Bioscience and Bioengineering, 2011, 112, 292-298.	1.1	108
15	MRMPROBS: A Data Assessment and Metabolite Identification Tool for Large-Scale Multiple Reaction Monitoring Based Widely Targeted Metabolomics. Analytical Chemistry, 2013, 85, 5191-5199.	3.2	102
16	Advances in computational metabolomics and databases deepen the understanding of metabolisms. Current Opinion in Biotechnology, 2018, 54, 10-17.	3.3	89
17	Comprehensive comparison of in silico MS/MS fragmentation tools of the CASMI contest: database boosting is needed to achieve 93% accuracy. Journal of Cheminformatics, 2017, 9, 32.	2.8	80
18	MRMPROBS suite for metabolomics using large-scale MRM assays. Bioinformatics, 2014, 30, 2379-2380.	1.8	77

#	Article	IF	Citations
19	Chromosome-level genome assembly of Ophiorrhiza pumila reveals the evolution of camptothecin biosynthesis. Nature Communications, 2021, 12, 405.	5.8	77
20	Discovering Regulated Metabolite Families in Untargeted Metabolomics Studies. Analytical Chemistry, 2016, 88, 8082-8090.	3.2	72
21	Lipid Annotator: Towards Accurate Annotation in Non-Targeted Liquid Chromatography High-Resolution Tandem Mass Spectrometry (LC-HRMS/MS) Lipidomics Using a Rapid and User-Friendly Software. Metabolites, 2020, 10, 101.	1.3	69
22	MS-CleanR: A Feature-Filtering Workflow for Untargeted LCâ€“MS Based Metabolomics. Analytical Chemistry, 2020, 92, 9971-9981.	3.2	55
23	Defining the Scope of Exposome Studies and Research Needs from a Multidisciplinary Perspective. Environmental Science and Technology Letters, 2021, 8, 839-852.	3.9	55
24	Comprehensive identification of sphingolipid species by in silico retention time and tandem mass spectral library. Journal of Cheminformatics, 2017, 9, 19.	2.8	54
25	Highly sensitive and selective analysis of widely targeted metabolomics using gas chromatography/triple-quadrupole mass spectrometry. Journal of Bioscience and Bioengineering, 2014, 117, 122-128.	1.1	52
26	Characterization of Lipid Profiles after Dietary Intake of Polyunsaturated Fatty Acids Using Integrated Untargeted and Targeted Lipidomics. Metabolites, 2019, 9, 241.	1.3	48
27	Correlation-Based Deconvolution (CorrDec) To Generate High-Quality MS2 Spectra from Data-Independent Acquisition in Multisample Studies. Analytical Chemistry, 2020, 92, 11310-11317.	3.2	46
28	Metabolomics and complementary techniques to investigate the plant phytochemical cosmos. Natural Product Reports, 2021, 38, 1729-1759.	5.2	46
29	Integrated Strategy for Unknown Elâ€“MS Identification Using Quality Control Calibration Curve, Multivariate Analysis, Elâ€“MS Spectral Database, and Retention Index Prediction. Analytical Chemistry, 2017, 89, 6766-6773.	3.2	38
30	Method for Assessing the Statistical Significance of Mass Spectral Similarities Using Basic Local Alignment Search Tool Statistics. Analytical Chemistry, 2013, 85, 8291-8297.	3.2	34
31	Elucidation of Gut Microbiota-Associated Lipids Using LC-MS/MS and 16S rRNA Sequence Analyses. IScience, 2020, 23, 101841.	1.9	33
32	Mass Spectrometry Data Repository Enhances Novel Metabolite Discoveries with Advances in Computational Metabolomics. Metabolites, 2019, 9, 119.	1.3	31
33	Creating a Reliable Mass Spectralâ€“Retention Time Library for All Ion Fragmentation-Based Metabolomics. Metabolites, 2019, 9, 251.	1.3	30
34	MRM-DIFF: data processing strategy for differential analysis in large scale MRM-based lipidomics studies. Frontiers in Genetics, 2014, 5, 471.	1.1	29
35	Identification of Biomarkers of Stent Restenosis With Serum Metabolomic Profiling Using Gas Chromatography/Mass Spectrometry. Circulation Journal, 2012, 76, 1864-1873.	0.7	23
36	Flavor characteristics of the juices from fresh market tomatoes differentiated from those from processing tomatoes by combined analysis of volatile profiles with sensory evaluation. Bioscience, Biotechnology and Biochemistry, 2016, 80, 2401-2411.	0.6	22

#	Article	IF	Citations
37	Using MS-FINDER for identifying 19 natural products in the CASMI 2016 contest. Phytochemistry Letters, 2017, 21, 306-312.	0.6	21
38	The importance of bioinformatics for connecting data-driven lipidomics and biological insights. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2017, 1862, 762-765.	1.2	19
39	Plasma metabolites associated with arterial stiffness in patients with type 2 diabetes. Cardiovascular Diabetology, 2020, 19, 75.	2.7	19
40	Metabolomics with ¹⁵N Labeling for Characterizing Missing Monoterpene Indole Alkaloids in Plants. Analytical Chemistry, 2020, 92, 5670-5675.	3.2	19
41	Food Lipidomics for 155 Agricultural Plant Products. Journal of Agricultural and Food Chemistry, 2021, 69, 8981-8990.	2.4	18
42	Different-batch metabolome analysis of Saccharomyces cerevisiae based on gas chromatography/mass spectrometry. Journal of Bioscience and Bioengineering, 2014, 117, 248-255.	1.1	17
43	Identification of Plasma Inositol and Indoxyl Sulfate as Novel Biomarker Candidates for Atherosclerosis in Patients with Type 2 Diabetes. -Findings from Metabolome Analysis Using GC/MS-. Journal of Atherosclerosis and Thrombosis, 2020, 27, 1053-1067.	0.9	15
44	Automation of chemical assignment for identifying molecular formula of S-containing metabolites by combining metabolomics and chemoinformatics with 34S labeling. Metabolomics, 2016, 12, 1.	1.4	12
45	Metabolome-Based Discrimination Analysis of Shallot Landraces and Bulb Onion Cultivars Associated with Differences in the Amino Acid and Flavonoid Profiles. Molecules, 2020, 25, 5300.	1.7	12
46	Novel Strategy for Non-Targeted Isotope-Assisted Metabolomics by Means of Metabolic Turnover and Multivariate Analysis. Metabolites, 2014, 4, 722-739.	1.3	10
47	Boosting Sensitivity in Liquid Chromatographyâ€“Fourier Transform Ion Cyclotron Resonanceâ€“Tandem Mass Spectrometry for Product Ion Analysis of Monoterpene Indole Alkaloids. Frontiers in Plant Science, 2015, 6, 1127.	1.7	9
48	Global profiling of gut microbiota-associated lipid metabolites in antibiotic-treated mice by LC-MS/MS-based analyses. STAR Protocols, 2021, 2, 100492.	0.5	9
49	Stage-Specific De Novo Synthesis of Very-Long-Chain Dihydroceramides Confers Dormancy to Entamoeba Parasites. MSphere, 2021, 6, .	1.3	8
50	Lipidomics and Redox Lipidomics Indicate Early Stage Alcoholâ€Induced Liver Damage. Hepatology Communications, 2022, 6, 513-525.	2.0	6
51	OS-PCA: Orthogonal Smoothed Principal Component Analysis Applied to Metabolome Data. Metabolites, 2021, 11, 149.	1.3	4
52	The Guide for Metabolite Annotation/Identification in Untargeted Metabolomics. Journal of the Mass Spectrometry Society of Japan, 2017, 65, 203-209.	0.0	1
53	Computational MS/MS Fragmentation and Structure Elucidation Using MS-FINDER Software. , 2020, , 189-210.		1
54	Gas Chromatography/Mass Spectrometry Analysis: Nontargeted Metabolomics Based on Scan Mode Analysis. , 2014, , 103-135.		0

#	Article	IF	Citations
55	LC/QqQ/MS Analysis: Widely Targeted Metabolomics on the Basis of Multiple Reaction Monitoring. , 2014, , 137-169.		0
56	Computational Mass Spectrometry Deepens The Understanding Of Metabolisms. , 2018, , .		0
57	Data Analysis in Untargeted Lipidomics. Oleoscience, 2022, 22, 297-306.	0.0	0
58	Predicting Molecular Formula from Mass Spectrometry Data. Journal of the Mass Spectrometry Society of Japan, 2022, 70, 133-134.	0.0	0