Hiroshi Tsugawa

List of Publications by Year in Descending Order

57 papers	3,586 citations	24 h-index	59 g-index
64 ext. papers	5,185 ext. citations	8.1 avg, IF	5.46 L-index

#	Paper	IF	Citations
57	Stage-Specific Synthesis of Very-Long-Chain Dihydroceramides Confers Dormancy to Parasites. *MSphere*, **2021**, 6,	5	1
56	Global profiling of gut microbiota-associated lipid metabolites in antibiotic-treated mice by LC-MS/MS-based analyses. *STAR Protocols*, **2021**, 2, 100492	1.4	2
55	Ion identity molecular networking for mass spectrometry-based metabolomics in the GNPS environment. *Nature Communications*, **2021**, 12, 3832	17.4	22
54	Chromosome-level genome assembly of Ophiorrhiza pumila reveals the evolution of camptothecin biosynthesis. *Nature Communications*, **2021**, 12, 405	17.4	24
53	Food Lipidomics for 155 Agricultural Plant Products. *Journal of Agricultural and Food Chemistry*, **2021**, 69, 8981-8990	5.7	11
52	Defining the Scope of Exposome Studies and Research Needs from a Multidisciplinary Perspective. *Environmental Science and Technology Letters*, **2021**, 8, 839-852	11	10
51	Metabolomics and complementary techniques to investigate the plant phytochemical cosmos. *Natural Product Reports*, **2021**, 38, 1729-1759	15.1	7
50	Elucidation of Gut Microbiota-Associated Lipids Using LC-MS/MS and 16S rRNA Sequence Analyses. *IScience*, **2020**, 23, 101841	6.1	13
49	Retip: Retention Time Prediction for Compound Annotation in Untargeted Metabolomics. *Analytical Chemistry*, **2020**, 92, 7515-7522	7.8	44
48	Plasma metabolites associated with arterial stiffness in patients with type 2 diabetes. *Cardiovascular Diabetology*, **2020**, 19, 75	8.7	9
47	A lipidome atlas in MS-DIAL 4. *Nature Biotechnology*, **2020**, 38, 1159-1163	44.5	141
46	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,	5.6	24
45	MS-CleanR: A Feature-Filtering Workflow for Untargeted LC-MS Based Metabolomics. *Analytical Chemistry*, **2020**, 92, 9971-9981	7.8	22
44	Metabolomics with N Labeling for Characterizing Missing Monoterpene Indole Alkaloids in Plants. *Analytical Chemistry*, **2020**, 92, 5670-5675	7.8	14
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	4	10
42	Computational MS/MS Fragmentation and Structure Elucidation Using MS-FINDER Software **2020**, 189-210		
41	Correlation-Based Deconvolution (CorrDec) To Generate High-Quality MS2 Spectra from Data-Independent Acquisition in Multisample Studies. *Analytical Chemistry*, **2020**, 92, 11310-11317	7.8	14

40	Metabolome-Based Discrimination Analysis of Shallot Landraces and Bulb Onion Cultivars Associated with Differences in the Amino Acid and Flavonoid Profiles. *Molecules*, **2020**, 25,	4.8	3
39	Feature-based molecular networking in the GNPS analysis environment. *Nature Methods*, **2020**, 17, 905-908	21.6	207
38	A cheminformatics approach to characterize metabolomes in stable-isotope-labeled organisms. *Nature Methods*, **2019**, 16, 295-298	21.6	99
37	Mass Spectrometry Data Repository Enhances Novel Metabolite Discoveries with Advances in Computational Metabolomics. *Metabolites*, **2019**, 9,	5.6	14
36	Creating a Reliable Mass Spectral-Retention Time Library for All Ion Fragmentation-Based Metabolomics. *Metabolites*, **2019**, 9,	5.6	15
35	Characterization of Lipid Profiles after Dietary Intake of Polyunsaturated Fatty Acids Using Integrated Untargeted and Targeted Lipidomics. *Metabolites*, **2019**, 9,	5.6	28
34	Advances in computational metabolomics and databases deepen the understanding of metabolisms. *Current Opinion in Biotechnology*, **2018**, 54, 10-17	11.4	58
33	Identification of small molecules using accurate mass MS/MS search. *Mass Spectrometry Reviews*, **2018**, 37, 513-532	11	194
32	Identifying metabolites by integrating metabolome databases with mass spectrometry cheminformatics. *Nature Methods*, **2018**, 15, 53-56	21.6	200
31	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	5	15
30	Integrated Strategy for Unknown EI-MS Identification Using Quality Control Calibration Curve, Multivariate Analysis, EI-MS Spectral Database, and Retention Index Prediction. *Analytical Chemistry* , **2017**, 89, 6766-6773	7.8	23
29	Comprehensive identification of sphingolipid species by in silico retention time and tandem mass spectral library. *Journal of Cheminformatics*, **2017**, 9, 19	8.6	39
28	Using MS-FINDER for identifying 19 natural products in the CASMI 2016 contest. *Phytochemistry Letters*, **2017**, 21, 306-312	1.9	10
27	Critical Assessment of Small Molecule Identification 2016: automated methods. *Journal of Cheminformatics*, **2017**, 9, 22	8.6	89
26	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	8.6	64
25	The Guide for Metabolite Annotation/Identification in Untargeted Metabolomics. *Journal of the Mass Spectrometry Society of Japan*, **2017**, 65, 203-209	0.2	1
24	Discovering Regulated Metabolite Families in Untargeted Metabolomics Studies. *Analytical Chemistry*, **2016**, 88, 8082-90	7.8	56
23	Hydrogen Rearrangement Rules: Computational MS/MS Fragmentation and Structure Elucidation Using MS-FINDER Software. *Analytical Chemistry*, **2016**, 88, 7946-58	7.8	292

22	Automation of chemical assignment for identifying molecular formula of S-containing metabolites by combining metabolomics and chemoinformatics with 34S labeling. *Metabolomics*, **2016**, 12, 1	4.7	8
21	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	2.1	17
20	MS-DIAL: data-independent MS/MS deconvolution for comprehensive metabolome analysis. *Nature Methods*, **2015**, 12, 523-6	21.6	1036
19	Bulk RNA degradation by nitrogen starvation-induced autophagy in yeast. *EMBO Journal*, **2015**, 34, 154-68	9	79
18	Boosting Sensitivity in Liquid Chromatography-Fourier Transform Ion Cyclotron Resonance-Tandem Mass Spectrometry for Product Ion Analysis of Monoterpene Indole Alkaloids. *Frontiers in Plant Science*, **2015**, 6, 1127	6.2	6
17	MRM-DIFF: data processing strategy for differential analysis in large scale MRM-based lipidomics studies. *Frontiers in Genetics*, **2014**, 5, 471	4.5	21
16	Gas Chromatography/Mass Spectrometry Analysis: Nontargeted Metabolomics Based on Scan Mode Analysis **2014**, 103-135		
15	LC/QqQ/MS Analysis: Widely Targeted Metabolomics on the Basis of Multiple Reaction Monitoring **2014**, 137-169		
14	Novel strategy for non-targeted isotope-assisted metabolomics by means of metabolic turnover and multivariate analysis. *Metabolites*, **2014**, 4, 722-39	5.6	8
13	MRMPROBS suite for metabolomics using large-scale MRM assays. *Bioinformatics*, **2014**, 30, 2379-80	7.2	37
12	Different-batch metabolome analysis of Saccharomyces cerevisiae based on gas chromatography/mass spectrometry. *Journal of Bioscience and Bioengineering*, **2014**, 117, 248-255	3.3	15
11	Highly sensitive and selective analysis of widely targeted metabolomics using gas chromatography/triple-quadrupole mass spectrometry. *Journal of Bioscience and Bioengineering*, **2014**, 117, 122-8	3.3	47
10	Method for assessing the statistical significance of mass spectral similarities using basic local alignment search tool statistics. *Analytical Chemistry*, **2013**, 85, 8291-7	7.8	26
9	Current metabolomics: technological advances. *Journal of Bioscience and Bioengineering*, **2013**, 116, 9-16	3.3	143
8	MRMPROBS: a data assessment and metabolite identification tool for large-scale multiple reaction monitoring based widely targeted metabolomics. *Analytical Chemistry*, **2013**, 85, 5191-9	7.8	67
7	Identification of biomarkers of stent restenosis with serum metabolomic profiling using gas chromatography/mass spectrometry. *Circulation Journal*, **2012**, 76, 1864-73	2.9	15
6	Practical non-targeted gas chromatography/mass spectrometry-based metabolomics platform for metabolic phenotype analysis. *Journal of Bioscience and Bioengineering*, **2011**, 112, 292-8	3.3	94
5	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	3.6	141

List of Publications

4	MS-CleanR: A feature-filtering approach to improve annotation rate in untargeted LC-MS based metabolomics	1
3	MS-DIAL 4: accelerating lipidomics using an MS/MS, CCS, and retention time atlas	8
2	Ion Identity Molecular Networking in the GNPS Environment	11
1	Feature-based Molecular Networking in the GNPS Analysis Environment	29