Takeshi Ara

List of Publications by Year
in descending order

42 papers	10,958 citations	394421 19 h-index	276875 41 g-index
43 all docs	43 docs citations	43 times ranked	14474 citing authors

#	Article	IF	Citations
1	Integration of bioassay and non-target metabolite analysis of tomato reveals that β-carotene and lycopene activate the adiponectin signaling pathway, including AMPK phosphorylation. PLoS ONE, 2022, 17, e0267248.	2.5	1
2	MassBase: A large-scaled depository of mass spectrometry datasets for metabolome analysis. Plant Biotechnology, 2021, 38, 167-171.	1.0	5
3	TOMATOMET: A metabolome database consists of 7118 accurate mass values detected in mature fruits of 25 tomato cultivars. Plant Direct, 2021, 5, e00318.	1.9	20
4	Metabolic analysis of unripe papaya (*Carica papaya* L.) to promote its utilization as a functional food. Bioscience, Biotechnology and Biochemistry, 2021, 85, 1194-1204.	1.3	8
5	Metabolome analysis using multiple data mining approaches suggests luteolin biosynthesis in <i>Physcomitrella patens</i>. Plant Biotechnology, 2020, 37, 377-381.	1.0	4
6	Metabolome profile of Negi-Nira chive, an interspecies hybrid of green spring onion (<i>Allium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542	1.0	0
7	A new mouse model for noninvasive fluorescence‐based monitoring of mitochondrial <scp>UCP</scp>1 expression. FEBS Letters, 2019, 593, 1201-1212.	2.8	8
8	Soy hydrolysate enhances the isoproterenol-stimulated lipolytic pathway through an increase in β-adrenergic receptor expression in adipocytes. Bioscience, Biotechnology and Biochemistry, 2019, 83, 1782-1789.	1.3	3
9	Endoplasmic Reticulum Stress Impaired Uncoupling Protein 1 Expression via the Suppression of Peroxisome Proliferator-Activated Receptor γ Binding Activity in Mice Beige Adipocytes. International Journal of Molecular Sciences, 2019, 20, 274.	4.1	25
10	Apo-12′-lycopenal, a Lycopene Metabolite, Promotes Adipocyte Differentiation via Peroxisome Proliferator-Activated Receptor γ Activation. Journal of Agricultural and Food Chemistry, 2018, 66, 13152-13161.	5.2	11
11	The Mevalonate Pathway Is Indispensable for Adipocyte Survival. IScience, 2018, 9, 175-191.	4.1	45
12	Pathway-specific metabolome analysis with 18O2-labeled Medicago truncatula via a mass spectrometry-based approach. Metabolomics, 2018, 14, 71.	3.0	19
13	β-adrenergic Receptor Stimulation Revealed a Novel Regulatory Pathway via Suppressing Histone Deacetylase 3 to Induce Uncoupling Protein 1 Expression in Mice Beige Adipocyte. International Journal of Molecular Sciences, 2018, 19, 2436.	4.1	10
14	Wide-range screening of anti-inflammatory compounds in tomato using LC-MS and elucidating the mechanism of their functions. PLoS ONE, 2018, 13, e0191203.	2.5	18
15	Over-expression of PPARα in obese mice adipose tissue improves insulin sensitivity. Biochemical and Biophysical Research Communications, 2017, 493, 108-114.	2.1	18
16	FlavonoidSearch: A system for comprehensive flavonoid annotation by mass spectrometry. Scientific Reports, 2017, 7, 1243.	3.3	41
17	Jatropha Metabolomics. Compendium of Plant Genomes, 2017, , 83-96.	0.5	1
18	Metabolonote: A Wiki-Based Database for Managing Hierarchical Metadata of Metabolome Analyses. Frontiers in Bioengineering and Biotechnology, 2015, 3, 38.	4.1	39

#	ARTICLE	IF	CITATIONS
19	Tools and Databases of the KOMICS Web Portal for Preprocessing, Mining, and Dissemination of Metabolomics Data. BioMed Research International, 2014, 2014, 1-11.	1.9	38
20	ShiftedIonsFinder: A standalone Java tool for finding peaks with specified mass differences by comparing mass spectra of isotope-labeled and unlabeled data sets. Plant Biotechnology, 2014, 31, 269-274.	1.0	9
21	An application of a relational database system for high-throughput prediction of elemental compositions from accurate mass values. Bioinformatics, 2013, 29, 290-291.	4.1	28
22	Development of KaPPA-View4 for omics studies on Jatropha and a database system KaPPA-Loader for construction of local omics databases. Plant Biotechnology, 2012, 29, 131-135.	1.0	9
23	MatchedIonsFinder: A software tool for revising alignment matrices of spectrograms from liquid chromatography-mass spectrometry. Plant Biotechnology, 2012, 29, 109-113.	1.0	5
24	Dynamic metabolic changes during fruit maturation in Jatropha curcas L.. Plant Biotechnology, 2012, 29, 175-178.	1.0	12
25	KaPPA-View4: a metabolic pathway database for representation and analysis of correlation networks of gene co-expression and metabolite co-accumulation and omics data. Nucleic Acids Research, 2011, 39, D677-D684.	14.5	69
26	MassBank: a public repository for sharing mass spectral data for life sciences. Journal of Mass Spectrometry, 2010, 45, 703-714.	1.6	1,831
27	Transient increase in salicylic acid and its glucose conjugates after wounding in Arabidopsis leaves. Plant Biotechnology, 2010, 27, 205-209.	1.0	23
28	Complete genome sequence and comparative analysis of Shewanella violacea, a psychrophilic and piezophilic bacterium from deep sea floor sediments. Molecular BioSystems, 2010, 6, 1216.	2.9	42
29	Using Alu Elements as Polyadenylation Sites: A Case of Retroposon Exaptation. Molecular Biology and Evolution, 2009, 26, 327-334.	8.9	81
30	ASTD: The Alternative Splicing and Transcript Diversity database. Genomics, 2009, 93, 213-220.	2.9	87
31	Improvement of the quantitative differential metabolome pipeline for gas chromatography-mass spectrometry data by automated reliable peak selection. Plant Biotechnology, 2009, 26, 445-449.	1.0	4
32	Beyond the 3′ end: experimental validation of extended transcript isoforms. Nucleic Acids Research, 2007, 35, 1947-1957.	14.5	18
33	Complete set of ORF clones of Escherichia coli ASKA library (A Complete Set of E. coli K-12 ORF) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.4	1,213
34	Construction of <i>Escherichia coli</i> K-12 in-frame, single-gene knockout mutants: the Keio collection. Molecular Systems Biology, 2006, 2, 2006.0008.	7.2	6,537
35	Conservation of alternative polyadenylation patterns in mammalian genes. BMC Genomics, 2006, 7, 189.	2.8	47
36	The disparate nature of "intergenic" polyadenylation sites. Rna, 2006, 12, 1794-1801.	3.5	25

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37	Large-scale identification of protein–protein interaction of <i>Escherichia coli</i> K-12. Genome Research, 2006, 16, 686-691.	5.5	368
38	Distribution of Repetitive Sequences on the Leading and Lagging Strands of the Escherichia coli Genome: Comparative Study of Long Direct Repeat (LDR) Sequences. DNA Research, 2002, 9, 1-10.	3.4	9
39	Conservation of Translation Initiation Sites Based on Dinucleotide Frequency and Codon Usage in Escherichia coli K-12 (W3110): Non-random Distribution of A/T-rich Sequences Immediately Upstream of the Translation Initiation Codon. DNA Research, 2002, 9, 19-24.	3.4	10
40	Complete Nucleotide Sequence of Plasmid Rts1: Implications for Evolution of Large Plasmid Genomes. Journal of Bacteriology, 2002, 184, 3194-3202.	2.2	66
41	Genome-wide analysis of deoxyadenosine methyltransferase-mediated control of gene expression in Escherichia coli. Molecular Microbiology, 2002, 45, 673-695.	2.5	147
42	Non-radioactive Adenosine 5′-Phosphosulfate Sulfotransferase Assay by Coupling with Sulfite Reductase andO-Acetylserine(thiol)lyase. Bioscience, Biotechnology and Biochemistry, 1997, 61, 621-624.	1.3	4