

Takeshi Ara

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

10,958
citations

394286

19
h-index

276775

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.	1.1	1
2	MassBase: A large-scaled depository of mass spectrometry datasets for metabolome analysis. Plant Biotechnology, 2021, 38, 167-171.	0.5	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.	0.8	20
4	Metabolic analysis of unripe papaya (<i>Carica papaya</i> L.) to promote its utilization as a functional food. Bioscience, Biotechnology and Biochemistry, 2021, 85, 1194-1204.	0.6	8
5	Metabolome analysis using multiple data mining approaches suggests luteolin biosynthesis in <i>Physcomitrella patens</i> . Plant Biotechnology, 2020, 37, 377-381.	0.5	4
6	Metabolome profile of Negi-Nira chive, an interspecies hybrid of green spring onion (<i>Allium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542	0.5	0
7	A new mouse model for noninvasive fluorescence-based monitoring of mitochondrial $\langle \text{sc} \rangle \text{UCP} \langle / \text{sc} \rangle 1$ expression. FEBS Letters, 2019, 593, 1201-1212.	1.3	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.	0.6	3
9	Endoplasmic Reticulum Stress Impaired Uncoupling Protein 1 Expression via the Suppression of Peroxisome Proliferator-Activated Receptor β Binding Activity in Mice Beige Adipocytes. International Journal of Molecular Sciences, 2019, 20, 274.	1.8	25
10	Apo-12-lycopenal, a Lycopene Metabolite, Promotes Adipocyte Differentiation via Peroxisome Proliferator-Activated Receptor β Activation. Journal of Agricultural and Food Chemistry, 2018, 66, 13152-13161.	2.4	11
11	The Mevalonate Pathway Is Indispensable for Adipocyte Survival. IScience, 2018, 9, 175-191.	1.9	45
12	Pathway-specific metabolome analysis with $^{18}\text{O}_2$ -labeled <i>Medicago truncatula</i> via a mass spectrometry-based approach. Metabolomics, 2018, 14, 71.	1.4	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.	1.8	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.	1.1	18
15	Over-expression of PPAR α in obese mice adipose tissue improves insulin sensitivity. Biochemical and Biophysical Research Communications, 2017, 493, 108-114.	1.0	18
16	FlavonoidSearch: A system for comprehensive flavonoid annotation by mass spectrometry. Scientific Reports, 2017, 7, 1243.	1.6	41
17	Jatropha Metabolomics. Compendium of Plant Genomes, 2017, , 83-96.	0.3	1
18	Metabolonote: A Wiki-Based Database for Managing Hierarchical Metadata of Metabolome Analyses. Frontiers in Bioengineering and Biotechnology, 2015, 3, 38.	2.0	39

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19	Tools and Databases of the KOMICS Web Portal for Preprocessing, Mining, and Dissemination of Metabolomics Data. <i>BioMed Research International</i> , 2014, 2014, 1-11.	0.9	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. <i>Plant Biotechnology</i> , 2014, 31, 269-274.	0.5	9
21	An application of a relational database system for high-throughput prediction of elemental compositions from accurate mass values. <i>Bioinformatics</i> , 2013, 29, 290-291.	1.8	28
22	Development of KaPPA-View4 for omics studies on <i>Jatropha</i> and a database system KaPPA-Loader for construction of local omics databases. <i>Plant Biotechnology</i> , 2012, 29, 131-135.	0.5	9
23	MatchedIonsFinder: A software tool for revising alignment matrices of spectrograms from liquid chromatography-mass spectrometry. <i>Plant Biotechnology</i> , 2012, 29, 109-113.	0.5	5
24	Dynamic metabolic changes during fruit maturation in <i>Jatropha curcas</i> L.. <i>Plant Biotechnology</i> , 2012, 29, 175-178.	0.5	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. <i>Nucleic Acids Research</i> , 2011, 39, D677-D684.	6.5	69
26	MassBank: a public repository for sharing mass spectral data for life sciences. <i>Journal of Mass Spectrometry</i> , 2010, 45, 703-714.	0.7	1,831
27	Transient increase in salicylic acid and its glucose conjugates after wounding in <i>Arabidopsis</i> leaves. <i>Plant Biotechnology</i> , 2010, 27, 205-209.	0.5	23
28	Complete genome sequence and comparative analysis of <i>Shewanella violacea</i> , a psychrophilic and piezophilic bacterium from deep sea floor sediments. <i>Molecular BioSystems</i> , 2010, 6, 1216.	2.9	42
29	Using Alu Elements as Polyadenylation Sites: A Case of Retroposon Exaptation. <i>Molecular Biology and Evolution</i> , 2009, 26, 327-334.	3.5	81
30	ASTD: The Alternative Splicing and Transcript Diversity database. <i>Genomics</i> , 2009, 93, 213-220.	1.3	87
31	Improvement of the quantitative differential metabolome pipeline for gas chromatography-mass spectrometry data by automated reliable peak selection. <i>Plant Biotechnology</i> , 2009, 26, 445-449.	0.5	4
32	Beyond the 3' end: experimental validation of extended transcript isoforms. <i>Nucleic Acids Research</i> , 2007, 35, 1947-1957.	6.5	18
33	Complete set of ORF clones of <i>Escherichia coli</i> ASKA library (A Complete Set of <i>E. coli</i> K-12 ORF) Tj ETQq1 1 0.784314 rgBT / Overlock 1,213	1.5	1,213
34	Construction of <i>Escherichia coli</i> K12 in-frame, single-gene knockout mutants: the Keio collection. <i>Molecular Systems Biology</i> , 2006, 2, 2006.0008.	3.2	6,537
35	Conservation of alternative polyadenylation patterns in mammalian genes. <i>BMC Genomics</i> , 2006, 7, 189.	1.2	47
36	The disparate nature of "intergenic" polyadenylation sites. <i>Rna</i> , 2006, 12, 1794-1801.	1.6	25

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37	Large-scale identification of protein-protein interaction of Escherichia coli K-12. <i>Genome Research</i> , 2006, 16, 686-691.	2.4	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. <i>DNA Research</i> , 2002, 9, 1-10.	1.5	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. <i>DNA Research</i> , 2002, 9, 19-24.	1.5	10
40	Complete Nucleotide Sequence of Plasmid Rts1: Implications for Evolution of Large Plasmid Genomes. <i>Journal of Bacteriology</i> , 2002, 184, 3194-3202.	1.0	66
41	Genome-wide analysis of deoxyadenosine methyltransferase-mediated control of gene expression in Escherichia coli. <i>Molecular Microbiology</i> , 2002, 45, 673-695.	1.2	147
42	Non-radioactive Adenosine 5'-Phosphosulfate Sulfotransferase Assay by Coupling with Sulfite Reductase and O-Acetylserine(thiol)lyase. <i>Bioscience, Biotechnology and Biochemistry</i> , 1997, 61, 621-624.	0.6	4