Eiichiro Fukusaki

List of Publications by Year in descending order

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302 papers 10,502 citations

²⁶⁶³⁰
56
h-index

84 g-index

307 all docs

307 docs citations

times ranked

307

14125 citing authors

#	Article	IF	CITATIONS
1	Chloroplast-mediated activation of plant immune signalling in Arabidopsis. Nature Communications, 2012, 3, 926.	12.8	332
2	Time-course metabolic profiling in Arabidopsis thaliana cell cultures after salt stress treatment*. Journal of Experimental Botany, 2007, 58, 415-424.	4.8	256
3	Current metabolomics: Practical applications. Journal of Bioscience and Bioengineering, 2013, 115, 579-589.	2.2	245
4	Current metabolomics: Technological advances. Journal of Bioscience and Bioengineering, 2013, 116, 9-16.	2.2	178
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.	2.6	171
6	Prediction of Japanese Green Tea Ranking by Gas Chromatography/Mass Spectrometry-Based Hydrophilic Metabolite Fingerprinting. Journal of Agricultural and Food Chemistry, 2007, 55, 231-236.	5.2	169
7	Plant metabolomics: potential for practical operation. Journal of Bioscience and Bioengineering, 2005, 100, 347-354.	2.2	158
8	Development of a method for comprehensive and quantitative analysis of plant hormones by highly sensitive nanoflow liquid chromatography–electrospray ionization-ion trap mass spectrometry. Analytica Chimica Acta, 2009, 648, 215-225.	5 . 4	134
9	Serum metabolomics as a novel diagnostic approach for gastrointestinal cancer. Biomedical Chromatography, 2012, 26, 548-558.	1.7	133
10	Glutamate Acts as a Key Signal Linking Glucose Metabolism to Incretin/cAMP Action to Amplify Insulin Secretion. Cell Reports, 2014, 9, 661-673.	6.4	128
11	High throughput and exhaustive analysis of diverse lipids by using supercritical fluid chromatography-mass spectrometry for metabolomics. Journal of Bioscience and Bioengineering, 2008, 105, 460-469.	2.2	122
12	Adiponectin/T-cadherin system enhances exosome biogenesis and decreases cellular ceramides by exosomal release. JCI Insight, 2018, 3, .	5.0	122
13	Simultaneous analysis for water- and fat-soluble vitamins by a novel single chromatography technique unifying supercritical fluid chromatography and liquid chromatography. Journal of Chromatography A, 2014, 1362, 270-277.	3.7	121
14	¹ H NMR Based Metabolic Profiling in the Evaluation of Japanese Green Tea Quality. Journal of Agricultural and Food Chemistry, 2007, 55, 9330-9336.	5.2	120
15	Metabolic profiling of lipids by supercritical fluid chromatography/mass spectrometry. Journal of Chromatography A, 2012, 1250, 212-219.	3.7	118
16	Metabolic turnover analysis by a combination of in vivo13C-labelling from 13CO2 and metabolic profiling with CE-MS/MS reveals rate-limiting steps of the C3 photosynthetic pathway in Nicotiana tabacum leaves. Journal of Experimental Botany, 2010, 61, 1041-1051.	4.8	117
17	Flower color modulations of Torenia hybrida by downregulation of chalcone synthase genes with RNA interference. Journal of Biotechnology, 2004, 111, 229-240.	3.8	116
18	Cloning and Characterization of Mevalonate Pathway Genes in a Natural Rubber Producing Plant, <i>Hevea brasiliensis </i> . Bioscience, Biotechnology and Biochemistry, 2008, 72, 2049-2060.	1.3	115

#	Article	IF	CITATIONS
19	High-Throughput Technique for Comprehensive Analysis of Japanese Green Tea Quality Assessment Using Ultra-performance Liquid Chromatography with Time-of-Flight Mass Spectrometry (UPLC/TOF) Tj ETQq1 1	0.7824314	· rgBIA/Overlo
20	Bulk <scp>RNA</scp> degradation by nitrogen starvationâ€induced autophagy in yeast. EMBO Journal, 2015, 34, 154-168.	7.8	114
21	Development of a lipid profiling system using reverse-phase liquid chromatography coupled to high-resolution mass spectrometry with rapid polarity switching and an automated lipid identification software. Journal of Chromatography A, 2013, 1292, 211-218.	3.7	112
22	Practical non-targeted gas chromatography/mass spectrometry-based metabolomics platform for metabolic phenotype analysis. Journal of Bioscience and Bioengineering, 2011, 112, 292-298.	2.2	108
23	Serum metabolomics as a novel diagnostic approach for pancreatic cancer. Metabolomics, 2010, 6, 518-528.	3.0	105
24	<i>Drosophila</i> Sirt2/mammalian SIRT3 deacetylates ATP synthase \hat{l}^2 and regulates complex V activity. Journal of Cell Biology, 2014, 206, 289-305.	5. 2	104
25	MRMPROBS: A Data Assessment and Metabolite Identification Tool for Large-Scale Multiple Reaction Monitoring Based Widely Targeted Metabolomics. Analytical Chemistry, 2013, 85, 5191-5199.	6.5	102
26	Simultaneous profiling of polar lipids by supercritical fluid chromatography/tandem mass spectrometry with methylation. Journal of Chromatography A, 2013, 1279, 98-107.	3.7	95
27	Supercritical fluid chromatography/Orbitrap mass spectrometry based lipidomics platform coupled with automated lipid identification software for accurate lipid profiling. Journal of Chromatography A, 2013, 1301, 237-242.	3.7	94
28	Selection of Discriminant Markers for Authentication of Asian Palm Civet Coffee (Kopi Luwak): A Metabolomics Approach. Journal of Agricultural and Food Chemistry, 2013, 61, 7994-8001.	5.2	93
29	Application of supercritical fluid chromatography/mass spectrometry to lipid profiling of soybean. Journal of Bioscience and Bioengineering, 2012, 113, 262-268.	2.2	85
30	GCâ€MSâ€based metabolomics reveals mechanism of action for hydrazine induced hepatotoxicity in rats. Journal of Applied Toxicology, 2011, 31, 524-535.	2.8	84
31	The complete nucleotide sequence of the xylanase gene (xynA) ofBacillus pumilus. FEBS Letters, 1984, 171, 197-201.	2.8	82
32	Supergiant Ampholytic Sugar Chains with Imbalanced Charge Ratio Form Saline Ultra-absorbent Hydrogels. Macromolecules, 2008, 41, 4061-4064.	4.8	81
33	Predication of Japanese green tea (Sen-cha) ranking by volatile profiling using gas chromatography mass spectrometry and multivariate analysis. Journal of Bioscience and Bioengineering, 2011, 112, 252-255.	2.2	80
34	Metabolomics-driven approach to solving a CoA imbalance for improved 1-butanol production in Escherichia coli. Metabolic Engineering, 2017, 41, 135-143.	7.0	79
35	Highly sensitive and accurate profiling of carotenoids by supercritical fluid chromatography coupled with mass spectrometry. Journal of Separation Science, 2009, 32, 1459-1464.	2.5	78
36	High-throughput phospholipid profiling system based on supercritical fluid extraction–supercritical fluid chromatography/mass spectrometry for dried plasma spot analysis. Journal of Chromatography A, 2012, 1250, 69-75.	3.7	78

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37	Vascular plant oneâ€zincâ€finger protein 1/2 transcription factors regulate abiotic and biotic stress responses in Arabidopsis. Plant Journal, 2013, 73, 761-775.	5.7	78
38	Overexpression of an ADPâ€ribose pyrophosphatase, <i>AtNUDX2</i> , confers enhanced tolerance to oxidative stress in Arabidopsis plants. Plant Journal, 2009, 57, 289-301.	5.7	77
39	Modulation of the Poly(ADP-ribosyl)ation Reaction via the Arabidopsis ADP-Ribose/NADH Pyrophosphohydrolase, AtNUDX7, Is Involved in the Response to Oxidative Stress Â. Plant Physiology, 2009, 151, 741-754.	4.8	75
40	High-throughput simultaneous analysis of pesticides by supercritical fluid chromatography/tandem mass spectrometry. Journal of Chromatography A, 2012, 1266, 143-148.	3.7	73
41	Metabolic profiling of urine and blood plasma in rat models of drug addiction on the basis of morphine, methamphetamine, and cocaine-induced conditioned place preference. Analytical and Bioanalytical Chemistry, 2014, 406, 1339-1354.	3.7	72
42	Cloning and Characterization of the 2- <i>C</i> -Methyl- <scp>D</scp> -erythritol 4-Phosphate (MEP) Pathway Genes of a Natural-Rubber Producing Plant, <i>Hevea brasiliensis</i> - Bioscience, Biotechnology and Biochemistry, 2008, 72, 2903-2917.	1.3	71
43	Influences of methamphetamine-induced acute intoxication on urinary and plasma metabolic profiles in the rat. Toxicology, 2011, 287, 29-37.	4.2	71
44	AtNUDX6, an ADP-Ribose/NADH Pyrophosphohydrolase in Arabidopsis, Positively Regulates NPR1-Dependent Salicylic Acid Signaling. Plant Physiology, 2010, 152, 2000-2012.	4.8	69
45	Molar-Based Targeted Metabolic Profiling of Cyanobacterial Strains with Potential for Biological Production. Metabolites, 2014, 4, 499-516.	2.9	69
46	Gas chromatography/mass spectrometry based component profiling and quality prediction for Japanese sake. Journal of Bioscience and Bioengineering, 2014, 118, 406-414.	2.2	69
47	Metabolomics-based component profiling of hard and semi-hard natural cheeses with gas chromatography/time-of-flight-mass spectrometry, and its application to sensory predictive modeling. Journal of Bioscience and Bioengineering, 2012, 113, 751-758.	2.2	63
48	Analysis of the correlation between dipeptides and taste differences among soy sauces by using metabolomics-based component profiling. Journal of Bioscience and Bioengineering, 2014, 118, 56-63.	2.2	63
49	Quantitative analysis of anionic metabolites for Catharanthus roseus by capillary electrophoresis using sulfonated capillary coupled with electrospray ionization-tandem mass spectrometry. Journal of Bioscience and Bioengineering, 2008, 105, 249-260.	2.2	62
50	Influence of yeast and lactic acid bacterium on the constituent profile of soy sauce during fermentation. Journal of Bioscience and Bioengineering, 2017, 123, 203-208.	2.2	62
51	DNA as a â€~Nanomaterial'. Journal of Molecular Catalysis B: Enzymatic, 2004, 28, 155-166.	1.8	61
52	Pressure-assisted capillary electrophoresis mass spectrometry using combination of polarity reversion and electroosmotic flow for metabolomics anion analysis. Journal of Bioscience and Bioengineering, 2006, 101, 403-409.	2.2	61
53	Distinct signatures of dental plaque metabolic byproducts dictated by periodontal inflammatory status. Scientific Reports, 2017, 7, 42818.	3.3	61
54	Metabolomicsâ€based systematic prediction of yeast lifespan and its application for semiâ€rational screening of ageingâ€related mutants. Aging Cell, 2010, 9, 616-625.	6.7	60

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55	Metabolic profiling of Angelica acutiloba roots utilizing gas chromatography–time-of-flight–mass spectrometry for quality assessment based on cultivation area and cultivar via multivariate pattern recognition. Journal of Bioscience and Bioengineering, 2008, 105, 655-659.	2.2	58
56	Quality Evaluation and Prediction of Citrullus lanatus by ¹ H NMR-Based Metabolomics and Multivariate Analysis. Journal of Agricultural and Food Chemistry, 2008, 56, 5827-5835.	5.2	58
57	Influences of biofluid sample collection and handling procedures on GC–MS based metabolomic studies. Journal of Bioscience and Bioengineering, 2010, 110, 491-499.	2.2	58
58	Metabolic Profiling Approach To Explore Compounds Related to the Umami Intensity of Soy Sauce. Journal of Agricultural and Food Chemistry, 2014, 62, 7317-7322.	5.2	58
59	Prediction of Japanese Green Tea Ranking by Fourier Transform Near-Infrared Reflectance Spectroscopy. Journal of Agricultural and Food Chemistry, 2007, 55, 9908-9912.	5.2	57
60	Profiling of regioisomeric triacylglycerols in edible oils by supercritical fluid chromatography/tandem mass spectrometry. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2014, 966, 193-199.	2.3	57
61	In vitro selection of hematoporphyrin binding DNA aptamers. Bioorganic and Medicinal Chemistry Letters, 2000, 10, 2653-2656.	2.2	56
62	Simultaneous and rapid analysis of bile acids including conjugates by supercritical fluid chromatography coupled to tandem mass spectrometry. Journal of Chromatography A, 2013, 1299, 103-109.	3.7	56
63	Free D-amino acids produced by commensal bacteria in the colonic lumen. Scientific Reports, 2018, 8, 17915.	3.3	55
64	High-Throughput Simultaneous Analysis of Pesticides by Supercritical Fluid Chromatography Coupled with High-Resolution Mass Spectrometry. Journal of Agricultural and Food Chemistry, 2015, 63, 4457-4463.	5.2	54
65	Quality evaluation of Angelica acutiloba Kitagawa roots by 1H NMR-based metabolic fingerprinting. Journal of Pharmaceutical and Biomedical Analysis, 2008, 48, 42-48.	2.8	53
66	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.	2.2	52
67	GC/MS based metabolite profiling of Indonesian specialty coffee from different species and geographical origin. Metabolomics, 2019, 15, 126.	3.0	52
68	Quality Prediction of Japanese Green Tea Using Pyrolyzer Coupled GC/MS Based Metabolic Fingerprinting. Journal of Agricultural and Food Chemistry, 2008, 56, 744-750.	5.2	51
69	Microbe participation in aroma production during soy sauce fermentation. Journal of Bioscience and Bioengineering, 2018, 125, 688-694.	2.2	51
70	Quantification of coffee blends for authentication of Asian palm civet coffee (KopiÂLuwak) via metabolomics: A proof of concept. Journal of Bioscience and Bioengineering, 2016, 122, 79-84.	2.2	50
71	Tandem Mass Spectrometry Imaging Reveals Distinct Accumulation Patterns of Steroid Structural Isomers in Human Adrenal Glands. Analytical Chemistry, 2019, 91, 8918-8925.	6.5	48
72	Histochemical study of detailed laticifer structure and rubber biosynthesis-related protein localization in Hevea brasiliensis using spectral confocal laser scanning microscopy. Planta, 2009, 230, 215-225.	3.2	47

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73	Development of a liquid chromatography-tandem mass spectrometry method for quantitative analysis of trace d-amino acids. Journal of Bioscience and Bioengineering, 2017, 123, 134-138.	2.2	47
74	Hypoxanthine Secretion from Human Adipose Tissue and its Increase in Hypoxia. Obesity, 2018, 26, 1168-1178.	3.0	47
75	Ceramide kinase regulates phospholipase C and phosphatidylinositol 4, 5, bisphosphate in phototransduction. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20063-20068.	7.1	45
76	New Insight into the Role of the Calvin Cycle: Reutilization of CO2 Emitted through Sugar Degradation. Scientific Reports, 2015, 5, 11617.	3.3	45
77	Lipase-catalyzed kinetic resolution of methyl 4-hydroxy-5-tetradecynoate and its application to a facile synthesis of japanese beetle pheromone. Tetrahedron, 1991, 47, 6223-6230.	1.9	44
78	Fast GCâ€FID based metabolic fingerprinting of Japanese green tea leaf for its quality ranking prediction. Journal of Separation Science, 2009, 32, 2296-2304.	2.5	43
79	Development of oxidized phosphatidylcholine isomer profiling method using supercritical fluid chromatography/tandem mass spectrometry. Journal of Chromatography A, 2012, 1250, 205-211.	3.7	43
80	Metabolite profiling of soy sauce using gas chromatography with time-of-flight mass spectrometry and analysis of correlation with quantitative descriptive analysis. Journal of Bioscience and Bioengineering, 2012, 114, 170-175.	2.2	42
81	High-throughput and sensitive analysis of 3-monochloropropane-1,2-diol fatty acid esters in edible oils by supercritical fluid chromatography/tandem mass spectrometry. Journal of Chromatography A, 2012, 1250, 99-104.	3.7	42
82	Methanol production is enhanced by expression of an Aspergillus niger pectin methylesterase in tobacco cells. Journal of Biotechnology, 2003, 106, 45-52.	3.8	41
83	Canonical correlation analysis for multivariate regression and its application to metabolic fingerprinting. Biochemical Engineering Journal, 2008, 40, 199-204.	3.6	40
84	Changes in Transcription and Metabolism During the Early Stage of Replicative Cellular Senescence in Budding Yeast. Journal of Biological Chemistry, 2014, 289, 32081-32093.	3.4	40
85	Metabolite analysis by supercritical fluid chromatography. Bioanalysis, 2010, 2, 27-34.	1.5	39
86	Metabolomic approach for improving ethanol stress tolerance in Saccharomyces cerevisiae. Journal of Bioscience and Bioengineering, 2016, 121, 399-405.	2.2	39
87	Increased Dynamics of Tricarboxylic Acid Cycle and Glutamate Synthesis in Obese Adipose Tissue. Journal of Biological Chemistry, 2017, 292, 4469-4483.	3.4	39
88	Expression of fungal pectin methylesterase in transgenic tobacco leads to alteration in cell wall metabolism and a dwarf phenotype. Journal of Biotechnology, 2004, 111, 241-251.	3.8	38
89	Integrated Strategy for Unknown El–MS Identification Using Quality Control Calibration Curve, Multivariate Analysis, El–MS Spectral Database, and Retention Index Prediction. Analytical Chemistry, 2017, 89, 6766-6773.	6.5	38
90	Novel high-throughput and widely-targeted liquid chromatography–time ofÂflight mass spectrometry method for d-amino acids in foods. Journal of Bioscience and Bioengineering, 2017, 123, 126-133.	2.2	38

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91	Tailor-made poly-Î ³ -glutamic acid production. Metabolic Engineering, 2019, 55, 239-248.	7.0	38
92	Metabolome Analysis of Drosophila melanogaster during Embryogenesis. PLoS ONE, 2014, 9, e99519.	2.5	37
93	High-accuracy analysis system for the redox status of coenzyme Q10 by online supercritical fluid extraction–supercritical fluid chromatography/mass spectrometry. Journal of Chromatography A, 2012, 1250, 76-79.	3.7	36
94	Production of Eucommia-rubber from Eucommia ulmoides Oliv. (Hardy Rubber Tree). Plant Biotechnology, 2009, 26, 71-79.	1.0	34
95	Sphingosine kinases and their metabolites modulate endolysosomal trafficking in photoreceptors. Journal of Cell Biology, 2011, 192, 557-567.	5.2	34
96	Method for Assessing the Statistical Significance of Mass Spectral Similarities Using Basic Local Alignment Search Tool Statistics. Analytical Chemistry, 2013, 85, 8291-8297.	6.5	34
97	Supercritical fluid chromatography/mass spectrometry in metabolite analysis. Bioanalysis, 2014, 6, 1679-1689.	1.5	34
98	Application of gas chromatography/flame ionization detector-based metabolite fingerprinting for authentication of Asian palm civet coffee (Kopi Luwak). Journal of Bioscience and Bioengineering, 2015, 120, 555-561.	2.2	34
99	In Vivo 15N-Enrichment of Metabolites in Suspension Cultured Cells and Its Application to Metabolomics. Biotechnology Progress, 2006, 22, 1003-1011.	2.6	33
100	Extra-facile chiral separation of amino acid enantiomers by LC-TOFMS analysis. Journal of Bioscience and Bioengineering, 2016, 121, 349-353.	2.2	33
101	Iterative cycle of widely targeted metabolic profiling for the improvement of 1-butanol titer and productivity in Synechococcus elongatus. Biotechnology for Biofuels, 2018, 11, 188.	6.2	33
102	GC-MS Based Metabolite Profiling to Monitor Ripening-Specific Metabolites in Pineapple (Ananas) Tj ETQq0 0 0	rgB <u>T</u> JOver	ock 10 Tf 50
103	Expression of a xylanase gene of Bacillus pumilus in Escherichia coli and Bacillus subtilis. Applied Microbiology and Biotechnology, 1985, 22, 259.	3. 6	32
104	Nonâ€targeted metabolite fingerprinting of oriental folk medicine <i>Angelica acutiloba</i> roots by ultra performance liquid chromatography timeâ€ofâ€flight mass spectrometry. Journal of Separation Science, 2009, 32, 2233-2244.	2.5	32
105	A novel application of metabolomics in vertebrate development. Biochemical and Biophysical Research Communications, 2009, 386, 268-272.	2.1	32
106	Lipidomic analysis of plasma lipoprotein fractions in myocardial infarction-prone rabbits. Journal of Bioscience and Bioengineering, 2015, 120, 476-482.	2.2	32
107	Planteose as a storage carbohydrate required for early stage of germination of Orobanche minor and its metabolism as a possible target for selective control. Journal of Experimental Botany, 2015, 66, 3085-3097.	4.8	32
108	Metabolome analysis reveals the effect of carbon catabolite control on the poly(\hat{I}^3 -glutamic acid) biosynthesis of Bacillus licheniformis ATCC 9945. Journal of Bioscience and Bioengineering, 2016, 121, 413-419.	2.2	32

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109	Metabolic engineering for isopropanol production by an engineered cyanobacterium, Synechococcus elongatus PCC 7942, under photosynthetic conditions. Journal of Bioscience and Bioengineering, 2017, 123, 39-45.	2.2	32
110	Development of a practical metabolite identification technique for non-targeted metabolomics. Journal of Chromatography A, 2013, 1301, 73-79.	3.7	31
111	Epigenetic regulation of starvation-induced autophagy in Drosophila by histone methyltransferase G9a. Scientific Reports, 2017, 7, 7343.	3.3	31
112	Inflammation and Resolution Are Associated with Upregulation of Fatty Acid \hat{l}^2 -Oxidation in Zymosan-Induced Peritonitis. PLoS ONE, 2013, 8, e66270.	2.5	31
113	Application of gas chromatography-mass spectrometry-based metabolomics in food science and technology. Journal of Bioscience and Bioengineering, 2022, 133, 425-435.	2.2	31
114	High-efficiency bioaffinity separation of cells and proteins using novel thermoresponsive biotinylated magnetic nanoparticles. Nanobiotechnology, 2006, 2, 43-49.	1.2	30
115	Glutamate production from ammonia via glutamate dehydrogenase 2 activity supports cancer cell proliferation under glutamine depletion. Biochemical and Biophysical Research Communications, 2018, 495, 761-767.	2.1	30
116	Structure and expression of genes coding for xylan-degrading enzymes of Bacillus pumilus. FEBS Journal, 1987, 166, 539-545.	0.2	29
117	GABA metabolism pathway genes, UGA1 and GAD1, regulate replicative lifespan in Saccharomyces cerevisiae. Biochemical and Biophysical Research Communications, 2011, 407, 185-190.	2.1	29
118	Metabolic profiling of βâ€cryptoxanthin and its fatty acid esters by supercritical fluid chromatography coupled with triple quadrupole mass spectrometry. Journal of Separation Science, 2011, 34, 3546-3552.	2.5	29
119	MRM-DIFF: data processing strategy for differential analysis in large scale MRM-based lipidomics studies. Frontiers in Genetics, 2014, 5, 471.	2.3	29
120	A metabolomics-based strategy for identification of gene targets for phenotype improvement and its application to 1-butanol tolerance in Saccharomyces cerevisiae. Biotechnology for Biofuels, 2015, 8, 144.	6.2	29
121	Integrated metabolite and gene expression profiling revealing phytochrome A regulation of polyamine biosynthesis of Arabidopsis thaliana. Journal of Experimental Botany, 2008, 59, 1187-1200.	4.8	28
122	Profiling of primary metabolite by means of capillary electrophoresis-mass spectrometry and its application for plant science. Plant Biotechnology, 2009, 26, 47-52.	1.0	28
123	Quantitative target analysis and kinetic profiling of acyl-CoAs reveal the rate-limiting step in cyanobacterial 1-butanol production. Metabolomics, 2016, 12, 26.	3.0	28
124	Mechanistic study on the high-selectivity enantioseparation of amino acids using a chiral crown ether-bonded stationary phase and acidic, highly organic mobile phase by liquid chromatography/time-of-flight mass spectrometry. Journal of Chromatography A, 2018, 1578, 35-44.	3.7	28
125	Identification of Metabolites Associated with Onset of CAD in Diabetic Patients Using CE-MS Analysis: A Pilot Study. Journal of Atherosclerosis and Thrombosis, 2019, 26, 233-245.	2.0	28
126	Development of a practical online supercritical fluid extraction–supercritical fluid chromatography/mass spectrometry system with an integrated split-flow method. Journal of Chromatography A, 2019, 1592, 161-172.	3.7	28

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127	Metabolite profiles of polyhydroxyalkanoate-producing Ralstonia eutropha H16. Metabolomics, 2014, 10, 190-202.	3.0	27
128	Influence of nitrogen source and pH value on undesired poly(\hat{I}^3 -glutamic acid) formation of a protease producing <i>Bacillus licheniformis</i> strain. Journal of Industrial Microbiology and Biotechnology, 2015, 42, 1203-1215.	3.0	27
129	Poly- \hat{l}^3 -glutamic acid production by Bacillus subtilis 168 using glucose as the sole carbon source: A metabolomic analysis. Journal of Bioscience and Bioengineering, 2020, 130, 272-282.	2.2	26
130	High-sensitive liquid chromatography-tandem mass spectrometry-based chiral metabolic profiling focusing on amino acids and related metabolites. Journal of Bioscience and Bioengineering, 2019, 127, 520-527.	2.2	25
131	Orthogonal partial least squares/projections to latent structures regression-based metabolomics approach for identification of gene targets for improvement of 1-butanol production in Escherichia coli. Journal of Bioscience and Bioengineering, 2017, 124, 498-505.	2.2	24
132	Highly Accurate Detection and Identification Methodology of Xenobiotic Metabolites Using Stable Isotope Labeling, Data Mining Techniques, and Time-Dependent Profiling Based on LC/HRMS/MS. Analytical Chemistry, 2018, 90, 9068-9076.	6.5	24
133	Efficient kinetic resolution of organosilicon compounds by stereoselective esterification with hydrolases in organic solvent. Applied Microbiology and Biotechnology, 1993, 38, 482.	3.6	23
134	Sex Pheromonal Activity of Geometric and Optical Isomers of Synthetic Contact Pheromone to Males of the Yellow-Spotted Longicorn Beetle, Psacothea hilaris (PASCOE) (Coleoptera: Cerambycidae). Applied Entomology and Zoology, 1997, 32, 654-656.	1.2	23
135	Removal of Magnesium by Mg-dechelatase Is a Major Step in the Chlorophyll-Degrading Pathway in Ginkgo biloba in the Process of Autumnal Tints. Zeitschrift Fur Naturforschung - Section C Journal of Biosciences, 2000, 55, 923-926.	1.4	23
136	Reproductive organs regulate leaf nitrogen metabolism mediated by cytokinin signal. Planta, 2009, 229, 633-644.	3.2	23
137	Application of supercritical fluid carbon dioxide to the extraction and analysis of lipids. Bioanalysis, 2012, 4, 2413-2422.	1.5	23
138	Metabolic fingerprinting of hard and semi-hard natural cheeses using gas chromatography with flame ionization detector for practical sensory prediction modeling. Journal of Bioscience and Bioengineering, 2012, 114, 506-511.	2.2	23
139	Survival Response to Increased Ceramide Involves Metabolic Adaptation through Novel Regulators of Glycolysis and Lipolysis. PLoS Genetics, 2013, 9, e1003556.	3.5	23
140	Determination of Niacin and Its Metabolites Using Supercritical Fluid Chromatography Coupled to Tandem Mass Spectrometry. Mass Spectrometry, 2014, 3, A0029-A0029.	0.6	23
141	Solid-phase analytical derivatization for gas-chromatography–mass-spectrometry-based metabolomics. Journal of Bioscience and Bioengineering, 2017, 124, 700-706.	2.2	23
142	Serine racemase enhances growth of colorectal cancer by producing pyruvate from serine. Nature Metabolism, 2020, 2, 81-96.	11.9	23
143	Metabolic Profiling of Retrograde Pathway Transcription Factors Rtg1 and Rtg3 Knockout Yeast. Metabolites, 2014, 4, 580-598.	2.9	22
144	A High Phosphorus Diet Affects Lipid Metabolism in Rat Liver: A DNA Microarray Analysis. PLoS ONE, 2016, 11, e0155386.	2.5	22

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145	Quality evaluation of green tea leaf cultured under artificial light condition using gas chromatography/mass spectrometry. Journal of Bioscience and Bioengineering, 2017, 123, 197-202.	2.2	22
146	Directed strain evolution restructures metabolism for 1-butanol production in minimal media. Metabolic Engineering, 2018, 49, 153-163.	7.0	22
147	Acquisition of thermotolerant yeast <i>Saccharomyces cerevisiae </i> by breeding via stepwise adaptation. Biotechnology Progress, 2013, 29, 1116-1123.	2.6	21
148	Comparison of Isomerase and Weimberg Pathway for \hat{I}^3 -PGA Production From Xylose by Engineered Bacillus subtilis. Frontiers in Bioengineering and Biotechnology, 2019, 7, 476.	4.1	21
149	High-resolution spatial and temporal analysis of phytoalexin production in oats. Planta, 2009, 229, 931-943.	3.2	20
150	Supercritical fluid extraction as a preparation method for mass spectrometry of dried blood spots. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2014, 969, 199-204.	2.3	20
151	High-quality green tea leaf production by artificial cultivation under growth chamber conditions considering amino acids profile. Journal of Bioscience and Bioengineering, 2014, 118, 710-715.	2.2	20
152	Metabolic profiling of Garcinia mangostana (mangosteen) based on ripening stages. Journal of Bioscience and Bioengineering, 2018, 125, 238-244.	2.2	20
153	Metabolic repair through emergence of new pathways in Escherichia coli. Nature Chemical Biology, 2018, 14, 1005-1009.	8.0	20
154	Gas chromatography/mass spectrometry-based metabolite profiling of coffee beans obtained from different altitudes and origins with various postharvest processing. Metabolomics, 2021, 17, 69.	3.0	20
155	Biosynthetic Pathway for the C45 Polyprenol, Solanesol, in Tobacco. Bioscience, Biotechnology and Biochemistry, 2004, 68, 1988-1990.	1.3	19
156	c-Src-induced activation of ceramide metabolism impairs membrane microdomains and promotes malignant progression by facilitating the translocation of c-Src to focal adhesions. Biochemical Journal, 2014, 458, 81-93.	3.7	19
157	Application of Metabolomics for High Resolution Phenotype Analysis. Mass Spectrometry, 2014, 3, S0045-S0045.	0.6	19
158	Online monitoring of the respiratory quotient reveals metabolic phases during microaerobic 2,3â€butanediol production with ⟨i⟩Bacillus licheniformis⟨/i⟩. Engineering in Life Sciences, 2020, 20, 133-144.	3.6	19
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