

Fumio Matsuda

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112
papers

5,017
citations

27
h-index

70
g-index

121
ext. papers

6,040
ext. citations

5.1
avg, IF

5.53
L-index

#	Paper	IF	Citations
112	MassBank: a public repository for sharing mass spectral data for life sciences. <i>Journal of Mass Spectrometry</i> , 2010 , 45, 703-14	2.2	1321
111	Metabolomics for functional genomics, systems biology, and biotechnology. <i>Annual Review of Plant Biology</i> , 2010 , 61, 463-89	30.7	521
110	Comprehensive flavonol profiling and transcriptome coexpression analysis leading to decoding gene-metabolite correlations in Arabidopsis. <i>Plant Cell</i> , 2008 , 20, 2160-76	11.6	308
109	RIKEN tandem mass spectral database (ReSpect) for phytochemicals: a plant-specific MS/MS-based data resource and database. <i>Phytochemistry</i> , 2012 , 82, 38-45	4	214
108	MS/MS spectral tag-based annotation of non-targeted profile of plant secondary metabolites. <i>Plant Journal</i> , 2009 , 57, 555-77	6.9	191
107	Current metabolomics: practical applications. <i>Journal of Bioscience and Bioengineering</i> , 2013 , 115, 579-89	3.3	188
106	Dissection of genotype-phenotype associations in rice grains using metabolome quantitative trait loci analysis. <i>Plant Journal</i> , 2012 , 70, 624-36	6.9	155
105	AtMetExpress development: a phytochemical atlas of Arabidopsis development. <i>Plant Physiology</i> , 2010 , 152, 566-78	6.6	149
104	Genetic engineering to enhance the Ehrlich pathway and alter carbon flux for increased isobutanol production from glucose by <i>Saccharomyces cerevisiae</i> . <i>Journal of Biotechnology</i> , 2012 , 159, 32-7	3.7	131
103	Acetate-mediated novel survival strategy against drought in plants. <i>Nature Plants</i> , 2017 , 3, 17097	11.5	129
102	Metabolome-genome-wide association study dissects genetic architecture for generating natural variation in rice secondary metabolism. <i>Plant Journal</i> , 2015 , 81, 13-23	6.9	114
101	Increased isobutanol production in <i>Saccharomyces cerevisiae</i> by eliminating competing pathways and resolving cofactor imbalance. <i>Microbial Cell Factories</i> , 2013 , 12, 119	6.4	102
100	Widely targeted metabolic profiling analysis of yeast central metabolites. <i>Journal of Bioscience and Bioengineering</i> , 2012 , 113, 665-73	3.3	81
99	OpenMebius: an open source software for isotopically nonstationary ¹³ C-based metabolic flux analysis. <i>BioMed Research International</i> , 2014 , 2014, 627014	3	72
98	PRIME Update: innovative content for plant metabolomics and integration of gene expression and metabolite accumulation. <i>Plant and Cell Physiology</i> , 2013 , 54, e5	4.9	72
97	Metabolic profiling and cytological analysis of proanthocyanidins in immature seeds of Arabidopsis thaliana flavonoid accumulation mutants. <i>Plant Journal</i> , 2010 , 62, 549-59	6.9	66
96	Integrated metabolic flux and omics analysis of <i>Synechocystis</i> sp. PCC 6803 under mixotrophic and photoheterotrophic conditions. <i>Plant and Cell Physiology</i> , 2014 , 55, 1605-12	4.9	60

95	Assessment of metabolome annotation quality: a method for evaluating the false discovery rate of elemental composition searches. <i>PLoS ONE</i> , 2009 , 4, e7490	3.7	56
94	Development of microbial cell factories for bio-refinery through synthetic bioengineering. <i>Journal of Biotechnology</i> , 2013 , 163, 204-16	3.7	46
93	Organosolv pretreatment of sorghum bagasse using a low concentration of hydrophobic solvents such as 1-butanol or 1-pentanol. <i>Biotechnology for Biofuels</i> , 2016 , 9, 27	7.8	45
92	Rewiring of embryonic glucose metabolism via suppression of PFK-1 and aldolase during mouse chorioallantoic branching. <i>Development (Cambridge)</i> , 2017 , 144, 63-73	6.6	43
91	Metabolic Adaptation to Nutritional Stress in Human Colorectal Cancer. <i>Scientific Reports</i> , 2016 , 6, 38415	4.9	39
90	Engineering strategy of yeast metabolism for higher alcohol production. <i>Microbial Cell Factories</i> , 2011 , 10, 70	6.4	38
89	C-metabolic flux analysis for mevalonate-producing strain of Escherichia coli. <i>Journal of Bioscience and Bioengineering</i> , 2017 , 123, 177-182	3.3	35
88	Construction of an artificial pathway for isobutanol biosynthesis in the cytosol of Saccharomyces cerevisiae. <i>Bioscience, Biotechnology and Biochemistry</i> , 2012 , 76, 2139-41	2.1	30
87	Technical Challenges in Mass Spectrometry-Based Metabolomics. <i>Mass Spectrometry</i> , 2016 , 5, S0052	1.7	29
86	Overexpressing enzymes of the Ehrlich pathway and deleting genes of the competing pathway in Saccharomyces cerevisiae for increasing 2-phenylethanol production from glucose. <i>Journal of Bioscience and Bioengineering</i> , 2016 , 122, 34-9	3.3	27
85	(13)C-metabolic flux analysis in S-adenosyl-L-methionine production by Saccharomyces cerevisiae. <i>Journal of Bioscience and Bioengineering</i> , 2015 , 120, 532-8	3.3	26
84	Metabolic engineering of Synechococcus elongatus PCC 7942 for improvement of 1,3-propanediol and glycerol production based on in silico simulation of metabolic flux distribution. <i>Microbial Cell Factories</i> , 2017 , 16, 212	6.4	26
83	Method for assessing the statistical significance of mass spectral similarities using basic local alignment search tool statistics. <i>Analytical Chemistry</i> , 2013 , 85, 8291-7	7.8	26
82	Rre37 stimulates accumulation of 2-oxoglutarate and glycogen under nitrogen starvation in Synechocystis sp. PCC 6803. <i>FEBS Letters</i> , 2014 , 588, 466-71	3.8	26
81	Three gene expression vector sets for concurrently expressing multiple genes in Saccharomyces cerevisiae. <i>FEMS Yeast Research</i> , 2014 , 14, 399-411	3.1	25
80	Mass spectra-based framework for automated structural elucidation of metabolome data to explore phytochemical diversity. <i>Frontiers in Plant Science</i> , 2011 , 2, 40	6.2	25
79	Synthetic metabolic bypass for a metabolic toggle switch enhances acetyl-CoA supply for isopropanol production by Escherichia coli. <i>Journal of Bioscience and Bioengineering</i> , 2017 , 123, 625-633	3.3	24
78	Absolute quantitation of glycolytic intermediates reveals thermodynamic shifts in Saccharomyces cerevisiae strains lacking PFK1 or ZWF1 genes. <i>Journal of Bioscience and Bioengineering</i> , 2015 , 120, 280-283	3.3	22

77	Winners of CASMI2013: Automated Tools and Challenge Data. <i>Mass Spectrometry</i> , 2014 , 3, S0039	1.7	22
76	Changes in Lignin and Polysaccharide Components in 13 Cultivars of Rice Straw following Dilute Acid Pretreatment as Studied by Solution-State 2D 1H-13C NMR. <i>PLoS ONE</i> , 2015 , 10, e0128417	3.7	21
75	Precipitate obtained following membrane separation of hydrothermally pretreated rice straw liquid revealed by 2D NMR to have high lignin content. <i>Biotechnology for Biofuels</i> , 2015 , 8, 88	7.8	20
74	Toward the complete utilization of rice straw: Methane fermentation and lignin recovery by a combinational process involving mechanical milling, supporting material and nanofiltration. <i>Bioresource Technology</i> , 2016 , 216, 830-7	11	20
73	Transomics data-driven, ensemble kinetic modeling for system-level understanding and engineering of the cyanobacteria central metabolism. <i>Metabolic Engineering</i> , 2019 , 52, 273-283	9.7	20
72	Learning from quantitative data to understand central carbon metabolism. <i>Biotechnology Advances</i> , 2017 , 35, 971-980	17.8	18
71	Application of adaptive laboratory evolution to overcome a flux limitation in an Escherichia coli production strain. <i>Biotechnology and Bioengineering</i> , 2018 , 115, 1542-1551	4.9	17
70	Increased biomass production and glycogen accumulation in apcE gene deleted Synechocystis sp. PCC 6803. <i>AMB Express</i> , 2014 , 4, 17	4.1	17
69	Metabolome analysis of Saccharomyces cerevisiae and optimization of culture medium for S-adenosyl-L-methionine production. <i>AMB Express</i> , 2016 , 6, 38	4.1	17
68	A pyruvate carbon flux tugging strategy for increasing 2,3-butanediol production and reducing ethanol subgeneration in the yeast. <i>Biotechnology for Biofuels</i> , 2018 , 11, 180	7.8	16
67	^{13}C -based metabolic flux analysis of Saccharomyces cerevisiae with a reduced Crabtree effect. <i>Journal of Bioscience and Bioengineering</i> , 2015 , 120, 140-4	3.3	16
66	Metabolic engineering of mevalonate-producing Escherichia coli strains based on thermodynamic analysis. <i>Metabolic Engineering</i> , 2018 , 47, 1-9	9.7	15
65	Transcriptome analysis of the cyanobacterium Synechocystis sp. PCC 6803 and mechanisms of photoinhibition tolerance under extreme high light conditions. <i>Journal of Bioscience and Bioengineering</i> , 2018 , 126, 596-602	3.3	15
64	Inter-Laboratory Comparison of Metabolite Measurements for Metabolomics Data Integration. <i>Metabolites</i> , 2019 , 9,	5.6	15
63	Metabolic engineering of isopropyl alcohol-producing Escherichia coli strains with C-metabolic flux analysis. <i>Biotechnology and Bioengineering</i> , 2017 , 114, 2782-2793	4.9	15
62	Metabolic flux of the oxidative pentose phosphate pathway under low light conditions in Synechocystis sp. PCC 6803. <i>Journal of Bioscience and Bioengineering</i> , 2018 , 126, 38-43	3.3	14
61	Metabolic Flux Analysis of the Synechocystis sp. PCC 6803 Δ rtABCD Mutant Reveals a Mechanism for Metabolic Adaptation to Nitrogen-Limited Conditions. <i>Plant and Cell Physiology</i> , 2017 , 58, 537-545	4.9	14
60	Magnesium starvation improves production of malonyl-CoA-derived metabolites in Escherichia coli. <i>Metabolic Engineering</i> , 2019 , 52, 215-223	9.7	14

59	Targeted proteome analysis of single-gene deletion strains of <i>Saccharomyces cerevisiae</i> lacking enzymes in the central carbon metabolism. <i>PLoS ONE</i> , 2017 , 12, e0172742	3.7	13
58	Heterologous expression of bacterial phosphoenol pyruvate carboxylase and Entner-Doudoroff pathway in <i>Saccharomyces cerevisiae</i> for improvement of isobutanol production. <i>Journal of Bioscience and Bioengineering</i> , 2017 , 124, 263-270	3.3	12
57	Nano-scale liquid chromatography coupled to tandem mass spectrometry using the multiple reaction monitoring mode based quantitative platform for analyzing multiple enzymes associated with central metabolic pathways of <i>Saccharomyces cerevisiae</i> using ultra fast mass spectrometry. <i>Journal of Bioscience and Bioengineering</i> , 2015 , 119, 117-20	3.3	12
56	Investigation of useful carbon tracers for C-metabolic flux analysis of by considering five experimentally determined flux distributions. <i>Metabolic Engineering Communications</i> , 2016 , 3, 187-195	6.5	12
55	Rethinking Mass Spectrometry-Based Small Molecule Identification Strategies in Metabolomics. <i>Mass Spectrometry</i> , 2014 , 3, S0038	1.7	10
54	GC-MS/MS survey of collision-induced dissociation of tert-butyldimethylsilyl-derivatized amino acids and its application to (¹³ C)-metabolic flux analysis of <i>Escherichia coli</i> central metabolism. <i>Analytical and Bioanalytical Chemistry</i> , 2016 , 408, 6133-40	4.4	10
53	Metabolic characterization of cultured mammalian cells by mass balance analysis, tracer labeling experiments and computer-aided simulations. <i>Journal of Bioscience and Bioengineering</i> , 2015 , 120, 725-33	3.3	9
52	Comparison of metabolic profiles of yeasts based on the difference of the Crabtree positive and negative. <i>Journal of Bioscience and Bioengineering</i> , 2020 , 129, 52-58	3.3	9
51	C-metabolic flux analysis of ethanol-assimilating <i>Saccharomyces cerevisiae</i> for S-adenosyl-L-methionine production. <i>Microbial Cell Factories</i> , 2018 , 17, 82	6.4	9
50	Comparative Targeted Proteomics of the Central Metabolism and Photosystems in SigE Mutant Strains of sp. PCC 6803. <i>Molecules</i> , 2018 , 23,	4.8	8
49	Treatment of Retinoblastoma 1-Intact Hepatocellular Carcinoma With Cyclin-Dependent Kinase 4/6 Inhibitor Combination Therapy. <i>Hepatology</i> , 2021 , 74, 1971-1993	11.2	8
48	Evaluation of control mechanisms for <i>Saccharomyces cerevisiae</i> central metabolic reactions using metabolome data of eight single-gene deletion mutants. <i>Applied Microbiology and Biotechnology</i> , 2013 , 97, 3569-77	5.7	7
47	Assessment of Protein Content and Phosphorylation Level in sp. PCC 6803 under Various Growth Conditions Using Quantitative Phosphoproteomic Analysis. <i>Molecules</i> , 2020 , 25,	4.8	7
46	Prediction of Hopeless Peptides Unlikely to be Selected for Targeted Proteome Analysis. <i>Mass Spectrometry</i> , 2017 , 6, A0056	1.7	6
45	A Highly Specific Genome-Wide Association Study Integrated with Transcriptome Data Reveals the Contribution of Copy Number Variations to Specialized Metabolites in <i>Arabidopsis thaliana</i> Accessions. <i>Molecular Biology and Evolution</i> , 2017 , 34, 3111-3122	8.3	5
44	Computational data mining method for isotopomer analysis in the quantitative assessment of metabolic reprogramming. <i>Scientific Reports</i> , 2020 , 10, 286	4.9	5
43	Drought Stress Responses in Context-Specific Genome-Scale Metabolic Models of. <i>Metabolites</i> , 2020 , 10,	5.6	5
42	Seed-coat protective neolignans are produced by the dirigent protein AtDP1 and the laccase AtLAC5 in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2021 , 33, 129-152	11.6	5

41	Data science-based modeling of the lysine fermentation process. <i>Journal of Bioscience and Bioengineering</i> , 2020 , 130, 409-415	3-3	5
40	Time-resolved analysis of short term metabolic adaptation at dark transition in <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Bioscience and Bioengineering</i> , 2019 , 128, 424-428	3-3	4
39	Theophylline-inducible riboswitch accurately regulates protein expression at low level in <i>Escherichia coli</i> . <i>Biotechnology Letters</i> , 2019 , 41, 743-751	3	4
38	Effects of mutations of GID protein-coding genes on malate production and enzyme expression profiles in <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2020 , 104, 4971-4983	5-7	4
37	Regular expressions of MS/MS spectra for partial annotation of metabolite features. <i>Metabolomics</i> , 2016 , 12, 1	4-7	4
36	Mutations in hik26 and slr1916 lead to high-light stress tolerance in <i>Synechocystis</i> sp. PCC6803. <i>Communications Biology</i> , 2021 , 4, 343	6-7	4
35	Fragmentation of Dicarboxylic and Tricarboxylic Acids in the Krebs Cycle Using GC-EI-MS and GC-EI-MS/MS. <i>Mass Spectrometry</i> , 2019 , 8, A0073	1-7	4
34	Sugar phosphate analysis with baseline separation and soft ionization by gas chromatography-negative chemical ionization-mass spectrometry improves flux estimation of bidirectional reactions in cancer cells. <i>Metabolic Engineering</i> , 2019 , 51, 43-49	9-7	4
33	Targeted proteome analysis of microalgae under high-light conditions by optimized protein extraction of photosynthetic organisms. <i>Journal of Bioscience and Bioengineering</i> , 2019 , 127, 394-402	3-3	4
32	Mass Spectrometry-Based Method to Study Inhibitor-Induced Metabolic Redirection in the Central Metabolism of Cancer Cells. <i>Mass Spectrometry</i> , 2018 , 7, A0067	1-7	4
31	Molecular Components of Arabidopsis Intact Vacuoles Clarified with Metabolomic and Proteomic Analyses. <i>Plant and Cell Physiology</i> , 2018 , 59, 1353-1362	4-9	3
30	Comparative analysis of fermentation and enzyme expression profiles among industrial <i>Saccharomyces cerevisiae</i> strains. <i>Applied Microbiology and Biotechnology</i> , 2018 , 102, 7071-7081	5-7	3
29	Repression of mitochondrial metabolism for cytosolic pyruvate-derived chemical production in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2019 , 18, 177	6-4	3
28	Synthetic production of prenylated naringenins in yeast using promiscuous microbial prenyltransferases. <i>Metabolic Engineering Communications</i> , 2021 , 12, e00169	6-5	3
27	Differences in glucose yield of residues from among varieties of rice, wheat, and sorghum after dilute acid pretreatment. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017 , 81, 1650-1656	2-1	2
26	Lipoprotein profiling methodology based on determination of apolipoprotein concentration. <i>Bioanalysis</i> , 2017 , 9, 9-19	2-1	2
25	A Fusion Method to Develop an Expanded Artificial Genomic RNA Replicable by Q ϕ Replicase. <i>ChemBioChem</i> , 2019 , 20, 2331-2335	3-8	2
24	Random Transfer of Genes into Reveals a Complex Background of Heat Tolerance. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5-6	2

23	Expression of <i>Saccharomyces cerevisiae</i> cDNAs to enhance the growth of non-ethanol-producing <i>S. cerevisiae</i> strains lacking pyruvate decarboxylases. <i>Journal of Bioscience and Bioengineering</i> , 2018 , 126, 317-321	3.3	1
22	Evaluation of <i>Brachypodium distachyon</i> L-Tyrosine Decarboxylase Using L-Tyrosine Over-Producing <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2015 , 10, e0125488	3.7	1
21	Automated Recommendation of Research Keywords from PubMed That Suggest the Molecular Mechanism Associated with Biomarker Metabolites.. <i>Metabolites</i> , 2022 , 12,	5.6	1
20	Novel allosteric inhibition of phosphoribulokinase identified by ensemble kinetic modeling of sp. PCC 6803 metabolism. <i>Metabolic Engineering Communications</i> , 2020 , 11, e00153	6.5	1
19	Direct and quantitative analysis of altered metabolic flux distributions and cellular ATP production pathway in fumarate hydratase-diminished cells. <i>Scientific Reports</i> , 2020 , 10, 13065	4.9	1
18	Analyses of Lipid A Diversity in Gram-Negative Intestinal Bacteria Using Liquid Chromatography-Quadrupole Time-of-Flight Mass Spectrometry. <i>Metabolites</i> , 2021 , 11,	5.6	1
17	Positive effects of proline addition on the central metabolism of wild-type and lactic acid-producing <i>Saccharomyces cerevisiae</i> strains. <i>Bioprocess and Biosystems Engineering</i> , 2016 , 39, 1711-6	3.7	1
16	Soft-sensor development for monitoring the lysine fermentation process. <i>Journal of Bioscience and Bioengineering</i> , 2021 , 132, 183-189	3.3	1
15	Proteome analysis of response to different spectral light irradiation in <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Proteomics</i> , 2021 , 246, 104306	3.9	1
14	Survival of membrane-damaged <i>Escherichia coli</i> in a cytosol-mimicking solution. <i>Journal of Bioscience and Bioengineering</i> , 2019 , 128, 558-563	3.3	0
13	Increased carvone production in <i>Escherichia coli</i> by balancing limonene conversion enzyme expression via targeted quantification concatamer proteome analysis. <i>Scientific Reports</i> , 2021 , 11, 22126	4.9	0
12	Comparative C-metabolic flux analysis indicates elevation of ATP regeneration, carbon dioxide, and heat production in industrial <i>Saccharomyces cerevisiae</i> strains. <i>Biotechnology Journal</i> , 2021 , e2000438	5.6	0
11	Fake metabolomics chromatogram generation for facilitating deep learning of peak-picking neural networks. <i>Journal of Bioscience and Bioengineering</i> , 2021 , 131, 207-212	3.3	0
10	mfapy: An open-source Python package for C-based metabolic flux analysis. <i>Metabolic Engineering Communications</i> , 2021 , 13, e00177	6.5	0
9	Metabolomics-based phenotypic screens for evaluation of drug synergy via direct-infusion mass spectrometry.. <i>iScience</i> , 2022 , 25, 104221	6.1	0
8	Omics-Integrated Approach for Metabolic State Analysis of Microbial Processes 2017 , 213-236		
7	Integrative Analysis of Secondary Metabolism and Transcript Regulation in <i>Arabidopsis Thaliana</i> 2013 , 175-195		
6	Application Studies Using Metabolomics. <i>Journal of the Mass Spectrometry Society of Japan</i> , 2017 , 65, 220-222	0.2	

- 5 Analysis of Metabolic Dynamics in Metabolomics: Measurement of Metabolic Dynamics by Mass Spectrometry via Isotope Labeling Kinetics. *Journal of the Mass Spectrometry Society of Japan*, **2017**, 65, 210-214 0.2
- 4 Hydrophilic Metabolite Analysis. *Journal of the Mass Spectrometry Society of Japan*, **2017**, 65, 195-198 0.2
- 3 In Silico Metabolic Pathway Design and ¹³C-Based Metabolic Flux Analysis for Bio-Production. *Kagaku To Seibutsu*, **2015**, 53, 455-461 0
- 2 Effects of Organic Solvents on Cancer Metabolism. *Journal of the Mass Spectrometry Society of Japan*, **2020**, 68, 90-92 0.2
- 1 Rewiring of embryonic glucose metabolism via suppression of PFK-1 and aldolase during mouse chorioallantoic branching. *Journal of Cell Science*, **2017**, 130, e1.1-e1.1 5.3