

Fumio Matsuda

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Automated Recommendation of Research Keywords from PubMed That Suggest the Molecular Mechanism Associated with Biomarker Metabolites.. <i>Metabolites</i> , 2022 , 12,	5.6	1
111	Metabolomics-based phenotypic screens for evaluation of drug synergy via direct-infusion mass spectrometry.. <i>IScience</i> , 2022 , 25, 104221	6.1	0
110	Increased carvone production in Escherichia coli by balancing limonene conversion enzyme expression via targeted quantification concatamer proteome analysis. <i>Scientific Reports</i> , 2021 , 11, 221264.9	4.9	0
109	Seed-coat protective neolignans are produced by the dirigent protein AtDP1 and the laccase AtLAC5 in Arabidopsis. <i>Plant Cell</i> , 2021 , 33, 129-152	11.6	5
108	Mutations in hik26 and slr1916 lead to high-light stress tolerance in Synechocystis sp. PCC6803. <i>Communications Biology</i> , 2021 , 4, 343	6.7	4
107	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
106	Random Transfer of Genes into Reveals a Complex Background of Heat Tolerance. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	2
105	Comparative C-metabolic flux analysis indicates elevation of ATP regeneration, carbon dioxide, and heat production in industrial Saccharomyces cerevisiae strains. <i>Biotechnology Journal</i> , 2021 , e2000438	5.6	0
104	Synthetic production of prenylated naringenins in yeast using promiscuous microbial prenyltransferases. <i>Metabolic Engineering Communications</i> , 2021 , 12, e00169	6.5	3
103	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
102	Soft-sensor development for monitoring the lysine fermentation process. <i>Journal of Bioscience and Bioengineering</i> , 2021 , 132, 183-189	3.3	1
101	Proteome analysis of response to different spectral light irradiation in Synechocystis sp. PCC 6803. <i>Journal of Proteomics</i> , 2021 , 246, 104306	3.9	1
100	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
99	mfapy: An open-source Python package for C-based metabolic flux analysis. <i>Metabolic Engineering Communications</i> , 2021 , 13, e00177	6.5	0
98	Computational data mining method for isotopomer analysis in the quantitative assessment of metabolic reprogramming. <i>Scientific Reports</i> , 2020 , 10, 286	4.9	5
97	Effects of mutations of GID protein-coding genes on malate production and enzyme expression profiles in Saccharomyces cerevisiae. <i>Applied Microbiology and Biotechnology</i> , 2020 , 104, 4971-4983	5.7	4
96	Drought Stress Responses in Context-Specific Genome-Scale Metabolic Models of. <i>Metabolites</i> , 2020 , 10,	5.6	5

95	Effects of Organic Solvents on Cancer Metabolism. <i>Journal of the Mass Spectrometry Society of Japan</i> , 2020 , 68, 90-92	0.2	
94	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
93	Data science-based modeling of the lysine fermentation process. <i>Journal of Bioscience and Bioengineering</i> , 2020 , 130, 409-415	3.3	5
92	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
91	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
90	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
89	Survival of membrane-damaged Escherichia coli in a cytosol-mimicking solution. <i>Journal of Bioscience and Bioengineering</i> , 2019 , 128, 558-563	3.3	0
88	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
87	Time-resolved analysis of short term metabolic adaptation at dark transition in Synechocystis sp. PCC 6803. <i>Journal of Bioscience and Bioengineering</i> , 2019 , 128, 424-428	3.3	4
86	Theophylline-inducible riboswitch accurately regulates protein expression at low level in Escherichia coli. <i>Biotechnology Letters</i> , 2019 , 41, 743-751	3	4
85	Inter-Laboratory Comparison of Metabolite Measurements for Metabolomics Data Integration. <i>Metabolites</i> , 2019 , 9,	5.6	15
84	Repression of mitochondrial metabolism for cytosolic pyruvate-derived chemical production in Saccharomyces cerevisiae. <i>Microbial Cell Factories</i> , 2019 , 18, 177	6.4	3
83	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
82	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
81	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
80	Magnesium starvation improves production of malonyl-CoA-derived metabolites in Escherichia coli. <i>Metabolic Engineering</i> , 2019 , 52, 215-223	9.7	14
79	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
78	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

77	Metabolic flux of the oxidative pentose phosphate pathway under low light conditions in <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Bioscience and Bioengineering</i> , 2018 , 126, 38-43	3.3	14
76	Metabolic engineering of mevalonate-producing <i>Escherichia coli</i> strains based on thermodynamic analysis. <i>Metabolic Engineering</i> , 2018 , 47, 1-9	9.7	15
75	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
74	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
73	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
72	Transcriptome analysis of the cyanobacterium <i>Synechocystis</i> 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
71	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
70	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
69	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
68	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
67	Omics-Integrated Approach for Metabolic State Analysis of Microbial Processes 2017 , 213-236		
66	Synthetic metabolic bypass for a metabolic toggle switch enhances acetyl-CoA supply for isopropanol production by <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 2017 , 123, 625-633	3.3	24
65	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
64	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
63	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
62	Lipoprotein profiling methodology based on determination of apolipoprotein concentration. <i>Bioanalysis</i> , 2017 , 9, 9-19	2.1	2
61	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
60	Metabolic engineering of <i>Synechococcus elongatus</i> 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

59	Learning from quantitative data to understand central carbon metabolism. <i>Biotechnology Advances</i> , 2017 , 35, 971-980	17.8	18
58	Metabolic engineering of isopropyl alcohol-producing <i>Escherichia coli</i> strains with C-metabolic flux analysis. <i>Biotechnology and Bioengineering</i> , 2017 , 114, 2782-2793	4.9	15
57	Metabolic Flux Analysis of the <i>Synechocystis</i> sp. PCC 6803 Δ trtABCD Mutant Reveals a Mechanism for Metabolic Adaptation to Nitrogen-Limited Conditions. <i>Plant and Cell Physiology</i> , 2017 , 58, 537-545	4.9	14
56	Acetate-mediated novel survival strategy against drought in plants. <i>Nature Plants</i> , 2017 , 3, 17097	11.5	129
55	C-metabolic flux analysis for mevalonate-producing strain of <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 2017 , 123, 177-182	3.3	35
54	Application Studies Using Metabolomics. <i>Journal of the Mass Spectrometry Society of Japan</i> , 2017 , 65, 220-222	0.2	
53	Analysis of Metabolic Dynamics in Metabolomics: Measurement of Metabolic Dynamics by Mass Spectrometry via Isotope Labeling Kinetics. <i>Journal of the Mass Spectrometry Society of Japan</i> , 2017 , 65, 210-214	0.2	
52	Prediction of Hopeless Peptides Unlikely to be Selected for Targeted Proteome Analysis. <i>Mass Spectrometry</i> , 2017 , 6, A0056	1.7	6
51	Hydrophilic Metabolite Analysis. <i>Journal of the Mass Spectrometry Society of Japan</i> , 2017 , 65, 195-198	0.2	
50	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
49	Rewiring of embryonic glucose metabolism via suppression of PFK-1 and aldolase during mouse chorioallantoic branching. <i>Journal of Cell Science</i> , 2017 , 130, e1.1-e1.1	5.3	
48	Technical Challenges in Mass Spectrometry-Based Metabolomics. <i>Mass Spectrometry</i> , 2016 , 5, S0052	1.7	29
47	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
46	Regular expressions of MS/MS spectra for partial annotation of metabolite features. <i>Metabolomics</i> , 2016 , 12, 1	4.7	4
45	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
44	Overexpressing enzymes of the Ehrlich pathway and deleting genes of the competing pathway in <i>Saccharomyces cerevisiae</i> for increasing 2-phenylethanol production from glucose. <i>Journal of Bioscience and Bioengineering</i> , 2016 , 122, 34-9	3.3	27
43	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
42	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, 1711-8	3.7	1

41	Metabolic Adaptation to Nutritional Stress in Human Colorectal Cancer. <i>Scientific Reports</i> , 2016 , 6, 38415-9	4.9	39
40	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
39	Metabolome analysis of <i>Saccharomyces cerevisiae</i> and optimization of culture medium for S-adenosyl-L-methionine production. <i>AMB Express</i> , 2016 , 6, 38	4.1	17
38	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
37	(13)C-metabolic flux analysis in S-adenosyl-L-methionine production by <i>Saccharomyces cerevisiae</i> . <i>Journal of Bioscience and Bioengineering</i> , 2015 , 120, 532-8	3.3	26
36	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, 725-31	3.3	9
35	Absolute quantitation of glycolytic intermediates reveals thermodynamic shifts in <i>Saccharomyces cerevisiae</i> strains lacking PFK1 or ZWF1 genes. <i>Journal of Bioscience and Bioengineering</i> , 2015 , 120, 280-6	3.3	22
34	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
33	In Silico Metabolic Pathway Design and 13C-Based Metabolic Flux Analysis for Bio-Production. <i>Kagaku To Seibutsu</i> , 2015 , 53, 455-461	0	
32	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
31	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
30	13C-based metabolic flux analysis of <i>Saccharomyces cerevisiae</i> with a reduced Crabtree effect. <i>Journal of Bioscience and Bioengineering</i> , 2015 , 120, 140-4	3.3	16
29	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
28	Three gene expression vector sets for concurrently expressing multiple genes in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2014 , 14, 399-411	3.1	25
27	Increased biomass production and glycogen accumulation in <i>apcE</i> gene deleted <i>Synechocystis</i> sp. PCC 6803. <i>AMB Express</i> , 2014 , 4, 17	4.1	17
26	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
25	Rethinking Mass Spectrometry-Based Small Molecule Identification Strategies in Metabolomics. <i>Mass Spectrometry</i> , 2014 , 3, S0038	1.7	10
24	Winners of CASMI2013: Automated Tools and Challenge Data. <i>Mass Spectrometry</i> , 2014 , 3, S0039	1.7	22

23	OpenMebius: an open source software for isotopically nonstationary ¹³ C-based metabolic flux analysis. <i>BioMed Research International</i> , 2014 , 2014, 627014	3	72
22	Rre37 stimulates accumulation of 2-oxoglutarate and glycogen under nitrogen starvation in <i>Synechocystis</i> sp. PCC 6803. <i>FEBS Letters</i> , 2014 , 588, 466-71	3.8	26
21	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
20	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
19	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
18	Integrative Analysis of Secondary Metabolism and Transcript Regulation in <i>Arabidopsis Thaliana</i> 2013 , 175-195		
17	Current metabolomics: practical applications. <i>Journal of Bioscience and Bioengineering</i> , 2013 , 115, 579-89	3.3	188
16	Development of microbial cell factories for bio-refinery through synthetic bioengineering. <i>Journal of Biotechnology</i> , 2013 , 163, 204-16	3.7	46
15	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
14	Widely targeted metabolic profiling analysis of yeast central metabolites. <i>Journal of Bioscience and Bioengineering</i> , 2012 , 113, 665-73	3.3	81
13	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
12	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
11	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
10	Construction of an artificial pathway for isobutanol biosynthesis in the cytosol of <i>Saccharomyces cerevisiae</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2012 , 76, 2139-41	2.1	30
9	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
8	Engineering strategy of yeast metabolism for higher alcohol production. <i>Microbial Cell Factories</i> , 2011 , 10, 70	6.4	38
7	Metabolic profiling and cytological analysis of proanthocyanidins in immature seeds of <i>Arabidopsis thaliana</i> flavonoid accumulation mutants. <i>Plant Journal</i> , 2010 , 62, 549-59	6.9	66
6	AtMetExpress development: a phytochemical atlas of <i>Arabidopsis</i> development. <i>Plant Physiology</i> , 2010 , 152, 566-78	6.6	149

5	Metabolomics for functional genomics, systems biology, and biotechnology. <i>Annual Review of Plant Biology</i> , 2010 , 61, 463-89	30.7	521
4	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
3	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
2	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
1	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