

Fumio Matsuda

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7703780/publications.pdf>

Version: 2024-02-01

117
papers

6,753
citations

159525

30
h-index

64755

79
g-index

121
all docs

121
docs citations

121
times ranked

8897
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Metabolomics for Functional Genomics, Systems Biology, and Biotechnology. <i>Annual Review of Plant Biology</i> , 2010, 61, 463-489.	8.6	647
3	Comprehensive Flavonol Profiling and Transcriptome Coexpression Analysis Leading to Decoding Gene-Metabolite Correlations in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2008, 20, 2160-2176.	3.1	347
4	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.	1.4	284
5	Current metabolomics: Practical applications. <i>Journal of Bioscience and Bioengineering</i> , 2013, 115, 579-589.	1.1	245
6	Acetate-mediated novel survival strategy against drought in plants. <i>Nature Plants</i> , 2017, 3, 17097.	4.7	232
7	MS/MS spectral tag-based annotation of non-targeted profile of plant secondary metabolites. <i>Plant Journal</i> , 2009, 57, 555-577.	2.8	208
8	Dissection of genotype-phenotype associations in rice grains using metabolome quantitative trait loci analysis. <i>Plant Journal</i> , 2012, 70, 624-636.	2.8	173
9	AtMetExpress Development: A Phytochemical Atlas of <i>Arabidopsis</i> Development. <i>Plant Physiology</i> , 2010, 152, 566-578.	2.3	161
10	Metabolome-genome-wide association study dissects genetic architecture for generating natural variation in rice secondary metabolism. <i>Plant Journal</i> , 2015, 81, 13-23.	2.8	152
11	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, 32-37.	1.9	150
12	Increased isobutanol production in <i>Saccharomyces cerevisiae</i> by eliminating competing pathways and resolving cofactor imbalance. <i>Microbial Cell Factories</i> , 2013, 12, 119.	1.9	126
13	Widely targeted metabolic profiling analysis of yeast central metabolites. <i>Journal of Bioscience and Bioengineering</i> , 2012, 113, 665-673.	1.1	94
14	OpenMebius: An Open Source Software for Isotopically Nonstationary ¹³ C-Based Metabolic Flux Analysis. <i>BioMed Research International</i> , 2014, 2014, 1-10.	0.9	87
15	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, 1605-1612.	1.5	86
16	Metabolic profiling and cytological analysis of proanthocyanidins in immature seeds of <i>Arabidopsis thaliana</i> flavonoid accumulation mutants. <i>Plant Journal</i> , 2010, 62, 549-559.	2.8	85
17	PRIME Update: Innovative Content for Plant Metabolomics and Integration of Gene Expression and Metabolite Accumulation. <i>Plant and Cell Physiology</i> , 2013, 54, e5-e5.	1.5	76
18	Rewiring of embryonic glucose metabolism via suppression of PFK-1 and aldolase during mouse chorioallantoic branching. <i>Development (Cambridge)</i> , 2017, 144, 63-73.	1.2	70

#	ARTICLE	IF	CITATIONS
19	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.	6.2	68
20	Assessment of Metabolome Annotation Quality: A Method for Evaluating the False Discovery Rate of Elemental Composition Searches. <i>PLoS ONE</i> , 2009, 4, e7490.	1.1	63
21	Development of microbial cell factories for bio-refinery through synthetic bioengineering. <i>Journal of Biotechnology</i> , 2013, 163, 204-216.	1.9	55
22	Metabolic Adaptation to Nutritional Stress in Human Colorectal Cancer. <i>Scientific Reports</i> , 2016, 6, 38415.	1.6	55
23	¹³ C-metabolic flux analysis for mevalonate-producing strain of <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 2017, 123, 177-182.	1.1	48
24	Engineering strategy of yeast metabolism for higher alcohol production. <i>Microbial Cell Factories</i> , 2011, 10, 70.	1.9	42
25	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, 34-39.	1.1	40
26	Technical Challenges in Mass Spectrometry-Based Metabolomics. <i>Mass Spectrometry</i> , 2016, 5, S0052-S0052.	0.2	38
27	Method for Assessing the Statistical Significance of Mass Spectral Similarities Using Basic Local Alignment Search Tool Statistics. <i>Analytical Chemistry</i> , 2013, 85, 8291-8297.	3.2	34
28	Inter-Laboratory Comparison of Metabolite Measurements for Metabolomics Data Integration. <i>Metabolites</i> , 2019, 9, 257.	1.3	34
29	Rre37 stimulates accumulation of 2-oxoglutarate and glycogen under nitrogen starvation in <i>Synechocystis</i> sp. PCC 6803. <i>FEBS Letters</i> , 2014, 588, 466-471.	1.3	33
30	Three gene expression vector sets for concurrently expressing multiple genes in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2014, 14, 399-411.	1.1	33
31	Construction of an Artificial Pathway for Isobutanol Biosynthesis in the Cytosol of <i>Saccharomyces cerevisiae</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 2139-2141.	0.6	32
32	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.	1.1	31
33	Metabolic flux analysis of <i>Synechocystis</i> sp. PCC 6803 ^Δ nrtABCD mutant reveals a mechanism for metabolic adaptation to nitrogen-limited conditions. <i>Plant and Cell Physiology</i> , 2017, 58, pcw233.	1.5	31
34	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.	1.9	31
35	Mass Spectra-Based Framework for Automated Structural Elucidation of Metabolome Data to Explore Phytochemical Diversity. <i>Frontiers in Plant Science</i> , 2011, 2, 40.	1.7	30
36	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.	1.4	30

#	ARTICLE	IF	CITATIONS
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, 532-538.	1.1	30
38	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, 280-286.	1.1	30
39	A pyruvate carbon flux tugging strategy for increasing 2,3-butanediol production and reducing ethanol subgeneration in the yeast <i>Saccharomyces cerevisiae</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 180.	6.2	30
40	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.	3.6	30
41	Metabolic engineering of isopropyl alcohol-producing <i>Escherichia coli</i> strains with ¹³ C-metabolic flux analysis. <i>Biotechnology and Bioengineering</i> , 2017, 114, 2782-2793.	1.7	26
42	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.	1.1	26
43	Winners of CASMI2013: Automated Tools and Challenge Data. <i>Mass Spectrometry</i> , 2014, 3, S0039-S0039.	0.2	24
44	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.	1.4	24
45	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, 830-837.	4.8	24
46	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.	1.1	24
47	Magnesium starvation improves production of malonyl-CoA-derived metabolites in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2019, 52, 215-223.	3.6	24
48	Learning from quantitative data to understand central carbon metabolism. <i>Biotechnology Advances</i> , 2017, 35, 971-980.	6.0	23
49	Application of adaptive laboratory evolution to overcome a flux limitation in an <i>Escherichia coli</i> production strain. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1542-1551.	1.7	23
50	Metabolic engineering of mevalonate-producing <i>Escherichia coli</i> strains based on thermodynamic analysis. <i>Metabolic Engineering</i> , 2018, 47, 1-9.	3.6	22
51	Treatment of Retinoblastoma – Intact Hepatocellular Carcinoma With Cyclin-Dependent Kinase 4/6 Inhibitor Combination Therapy. <i>Hepatology</i> , 2021, 74, 1971-1993.	3.6	22
52	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.	1.1	21
53	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.	1.1	21
54	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.	6.2	20

#	ARTICLE	IF	CITATIONS
55	13C-based metabolic flux analysis of <i>Saccharomyces cerevisiae</i> with a reduced Crabtree effect. <i>Journal of Bioscience and Bioengineering</i> , 2015, 120, 140-144.	1.1	18
56	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.	1.1	18
57	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-A0073.	0.2	17
58	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, 725-731.	1.1	16
59	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.	3.6	16
60	Rethinking Mass Spectrometry-Based Small Molecule Identification Strategies in Metabolomics. <i>Mass Spectrometry</i> , 2014, 3, S0038-S0038.	0.2	15
61	GC-MS/MS survey of collision-induced dissociation of tert-butyldimethylsilyl-derivatized amino acids and its application to 13C-metabolic flux analysis of <i>Escherichia coli</i> central metabolism. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 6133-6140.	1.9	15
62	Investigation of useful carbon tracers for 13 C-metabolic flux analysis of <i>Escherichia coli</i> by considering five experimentally determined flux distributions. <i>Metabolic Engineering Communications</i> , 2016, 3, 187-195.	1.9	15
63	Assessment of Protein Content and Phosphorylation Level in <i>Synechocystis</i> sp. PCC 6803 under Various Growth Conditions Using Quantitative Phosphoproteomic Analysis. <i>Molecules</i> , 2020, 25, 3582.	1.7	15
64	Drought Stress Responses in Context-Specific Genome-Scale Metabolic Models of <i>Arabidopsis thaliana</i> . <i>Metabolites</i> , 2020, 10, 159.	1.3	15
65	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.	3.5	14
66	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.	1.1	14
67	Comparative Targeted Proteomics of the Central Metabolism and Photosystems in SigE Mutant Strains of <i>Synechocystis</i> sp. PCC 6803. <i>Molecules</i> , 2018, 23, 1051.	1.7	13
68	Seed-coat protective neolignans are produced by the dirigent protein AtDPI and the laccase AtLAC5 in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2021, 33, 129-152.	3.1	13
69	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, 117-120.	1.1	12
70	13C-metabolic flux analysis of ethanol-assimilating <i>Saccharomyces cerevisiae</i> for S-adenosyl-l-methionine production. <i>Microbial Cell Factories</i> , 2018, 17, 82.	1.9	12
71	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.	1.1	12
72	Molecular components of <i>Arabidopsis</i> intact vacuoles clarified with metabolomic and proteomic analyses. <i>Plant and Cell Physiology</i> , 2018, 59, 1353-1362.	1.5	11

#	ARTICLE	IF	CITATIONS
73	Mass Spectrometry-Based Method to Study Inhibitor-Induced Metabolic Redirection in the Central Metabolism of Cancer Cells. <i>Mass Spectrometry</i> , 2018, 7, A0067-A0067.	0.2	11
74	Repression of mitochondrial metabolism for cytosolic pyruvate-derived chemical production in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2019, 18, 177.	1.9	11
75	Mutations in hik26 and slr1916 lead to high-light stress tolerance in <i>Synechocystis</i> sp. PCC6803. <i>Communications Biology</i> , 2021, 4, 343.	2.0	11
76	mfapy: An open-source Python package for 13C-based metabolic flux analysis. <i>Metabolic Engineering Communications</i> , 2021, 13, e00177.	1.9	11
77	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.	1.1	10
78	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.	1.6	10
79	Elevated Sporulation Efficiency in Fission Yeast <i>Schizosaccharomyces japonicus</i> Strains Isolated from <i>Drosophila</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 350.	1.5	10
80	Synthetic production of prenylated naringenins in yeast using promiscuous microbial prenyltransferases. <i>Metabolic Engineering Communications</i> , 2021, 12, e00169.	1.9	10
81	Soft-sensor development for monitoring the lysine fermentation process. <i>Journal of Bioscience and Bioengineering</i> , 2021, 132, 183-189.	1.1	10
82	Optogenetic reprogramming of carbon metabolism using light-powering microbial proton pump systems. <i>Metabolic Engineering</i> , 2022, 72, 227-236.	3.6	10
83	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, 3569-3577.	1.7	8
84	Theophylline-inducible riboswitch accurately regulates protein expression at low level in <i>Escherichia coli</i> . <i>Biotechnology Letters</i> , 2019, 41, 743-751.	1.1	8
85	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.	1.6	8
86	Metabolomics-based phenotypic screens for evaluation of drug synergy via direct-infusion mass spectrometry. <i>IScience</i> , 2022, 25, 104221.	1.9	8
87	Data science-based modeling of the lysine fermentation process. <i>Journal of Bioscience and Bioengineering</i> , 2020, 130, 409-415.	1.1	7
88	Computational data mining method for isotopomer analysis in the quantitative assessment of metabolic reprogramming. <i>Scientific Reports</i> , 2020, 10, 286.	1.6	7
89	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.	1.7	7
90	Analyses of Lipid A Diversity in Gram-Negative Intestinal Bacteria Using Liquid Chromatography-Quadrupole Time-of-Flight Mass Spectrometry. <i>Metabolites</i> , 2021, 11, 197.	1.3	7

#	ARTICLE	IF	CITATIONS
91	Random Transfer of <i>Ogataea polymorpha</i> Genes into <i>Saccharomyces cerevisiae</i> Reveals a Complex Background of Heat Tolerance. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 302.	1.5	7
92	Novel allosteric inhibition of phosphoribulokinase identified by ensemble kinetic modeling of <i>Synechocystis</i> sp. PCC 6803 metabolism. <i>Metabolic Engineering Communications</i> , 2020, 11, e00153.	1.9	7
93	Isotope Calculation Gadgets: A Series of Software for Isotope-Tracing Experiments in Garuda Platform. <i>Metabolites</i> , 2022, 12, 646.	1.3	7
94	Regular expressions of MS/MS spectra for partial annotation of metabolite features. <i>Metabolomics</i> , 2016, 12, 1.	1.4	6
95	Prediction of Hopeless Peptides Unlikely to be Selected for Targeted Proteome Analysis. <i>Mass Spectrometry</i> , 2017, 6, A0056-A0056.	0.2	6
96	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.	1.7	6
97	Improvement of 2,3-butanediol production by dCas9 gene expression system in <i>Saccharomyces cerevisiae</i> . <i>Journal of Bioscience and Bioengineering</i> , 2022, 133, 208-212.	1.1	5
98	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.	1.1	4
99	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, 1711-1716.	1.7	4
100	A Fusion Method to Develop an Expanded Artificial Genomic RNA Replicable by Q $\hat{1}$ Replicase. <i>ChemBioChem</i> , 2019, 20, 2331-2335.	1.3	4
101	Proteome analysis of response to different spectral light irradiation in <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Proteomics</i> , 2021, 246, 104306.	1.2	3
102	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.	0.6	2
103	Lipoprotein profiling methodology based on determination of apolipoprotein concentration. <i>Bioanalysis</i> , 2017, 9, 9-19.	0.6	2
104	Fake metabolomics chromatogram generation for facilitating deep learning of peak-picking neural networks. <i>Journal of Bioscience and Bioengineering</i> , 2021, 131, 207-212.	1.1	2
105	Comparative ¹³ 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> , 2022, 17, e2000438.	1.8	2
106	Hydrophilic Metabolite Analysis. <i>Journal of the Mass Spectrometry Society of Japan</i> , 2017, 65, 195-198.	0.0	1
107	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.	1.1	1
108	Editorial overview: Recent progress in analytical technologies for design-build-test-learn cycle in biotechnology. <i>Current Opinion in Biotechnology</i> , 2018, 54, 145-147.	3.3	1

#	ARTICLE	IF	CITATIONS
109	Survival of membrane-damaged <i>Escherichia coli</i> in a cytosol-mimicking solution. <i>Journal of Bioscience and Bioengineering</i> , 2019, 128, 558-563.	1.1	1
110	Comparative Evaluation of Plasma Metabolomic Data from Multiple Laboratories. <i>Metabolites</i> , 2022, 12, 135.	1.3	1
111	Automated Recommendation of Research Keywords from PubMed That Suggest the Molecular Mechanism Associated with Biomarker Metabolites. <i>Metabolites</i> , 2022, 12, 133.	1.3	1
112	Constitutive expression of the global regulator <i>AbrB</i> restores the growth defect of a genome-reduced <i>Bacillus subtilis</i> strain and improves its metabolite production. <i>DNA Research</i> , 2022, 29, .	1.5	1
113	<i>In Silico</i> Metabolic Pathway Design and ¹³ C-Based Metabolic Flux Analysis for Bio-Production. <i>Kagaku To Seibutsu</i> , 2015, 53, 455-461.	0.0	0
114	Application Studies Using Metabolomics. <i>Journal of the Mass Spectrometry Society of Japan</i> , 2017, 65, 220-222.	0.0	0
115	Analysis of Metabolic Dynamics in Metabolomics: Measurement of Metabolic Dynamics by Mass Spectrometry <i>via</i> Isotope Labeling Kinetics. <i>Journal of the Mass Spectrometry Society of Japan</i> , 2017, 65, 210-214.	0.0	0
116	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.	1.2	0
117	Effects of Organic Solvents on Cancer Metabolism. <i>Journal of the Mass Spectrometry Society of Japan</i> , 2020, 68, 90-92.	0.0	0