

Hiroshi Shimizu

List of Publications by Year in descending order

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242
papers

6,260
citations

71102

41
h-index

114465

63
g-index

255
all docs

255
docs citations

255
times ranked

8049
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive phenotypic analysis for identification of genes affecting growth under ethanol stress in <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2009, 9, 32-44.	2.3	199
2	Identification of target genes conferring ethanol stress tolerance to <i>Saccharomyces cerevisiae</i> based on DNA microarray data analysis. Journal of Biotechnology, 2007, 131, 34-44.	3.8	197
3	Agarose for a bioartificial pancreas. Journal of Biomedical Materials Research Part B, 1992, 26, 967-977.	3.1	137
4	Transcriptome analysis of parallel-evolved <i>Escherichia coli</i> strains under ethanol stress. BMC Genomics, 2010, 11, 579.	2.8	125
5	Comprehensive phenotypic analysis of single gene deletion and overexpression strains of <i>Saccharomyces cerevisiae</i> . Yeast, 2011, 28, 349-361.	1.7	124
6	Recent advances in amino acid production by microbial cells. Current Opinion in Biotechnology, 2016, 42, 133-146.	6.6	118
7	Development and experimental verification of a genome-scale metabolic model for <i>Corynebacterium glutamicum</i> . Microbial Cell Factories, 2009, 8, 43.	4.0	104
8	Flux analysis and metabolomics for systematic metabolic engineering of microorganisms. Biotechnology Advances, 2013, 31, 818-826.	11.7	103
9	Differential importance of trehalose accumulation in <i>Saccharomyces cerevisiae</i> in response to various environmental stresses. Journal of Bioscience and Bioengineering, 2010, 109, 262-266.	2.2	99
10	Enhanced kefir production by mixed culture of and. Journal of Biotechnology, 2003, 100, 43-53.	3.8	91
11	Beer Volatile Compounds and Their Application to Low-Malt Beer Fermentation. Journal of Bioscience and Bioengineering, 2008, 106, 317-323.	2.2	88
12	OpenMeibius: An Open Source Software for Isotopically Nonstationary ¹³ C-Based Metabolic Flux Analysis. BioMed Research International, 2014, 2014, 1-10.	1.9	87
13	Integrated Metabolic Flux and Omics Analysis of <i>Synechocystis</i> sp. PCC 6803 under Mixotrophic and Photoheterotrophic Conditions. Plant and Cell Physiology, 2014, 55, 1605-1612.	3.1	86
14	Nisin Production by a Mixed-Culture System Consisting of <i>Lactococcus lactis</i> and <i>Kluyveromyces marxianus</i> . Applied and Environmental Microbiology, 1999, 65, 3134-3141.	3.1	84
15	Interactions between <i>Lactobacillus kefirifaciens</i> and <i>Saccharomyces cerevisiae</i> in mixed culture for kefir production. Journal of Bioscience and Bioengineering, 2003, 96, 279-284.	2.2	79
16	Optimal production of glutathione by controlling the specific growth rate of yeast in fed-batch culture. Biotechnology and Bioengineering, 1991, 38, 196-205.	3.3	77
17	Distinct roles of two anaerobic pathways in glutamate production induced by biotin limitation in <i>Corynebacterium glutamicum</i> . Journal of Bioscience and Bioengineering, 2008, 106, 51-58.	2.2	73
18	Adaptation of <i>Saccharomyces cerevisiae</i> Cells to High Ethanol Concentration and Changes in Fatty Acid Composition of Membrane and Cell Size. PLoS ONE, 2008, 3, e2623.	2.5	73

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19	Study on roles of anaplerotic pathways in glutamate overproduction of <i>Corynebacterium glutamicum</i> by metabolic flux analysis. <i>Microbial Cell Factories</i> , 2007, 6, 19.	4.0	70
20	Effect of trehalose accumulation on response to saline stress in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2009, 26, 17-30.	1.7	70
21	Effect of amino acids on glutathione production by <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 1992, 36, 538.	3.6	67
22	Comparative analysis of transcriptional responses to saline stress in the laboratory and brewing strains of <i>Saccharomyces cerevisiae</i> with DNA microarray. <i>Applied Microbiology and Biotechnology</i> , 2006, 70, 346-357.	3.6	65
23	Increased 3-hydroxypropionic acid production from glycerol, by modification of central metabolism in <i>Escherichia coli</i> . <i>Microbial Cell Factories</i> , 2014, 13, 64.	4.0	63
24	Cysteine addition strategy for maximum glutathione production in fed-batch culture of <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 1992, 37, 141.	3.6	62
25	An on-line physiological state recognition system for the lysine fermentation process based on a metabolic reaction model. , 1997, 55, 170-181.		62
26	Reconstruction and verification of a genome-scale metabolic model for <i>Synechocystis</i> sp. PCC6803. <i>Applied Microbiology and Biotechnology</i> , 2011, 92, 347-358.	3.6	62
27	Effect of <i>odhA</i> overexpression and <i>odhA</i> antisense RNA expression on Tween-40-triggered glutamate production by <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 81, 1097-1106.	3.6	60
28	Fuzzy control of ethanol concentration its application to maximum glutathione production in yeast fed-batch culture. <i>Biotechnology and Bioengineering</i> , 1993, 41, 493-501.	3.3	59
29	Comparative study of flux redistribution of metabolic pathway in glutamate production by two coryneform bacteria. <i>Metabolic Engineering</i> , 2005, 7, 59-69.	7.0	59
30	An algorithmic approach to constructing the on-line estimation system for the specific growth rate. <i>Biotechnology and Bioengineering</i> , 1989, 33, 354-364.	3.3	58
31	Comparative studies of in vitro and in vivo function of three different shaped bioartificial pancreases made of agarose hydrogel. <i>Biomaterials</i> , 1994, 15, 113-120.	11.4	58
32	Requirement of de novo synthesis of the <i>OdhI</i> protein in penicillin-induced glutamate production by <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2010, 86, 911-920.	3.6	56
33	Integrated transcriptomic and metabolomic analysis of the central metabolism of <i>Synechocystis</i> sp. PCC 6803 under different trophic conditions. <i>Biotechnology Journal</i> , 2013, 8, 571-580.	3.5	56
34	Metabolic Adaptation to Nutritional Stress in Human Colorectal Cancer. <i>Scientific Reports</i> , 2016, 6, 38415.	3.3	55
35	Stable disruption of ethanol production by deletion of the genes encoding alcohol dehydrogenase isozymes in <i>Saccharomyces cerevisiae</i> . <i>Journal of Bioscience and Bioengineering</i> , 2012, 113, 192-195.	2.2	52
36	Combinatorial deletions of <i>glgC</i> and <i>phaCE</i> enhance ethanol production in <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Biotechnology</i> , 2016, 239, 13-19.	3.8	52

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37	Metabolic engineering of <i>Saccharomyces cerevisiae</i> to improve succinic acid production based on metabolic profiling. <i>Bioscience, Biotechnology and Biochemistry</i> , 2014, 78, 151-159.	1.3	51
38	Characterization of new isolated <i>Ralstonia eutropha</i> strain A-04 and kinetic study of biodegradable copolyester poly(3-hydroxybutyrate-co-4-hydroxybutyrate) production. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2008, 35, 1205-1215.	3.0	49
39	High-yielding rice Takanari has superior photosynthetic response to a commercial rice Koshihikari under fluctuating light. <i>Journal of Experimental Botany</i> , 2019, 70, 5287-5297.	4.8	49
40	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.	2.2	48
41	Investigating the effects of perturbations to <i>pgi</i> and <i>eno</i> gene expression on central carbon metabolism in <i>Escherichia coli</i> using ¹³ C metabolic flux analysis. <i>Microbial Cell Factories</i> , 2012, 11, 87.	4.0	47
42	An improved physico-chemical model of hybridization on high-density oligonucleotide microarrays. <i>Bioinformatics</i> , 2008, 24, 1278-1285.	4.1	45
43	Kinetic study of poly-d(3-hydroxybutyric acid (PHB) production and its molecular weight distribution control in a fed-batch culture of <i>Alcaligenes eutrophus</i> . <i>Journal of Bioscience and Bioengineering</i> , 1993, 76, 465-469.	0.9	43
44	FastPros: screening of reaction knockout strategies for metabolic engineering. <i>Bioinformatics</i> , 2014, 30, 981-987.	4.1	43
45	Metabolic engineering Integrating methodologies of molecular breeding and bioprocess systems engineering. <i>Journal of Bioscience and Bioengineering</i> , 2002, 94, 563-573.	2.2	42
46	Engineering strategy of yeast metabolism for higher alcohol production. <i>Microbial Cell Factories</i> , 2011, 10, 70.	4.0	42
47	Metabolic engineering of <i>Synechocystis</i> sp. PCC 6803 for enhanced ethanol production based on flux balance analysis. <i>Bioprocess and Biosystems Engineering</i> , 2017, 40, 791-796.	3.4	41
48	Analysis of adaptation to high ethanol concentration in <i>Saccharomyces cerevisiae</i> using DNA microarray. <i>Bioprocess and Biosystems Engineering</i> , 2009, 32, 681-688.	3.4	39
49	Optogenetic switch for controlling the central metabolic flux of <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2019, 55, 68-75.	7.0	38
50	Modelling and optimization of environmental conditions for kefiran production by <i>Lactobacillus kefiranofaciens</i> . <i>Applied Microbiology and Biotechnology</i> , 2001, 57, 639-646.	3.6	37
51	Development of an Automated Culture System for Laboratory Evolution. <i>Journal of the Association for Laboratory Automation</i> , 2014, 19, 478-482.	2.8	37
52	Investigation of phosphorylation status of <i>OdhI</i> protein during penicillin- and Tween 40-triggered glutamate overproduction by <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 143-151.	3.6	36
53	¹³ C-metabolic flux analysis in heterologous cellulase production by <i>Bacillus subtilis</i> genome-reduced strain. <i>Journal of Biotechnology</i> , 2014, 179, 42-49.	3.8	35
54	Metabolomic analysis of acid stress response in <i>Saccharomyces cerevisiae</i> . <i>Journal of Bioscience and Bioengineering</i> , 2015, 120, 396-404.	2.2	35

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55	The RB ^{IL-6} axis controls self-renewal and endocrine therapy resistance by fine-tuning mitochondrial activity. <i>Oncogene</i> , 2017, 36, 5145-5157.	5.9	35
56	Image analysis of mycelial morphology in virginiamycin production by batch culture of <i>Streptomyces virginiae</i> . <i>Journal of Bioscience and Bioengineering</i> , 1996, 81, 7-12.	0.9	34
57	Mining of Biological Data II : Assessing Data Structure and Class Homogeneity by Cluster Analysis. <i>Metabolic Engineering</i> , 2000, 2, 228-238.	7.0	33
58	Identification of alcohol stress tolerance genes of <i>Synechocystis</i> sp. PCC 6803 using adaptive laboratory evolution. <i>Biotechnology for Biofuels</i> , 2017, 10, 307.	6.2	33
59	Optimization of agitation and aeration conditions for maximum virginiamycin production. <i>Applied Microbiology and Biotechnology</i> , 1999, 51, 164-169.	3.6	32
60	Maximum production strategy for biodegradable copolymer P(HB-co-HV) in fed-batch culture of <i>Alcaligenes eutrophus</i> . , 1999, 62, 518-525.		32
61	Genome-wide expression analysis of <i>Saccharomyces pastorianus</i> orthologous genes using oligonucleotide microarrays. <i>Journal of Bioscience and Bioengineering</i> , 2010, 110, 602-607.	2.2	32
62	Comparison of transcriptional responses to osmotic stresses induced by NaCl and sorbitol additions in <i>Saccharomyces cerevisiae</i> using DNA microarray. <i>Journal of Bioscience and Bioengineering</i> , 2006, 102, 568-571.	2.2	31
63	Enhanced acetic acid and succinic acid production under microaerobic conditions by <i>Corynebacterium glutamicum</i> harboring <i>Escherichia coli</i> transhydrogenase gene <i>pntAB</i> . <i>Journal of General and Applied Microbiology</i> , 2014, 60, 112-118.	0.7	31
64	Metabolic flux analysis of <i>Synechocystis</i> sp. PCC 6803 Δ <i>nrtABCD</i> mutant reveals a mechanism for metabolic adaptation to nitrogen-limited conditions. <i>Plant and Cell Physiology</i> , 2017, 58, pcw233.	3.1	31
65	Maximizing yellow pigment production in fed-batch culture of <i>Monascus</i> sp.. <i>Journal of Bioscience and Bioengineering</i> , 2000, 90, 363-367.	2.2	30
66	Metabolic flux control analysis of branch points: an improved approach to obtain flux control coefficients from large perturbation data. <i>Metabolic Engineering</i> , 2004, 6, 391-400.	7.0	30
67	Phenotypic convergence in bacterial adaptive evolution to ethanol stress. <i>BMC Evolutionary Biology</i> , 2015, 15, 180.	3.2	30
68	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.	2.2	30
69	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.	2.2	30
70	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
71	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.	7.0	30
72	Evaluating ¹³ C enrichment data of free amino acids for precise metabolic flux analysis. <i>Biotechnology Journal</i> , 2011, 6, 1377-1387.	3.5	29

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73	A Vector Library for Silencing Central Carbon Metabolism Genes with Antisense RNAs in <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 564-573.	3.1	29
74	Prediction of Cross-resistance and Collateral Sensitivity by Gene Expression profiles and Genomic Mutations. <i>Scientific Reports</i> , 2017, 7, 14009.	3.3	29
75	On-line state recognition in a yeast fed-batch culture using error vectors. <i>Biotechnology and Bioengineering</i> , 1995, 47, 165-173.	3.3	28
76	Optimum autoregulator addition strategy for maximum virginiamycin production in batch culture of <i>Streptomyces virginiae</i> . <i>Biotechnology and Bioengineering</i> , 1995, 46, 437-442.	3.3	27
77	Utilization of <i>Saccharomyces cerevisiae</i> recombinant strain incapable of both ethanol and glycerol biosynthesis for anaerobic bioproduction. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 4811-4819.	3.6	27
78	Construction of a Genome-Scale Metabolic Model of <i>Arthrospira platensis</i> NIES-39 and Metabolic Design for Cyanobacterial Bioproduction. <i>PLoS ONE</i> , 2015, 10, e0144430.	2.5	27
79	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.	3.3	26
80	<i>Saccharomyces cerevisiae</i> and DNA microarray analyses: what did we learn from it for a better understanding and exploitation of yeast biotechnology?. <i>Applied Microbiology and Biotechnology</i> , 2010, 87, 391-400.	3.6	25
81	Mole fraction control of poly(3-hydroxybutyric-co-3-hydroxyvaleric) acid in fed-batch culture of <i>Alcaligenes eutrophus</i> . <i>Journal of Bioscience and Bioengineering</i> , 1996, 81, 422-428.	0.9	24
82	Experimental determination of group flux control coefficients in metabolic networks. , 1998, 58, 149-153.		24
83	Mining of Biological Data I: Identifying Discriminating Features Via Mean Hypothesis Testing. <i>Metabolic Engineering</i> , 2000, 2, 218-227.	7.0	24
84	Production of Glutamate and Glutamate-Related Amino Acids: Molecular Mechanism Analysis and <i>Metabolic Engineering</i> . , 2006, , 1-38.		24
85	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.	3.0	24
86	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.	2.2	24
87	Magnesium starvation improves production of malonyl-CoA-derived metabolites in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2019, 52, 215-223.	7.0	24
88	Bioprocess Fault Detection by Nonlinear Multivariate Analysis: Application of an Artificial Autoassociative Neural Network and Wavelet Filter Bank. <i>Biotechnology Progress</i> , 1998, 14, 79-87.	2.6	23
89	Application of a mathematical model and Differential Evolution algorithm approach to optimization of bacteriocin production by <i>Lactococcus lactis</i> C7. <i>Bioprocess and Biosystems Engineering</i> , 2005, 28, 15-26.	3.4	23
90	Precise metabolic flux analysis of coryneform bacteria by gas chromatography-mass spectrometry and verification by nuclear magnetic resonance. <i>Journal of Bioscience and Bioengineering</i> , 2006, 102, 413-424.	2.2	23

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91	In silico screening of triple reaction knockout <i>Escherichia coli</i> strains for overproduction of useful metabolites. <i>Journal of Bioscience and Bioengineering</i> , 2013, 115, 221-228.	2.2	23
92	Learning from quantitative data to understand central carbon metabolism. <i>Biotechnology Advances</i> , 2017, 35, 971-980.	11.7	23
93	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.	3.3	23
94	Integrated Analysis of the Transcriptome and Metabolome of <i>Corynebacterium glutamicum</i> during Penicillin-Induced Glutamic Acid Production. <i>Biotechnology Journal</i> , 2018, 13, e1700612.	3.5	23
95	Profile control of the specific growth rate in fed-batch experiments. <i>Applied Microbiology and Biotechnology</i> , 1989, 30, 276.	3.6	22
96	On-line fault diagnosis for optimal rice α -amylase production process of a temperature-sensitive mutant of <i>Saccharomyces cerevisiae</i> by an autoassociative neural network. <i>Journal of Bioscience and Bioengineering</i> , 1997, 83, 435-442.	0.9	22
97	Extracting the hidden features in saline osmotic tolerance in <i>Saccharomyces cerevisiae</i> from DNA microarray data using the self-organizing map: biosynthesis of amino acids. <i>Applied Microbiology and Biotechnology</i> , 2007, 75, 415-426.	3.6	22
98	Improving protein secretion of a transglutaminase-secreting <i>Corynebacterium glutamicum</i> recombinant strain on the basis of ^{13}C metabolic flux analysis. <i>Journal of Bioscience and Bioengineering</i> , 2011, 112, 595-601.	2.2	22
99	Metabolic engineering of mevalonate-producing <i>Escherichia coli</i> strains based on thermodynamic analysis. <i>Metabolic Engineering</i> , 2018, 47, 1-9.	7.0	22
100	Flux balance analysis of cyanobacteria reveals selective use of photosynthetic electron transport components under different spectral light conditions. <i>Photosynthesis Research</i> , 2020, 143, 31-43.	2.9	22
101	Treatment of Retinoblastoma – Intact Hepatocellular Carcinoma With Cyclin-Dependent Kinase 4/6 Inhibitor Combination Therapy. <i>Hepatology</i> , 2021, 74, 1971-1993.	7.3	22
102	Maximum virginiamycin production by optimization of cultivation conditions in batch culture with autoregulator addition. , 2000, 49, 437-444.		21
103	Clustering gene expression pattern and extracting relationship in gene network based on artificial neural networks. <i>Journal of Bioscience and Bioengineering</i> , 2003, 96, 421-428.	2.2	21
104	Simultaneous control of apparent extract and volatile compounds concentrations in low-malt beer fermentation. <i>Applied Microbiology and Biotechnology</i> , 2006, 73, 549-558.	3.6	21
105	Physiological analysis of yeast cells by flow cytometry during serial-repitching of low-malt beer fermentation. <i>Journal of Bioscience and Bioengineering</i> , 2007, 103, 451-456.	2.2	21
106	Metabolic impact of nutrient starvation in mevalonate-producing <i>Escherichia coli</i> . <i>Bioresource Technology</i> , 2017, 245, 1634-1640.	9.6	21
107	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.	2.2	21
108	Metabolic flux of the oxidative pentose phosphate pathway under low light conditions in <i>Synechocystis sp.</i> PCC 6803. <i>Journal of Bioscience and Bioengineering</i> , 2018, 126, 38-43.	2.2	21

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109	Multivariable control of alcohol concentrations in the production of polyhydroxyalkanoates (PHAs) by <i>Paracoccus denitrificans</i> . <i>Biotechnology and Bioengineering</i> , 2001, 74, 116-124.	3.3	20
110	Improvement of L-Lactate Production by <i>CYB2</i> Gene Disruption in a Recombinant <i>Saccharomyces cerevisiae</i> Strain under Low pH Condition. <i>Bioscience, Biotechnology and Biochemistry</i> , 2008, 72, 3063-3066.	1.3	20
111	Model-based analysis of non-specific binding for background correction of high-density oligonucleotide microarrays. <i>Bioinformatics</i> , 2009, 25, 36-41.	4.1	20
112	An in silico platform for the design of heterologous pathways in nonnative metabolite production. <i>BMC Bioinformatics</i> , 2012, 13, 93.	2.6	20
113	Understanding the mechanism of heat stress tolerance caused by high trehalose accumulation in <i>Saccharomyces cerevisiae</i> using DNA microarray. <i>Journal of Bioscience and Bioengineering</i> , 2012, 113, 526-528.	2.2	20
114	On-line monitoring of fungal cell concentration by dielectric spectroscopy. <i>Journal of Biotechnology</i> , 1999, 69, 115-123.	3.8	19
115	Proteomic analysis of responses to osmotic stress in laboratory and sake-brewing strains of <i>Saccharomyces cerevisiae</i> . <i>Process Biochemistry</i> , 2009, 44, 647-653.	3.7	19
116	Reliable Metabolic Flux Estimation in <i>Escherichia coli</i> Central Carbon Metabolism Using Intracellular Free Amino Acids. <i>Metabolites</i> , 2014, 4, 408-420.	2.9	19
117	¹³ C-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.	2.2	18
118	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.	2.5	18
119	Characterization and enzymatic degradation of microbial copolyester P(3HB-co-3HV)s produced by metabolic reaction model-based system. <i>Polymer Degradation and Stability</i> , 2006, 91, 2941-2950.	5.8	17
120	Investigating the effectiveness of DNA microarray analysis for identifying the genes involved in lactate production by <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 84, 1149-1159.	3.6	17
121	Systems Metabolic Engineering: The Creation of Microbial Cell Factories by Rational Metabolic Design and Evolution. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2012, 131, 1-23.	1.1	17
122	Light-inducible flux control of triosephosphate isomerase on glycolysis in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2019, 116, 3292-3300.	3.3	17
123	Fragmentation of Dicarboxylic and Tricarboxylic Acids in the Krebs Cycle Using GC-El-MS and GC-El-MS/MS. <i>Mass Spectrometry</i> , 2019, 8, A0073-A0073.	0.6	17
124	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.	2.2	16
125	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.	7.0	16
126	Molecular Mechanisms and Metabolic Engineering of Glutamate Overproduction in <i>Corynebacterium glutamicum</i> . <i>Sub-Cellular Biochemistry</i> , 2012, 64, 261-281.	2.4	15

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127	Enhanced dipicolinic acid production during the stationary phase in <i>Bacillus subtilis</i> by blocking acetoin synthesis. <i>Bioscience, Biotechnology and Biochemistry</i> , 2015, 79, 2073-2080.	1.3	15
128	Effect of malic enzyme on ethanol production by <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Bioscience and Bioengineering</i> , 2015, 119, 82-84.	2.2	15
129	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, 6133-6140.	3.7	15
130	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.	3.6	15
131	Effect of precise control of flux ratio between the glycolytic pathways on mevalonate production in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2019, 116, 1080-1088.	3.3	15
132	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.	3.8	15
133	Flux controlling technology for central carbon metabolism for efficient microbial bio-production. <i>Current Opinion in Biotechnology</i> , 2020, 64, 169-174.	6.6	15
134	Effect of Carbon and Nitrogen Additions on Consumption Activity of Apparent Extract of Yeast Cells in a Brewing Process. <i>Journal of the American Society of Brewing Chemists</i> , 2002, 60, 163-169.	1.1	14
135	Data preprocessing and output evaluation of an autoassociative neural network model for online fault detection in virginiamycin production. <i>Journal of Bioscience and Bioengineering</i> , 2002, 94, 70-77.	2.2	14
136	Robustness of cascade pH and dissolved oxygen control in symbiotic nisin production process system of <i>Lactococcus lactis</i> and <i>Kluyveromyces marxianus</i> . <i>Journal of Bioscience and Bioengineering</i> , 2006, 101, 274-276.	2.2	14
137	Dynamic change in promoter activation during lysine biosynthesis in <i>Escherichia coli</i> cells. <i>Molecular BioSystems</i> , 2008, 4, 128-134.	2.9	14
138	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.	2.2	14
139	A Maximum Production Strategy of Lysine Based on a Simplified Model Derived from a Metabolic Reaction Network. <i>Metabolic Engineering</i> , 1999, 1, 299-308.	7.0	13
140	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.	3.8	13
141	Model predictive controller for biodegradable polyhydroxyalkanoate production in fed-batch culture. <i>Journal of Biotechnology</i> , 2002, 95, 157-169.	3.8	12
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