

Hiroshi Shimizu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6695513/publications.pdf>

Version: 2024-02-01

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	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.	2.2	5
2	Optogenetic reprogramming of carbon metabolism using light-powering microbial proton pump systems. <i>Metabolic Engineering</i> , 2022, 72, 227-236.	7.0	10
3	Acceleration of target production in co-culture by enhancing intermediate consumption through adaptive laboratory evolution. <i>Biotechnology and Bioengineering</i> , 2022, 119, 936-945.	3.3	4
4	Metabolic pathway engineering for the non-growth-associated succinate production in <i>Escherichia coli</i> based on flux solution space. <i>Journal of Bioscience and Bioengineering</i> , 2022, 134, 29-33.	2.2	2
5	Systems Biology of Cyanobacteria for Investigating Light Adaptive Mechanisms. <i>Seibutsu Butsuri</i> , 2022, 62, 104-109.	0.1	0
6	Constitutive expression of the global regulator AbrB restores the growth defect of a genome-reduced <i>Bacillus subtilis</i> strain and improves its metabolite production. <i>DNA Research</i> , 2022, 29, .	3.4	1
7	Estimation of linear and cyclic electron flows in photosynthesis based on ¹³ C-metabolic flux analysis. <i>Journal of Bioscience and Bioengineering</i> , 2021, 131, 277-282.	2.2	6
8	Identification of a rate-limiting step in a metabolic pathway using the kinetic model and in vitro experiment. <i>Journal of Bioscience and Bioengineering</i> , 2021, 131, 271-276.	2.2	7
9	Role of type I NADH dehydrogenase in <i>Synechocystis</i> sp. PCC 6803 under phycobilisome excited red light. <i>Plant Science</i> , 2021, 304, 110798.	3.6	6
10	Thioredoxin pathway in <i>Anabaena</i> sp. PCC 7120: activity of NADPH-thioredoxin reductase C. <i>Journal of Biochemistry</i> , 2021, 169, 709-719.	1.7	3
11	Mutations in hik26 and slr1916 lead to high-light stress tolerance in <i>Synechocystis</i> sp. PCC6803. <i>Communications Biology</i> , 2021, 4, 343.	4.4	11
12	Random Transfer of <i>Ogataea polymorpha</i> Genes into <i>Saccharomyces cerevisiae</i> Reveals a Complex Background of Heat Tolerance. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 302.	3.5	7
13	Soft-sensor development for monitoring the lysine fermentation process. <i>Journal of Bioscience and Bioengineering</i> , 2021, 132, 183-189.	2.2	10
14	Proteome analysis of response to different spectral light irradiation in <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Proteomics</i> , 2021, 246, 104306.	2.4	3
15	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
16	Reactor control system in bacterial co-culture based on fluorescent proteins using an Arduino-based home-made device. <i>Biotechnology Journal</i> , 2021, 16, e2100169.	3.5	6
17	Recent advances in metabolic engineering – integration of in silico design and experimental analysis of metabolic pathways. <i>Journal of Bioscience and Bioengineering</i> , 2021, 132, 429-436.	2.2	5
18	mfapy: An open-source Python package for ¹³ C-based metabolic flux analysis. <i>Metabolic Engineering Communications</i> , 2021, 13, e00177.	3.6	11

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Data science-based modeling of the lysine fermentation process. <i>Journal of Bioscience and Bioengineering</i> , 2020, 130, 409-415.	2.2	7
22	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.	3.3	10
23	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
24	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
25	Transcription Factor ArcA is a Flux Sensor for the Oxygen Consumption Rate in <i>Escherichia coli</i> . <i>Biotechnology Journal</i> , 2020, 15, e1900353.	3.5	8
26	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.	3.6	7
27	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.	3.6	7
28	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
29	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
30	Repression of mitochondrial metabolism for cytosolic pyruvate-derived chemical production in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2019, 18, 177.	4.0	11
31	Prediction of Rate-Limiting Reactions for Growth-Associated Production Using a Constraint-Based Approach. <i>Biotechnology Journal</i> , 2019, 14, 1800431.	3.5	1
32	Optogenetic switch for controlling the central metabolic flux of <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2019, 55, 68-75.	7.0	38
33	¹³ C-Metabolic Flux Analysis Reveals Effect of Phenol on Central Carbon Metabolism in <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1010.	3.5	10
34	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.	2.2	12
35	Theophylline-inducible riboswitch accurately regulates protein expression at low level in <i>Escherichia coli</i> . <i>Biotechnology Letters</i> , 2019, 41, 743-751.	2.2	8
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	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
40	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
41	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.	2.2	10
42	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
43	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.	2.2	21
44	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
45	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.	2.2	1
46	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
47	Sclerotherapy for Rectal Varices by a Small-Bore Needle Puncture Through the Greater Sciatic Foramen. <i>CardioVascular and Interventional Radiology</i> , 2018, 41, 317-322.	2.0	6
48	Optimal ¹³ C-labeling of glycerol carbon source for precise flux estimation in <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 2018, 125, 301-305.	2.2	4
49	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.	0.6	11
50	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.	6.6	1
51	Transarterial Embolization for Life-Threatening Spontaneous Hemopneumothorax. <i>Interventional Radiology</i> , 2018, 3, 84-87.	0.4	0
52	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
53	¹³ 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.	4.0	12
54	Characterization of oil-producing yeast <i>Lipomyces starkeyi</i> on glycerol carbon source based on metabolomics and ¹³ C-labeling. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8909-8920.	3.6	9

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	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.	3.6	6
58	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
59	Metabolic impact of nutrient starvation in mevalonate-producing <i>Escherichia coli</i> . <i>Bioresource Technology</i> , 2017, 245, 1634-1640.	9.6	21
60	The RBâ€“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
61	Heterologous expression of bacterial phosphoenol pyruvate carboxylase and Entnerâ€“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
62	Prediction of Cross-resistance and Collateral Sensitivity by Gene Expression profiles and Genomic Mutations. <i>Scientific Reports</i> , 2017, 7, 14009.	3.3	29
63	Learning from quantitative data to understand central carbon metabolism. <i>Biotechnology Advances</i> , 2017, 35, 971-980.	11.7	23
64	Metabolic engineering of isopropyl alcoholâ€“producing <i>Escherichia coli</i> strains with ¹³ Câ€“metabolic flux analysis. <i>Biotechnology and Bioengineering</i> , 2017, 114, 2782-2793.	3.3	26
65	Metabolic flux analysis of <i>Synechocystis</i> sp. PCC 6803 ¹⁵ N <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
66	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
67	Prediction of Hopeless Peptides Unlikely to be Selected for Targeted Proteome Analysis. <i>Mass Spectrometry</i> , 2017, 6, A0056-A0056.	0.6	6
68	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
69	Pulmonary Tumor Thrombotic Microangiopathyâ€“ Antemortem Diagnosis With Pulmonary Artery Wedge Blood Cell Sampling in a Recurrent Breast Cancer Patient â€“. <i>Circulation Journal</i> , 2017, 81, 1959-1960.	1.6	6
70	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
71	Enhancement of 1,5-diaminopentane production in a recombinant strain of <i>Corynebacterium glutamicum</i> ; by Tween 40 addition. <i>Journal of General and Applied Microbiology</i> , 2016, 62, 42-45.	0.7	12
72	GC-MS/MS survey of collision-induced dissociation of tert-butyl dimethylsilyl-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

#	ARTICLE	IF	CITATIONS
73	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.	3.4	4
74	Metabolic Adaptation to Nutritional Stress in Human Colorectal Cancer. <i>Scientific Reports</i> , 2016, 6, 38415.	3.3	55
75	Recent advances in amino acid production by microbial cells. <i>Current Opinion in Biotechnology</i> , 2016, 42, 133-146.	6.6	118
76	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
77	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
78	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
79	A rare case of long-term survival with idiopathic dilatation of the pulmonary artery. <i>International Journal of Cardiology</i> , 2016, 223, 337-339.	1.7	1
80	Phenotypic convergence in bacterial adaptive evolution to ethanol stress. <i>BMC Evolutionary Biology</i> , 2015, 15, 180.	3.2	30
81	<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
82	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
83	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.	2.2	12
84	^{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
85	^{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
86	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
87	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
88	SSDesign: Computational metabolic pathway design based on flux variability using elementary flux modes. <i>Biotechnology and Bioengineering</i> , 2015, 112, 759-768.	3.3	12
89	Absolute quantitation of glycolytic intermediates reveals thermodynamic shifts in <i>Saccharomyces cerevisiae</i> strains lacking <i>PFK1</i> or <i>ZWF1</i> genes. <i>Journal of Bioscience and Bioengineering</i> , 2015, 120, 280-286.	2.2	30
90	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

#	ARTICLE	IF	CITATIONS
91	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
92	Developing Interpretation of Intracellular Metabolism of <i>Corynebacterium glutamicum</i> by Using Flux Analysis Technology. , 2015, , 25-38.		1
93	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
94	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
95	Potential of a <i>Saccharomyces cerevisiae</i> recombinant strain lacking ethanol and glycerol biosynthesis pathways in efficient anaerobic bioproduction. <i>Bioengineered</i> , 2014, 5, 123-128.	3.2	7
96	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
97	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
98	FastPros: screening of reaction knockout strategies for metabolic engineering. <i>Bioinformatics</i> , 2014, 30, 981-987.	4.1	43
99	OpenMebius: An Open Source Software for Isotopically Nonstationary ¹³ C-Based Metabolic Flux Analysis. <i>BioMed Research International</i> , 2014, 2014, 1-10.	1.9	87
100	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
101	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.	3.1	86
102	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
103	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
104	Flux analysis and metabolomics for systematic metabolic engineering of microorganisms. <i>Biotechnology Advances</i> , 2013, 31, 818-826.	11.7	103
105	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
106	Genome-wide identification of the targets for genetic manipulation to improve L-lactate production by <i>Saccharomyces cerevisiae</i> by using a single-gene deletion strain collection. <i>Journal of Biotechnology</i> , 2013, 168, 185-193.	3.8	3
107	ArtPathDesign: Rational heterologous pathway design system for the production of nonnative metabolites. <i>Journal of Bioscience and Bioengineering</i> , 2013, 116, 524-527.	2.2	5
108	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

#	ARTICLE	IF	CITATIONS
109	In silico screening of triple reaction knockout Escherichia coli strains for overproduction of useful metabolites. Journal of Bioscience and Bioengineering, 2013, 115, 221-228.	2.2	23
110	Systems metabolic engineering for the production of bio-nylon precursor. Biotechnology Journal, 2013, 8, 513-514.	3.5	7
111	Development of a Physical Model-Based Algorithm for the Detection of Single-Nucleotide Substitutions by Using Tiling Microarrays. PLoS ONE, 2013, 8, e54571.	2.5	6
112	An in silico platform for the design of heterologous pathways in nonnative metabolite production. BMC Bioinformatics, 2012, 13, 93.	2.6	20
113	Investigating the effects of perturbations to pgi and eno gene expression on central carbon metabolism in Escherichia coli using 13 C metabolic flux analysis. Microbial Cell Factories, 2012, 11, 87.	4.0	47
114	Systems Metabolic Engineering: The Creation of Microbial Cell Factories by Rational Metabolic Design and Evolution. Advances in Biochemical Engineering/Biotechnology, 2012, 131, 1-23.	1.1	17
115	Molecular Mechanisms and Metabolic Engineering of Glutamate Overproduction in Corynebacterium glutamicum. Sub-Cellular Biochemistry, 2012, 64, 261-281.	2.4	15
116	Design of Superior Cell Factories Based on Systems Wide Omics Analysis. , 2012, , 57-81.		3
117	Stable disruption of ethanol production by deletion of the genes encoding alcohol dehydrogenase isozymes in Saccharomyces cerevisiae. Journal of Bioscience and Bioengineering, 2012, 113, 192-195.	2.2	52
118	Understanding the mechanism of heat stress tolerance caused by high trehalose accumulation in Saccharomyces cerevisiae using DNA microarray. Journal of Bioscience and Bioengineering, 2012, 113, 526-528.	2.2	20
119	Improving protein secretion of a transglutaminase-secreting Corynebacterium glutamicum recombinant strain on the basis of 13C metabolic flux analysis. Journal of Bioscience and Bioengineering, 2011, 112, 595-601.	2.2	22
120	Evaluating ¹³ C enrichment data of free amino acids for precise metabolic flux analysis. Biotechnology Journal, 2011, 6, 1377-1387.	3.5	29
121	Investigation of phosphorylation status of OdhI protein during penicillin- and Tween 40-triggered glutamate overproduction by Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2011, 91, 143-151.	3.6	36
122	Reconstruction and verification of a genome-scale metabolic model for Synechocystis sp. PCC6803. Applied Microbiology and Biotechnology, 2011, 92, 347-358.	3.6	62
123	Engineering strategy of yeast metabolism for higher alcohol production. Microbial Cell Factories, 2011, 10, 70.	4.0	42
124	Comprehensive phenotypic analysis of single gene deletion and overexpression strains of Saccharomyces cerevisiae. Yeast, 2011, 28, 349-361.	1.7	124
125	Requirement of de novo synthesis of the OdhI protein in penicillin-induced glutamate production by Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2010, 86, 911-920.	3.6	56
126	Saccharomyces cerevisiae and DNA microarray analyses: what did we learn from it for a better understanding and exploitation of yeast biotechnology?. Applied Microbiology and Biotechnology, 2010, 87, 391-400.	3.6	25

#	ARTICLE	IF	CITATIONS
127	Transcriptome analysis of parallel-evolved <i>Escherichia coli</i> strains under ethanol stress. <i>BMC Genomics</i> , 2010, 11, 579.	2.8	125
128	Differential importance of trehalose accumulation in <i>Saccharomyces cerevisiae</i> in response to various environmental stresses. <i>Journal of Bioscience and Bioengineering</i> , 2010, 109, 262-266.	2.2	99
129	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
130	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
131	A model-based analysis method for detection of single-base substitution using resequencing microarrays. <i>Journal of Bioscience and Bioengineering</i> , 2009, 108, S160.	2.2	0
132	Flux balance analysis of <i>Corynebacterium glutamicum</i> using a genome-scale metabolic model. <i>Journal of Bioscience and Bioengineering</i> , 2009, 108, S166.	2.2	0
133	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
134	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
135	Investigating the effectiveness of DNA microarray analysis for identifying the genes involved in L-lactate production by <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 84, 1149-1159.	3.6	17
136	Effect of trehalose accumulation on response to saline stress in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2009, 26, 17-30.	1.7	70
137	Comprehensive phenotypic analysis for identification of genes affecting growth under ethanol stress in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2009, 9, 32-44.	2.3	199
138	Analysis of stochasticity in promoter activation by using a dual-fluorescence reporter system. <i>BioSystems</i> , 2009, 97, 160-164.	2.0	4
139	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
140	Analysis of metabolic network based on conservation of molecular structure. <i>BioSystems</i> , 2009, 95, 175-178.	2.0	5
141	Development and experimental verification of a genome-scale metabolic model for <i>Corynebacterium glutamicum</i> . <i>Microbial Cell Factories</i> , 2009, 8, 43.	4.0	104
142	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
143	Beer Volatile Compounds and Their Application to Low-Malt Beer Fermentation. <i>Journal of Bioscience and Bioengineering</i> , 2008, 106, 317-323.	2.2	88
144	Distinct roles of two anaplerotic pathways in glutamate production induced by biotin limitation in <i>Corynebacterium glutamicum</i> . <i>Journal of Bioscience and Bioengineering</i> , 2008, 106, 51-58.	2.2	73

#	ARTICLE	IF	CITATIONS
145	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
146	Genome-Wide Analysis of the Effects of Location and Number of Stress Response Elements on Gene Expression in <i>Saccharomyces cerevisiae</i> . <i>Journal of Bioscience and Bioengineering</i> , 2008, 106, 507-510.	2.2	5
147	Analysis of lager brewing yeast at low temperature fermentation using DNA microarray. <i>Journal of Biotechnology</i> , 2008, 136, S351-S352.	3.8	1
148	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
149	Adaptation of <i>Saccharomyces cerevisiae</i> Cells to High Ethanol Concentration and Changes in Fatty Acid Composition of Membrane and Cell Size. <i>PLoS ONE</i> , 2008, 3, e2623.	2.5	73
150	An improved physico-chemical model of hybridization on high-density oligonucleotide microarrays. <i>Bioinformatics</i> , 2008, 24, 1278-1285.	4.1	45
151	INVERSE METABOLIC ENGINEERING BY INTEGRATION OF MULTIPLE OMICS ANALYSES. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2007, 40, 19-24.	0.4	0
152	3P354 Analysis of the relationship between noise in gene expression and the regulatory structure in amino acid biosynthesis pathway (Others, Poster Presentations). <i>Seibutsu Butsuri</i> , 2007, 47, S291.	0.1	0
153	Identification of target genes conferring ethanol stress tolerance to <i>Saccharomyces cerevisiae</i> based on DNA microarray data analysis. <i>Journal of Biotechnology</i> , 2007, 131, 34-44.	3.8	197
154	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
155	Analysis of hemin effect on lactate reduction in <i>Lactococcus lactis</i> . <i>Journal of Bioscience and Bioengineering</i> , 2007, 103, 529-534.	2.2	8
156	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
157	Metabolic pathway recruiting through genomic data analysis for industrial application of <i>Saccharomyces cerevisiae</i> . <i>Biochemical Engineering Journal</i> , 2007, 36, 28-37.	3.6	8
158	Analysis of fluctuation in protein abundance without promoter regulation based on <i>Escherichia coli</i> continuous culture. <i>BioSystems</i> , 2007, 90, 614-622.	2.0	6
159	Kinetic modeling of kefiran production in mixed culture of <i>Lactobacillus kefiranofaciens</i> and <i>Saccharomyces cerevisiae</i> . <i>Process Biochemistry</i> , 2007, 42, 570-579.	3.7	9
160	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
161	Reduction of lactate production in <i>Lactococcus lactis</i> , a combined strategy: metabolic engineering by introducing foreign alanine dehydrogenase gene and hemin addition. <i>World Journal of Microbiology and Biotechnology</i> , 2007, 23, 947-953.	3.6	1
162	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

#	ARTICLE	IF	CITATIONS
163	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
164	Computational prediction of impact of rerouting the carbon flux in metabolic pathway on cell growth and nisin production by <i>Lactococcus lactis</i> . <i>Biochemical Engineering Journal</i> , 2006, 28, 220-230.	3.6	9
165	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
166	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
167	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
168	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
169	Production of Glutamate and Glutamate-Related Amino Acids: Molecular Mechanism Analysis and <i>Metabolic Engineering</i> . , 2006, , 1-38.		24
170	Analysis of Fluctuation in Gene Expression Based on Continuous Culture System. <i>Lecture Notes in Computer Science</i> , 2006, , 113-127.	1.3	0
171	Microbial Interaction in a Symbiotic Bioprocess of Lactic Acid Bacterium and Dairy Yeast. <i>Lecture Notes in Computer Science</i> , 2006, , 93-106.	1.3	3
172	Development of Co-Culture Systems of Lactic Acid Bacteria and Yeasts for Bioproduction. <i>Japanese Journal of Lactic Acid Bacteria</i> , 2005, 16, 2-10.	0.1	2
173	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
174	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
175	DNA microarray analysis on <i>Saccharomyces cerevisiae</i> under high carbon dioxide concentration in fermentation process. <i>Biotechnology and Bioprocess Engineering</i> , 2005, 10, 451-461.	2.6	8
176	On-Line Estimation and Control of Apparent Extract Concentration in Low-Malt Beer Fermentation. <i>Journal of the Institute of Brewing</i> , 2005, 111, 128-136.	2.3	8
177	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
178	Simultaneous Control of Apparent Extract and Volatile Compounds Concentrations in Beer Fermentation. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2004, 37, 451-456.	0.4	0
179	Analysis of Responses of Complex Bionetworks to Changes in Environmental Conditions. <i>Lecture Notes in Computer Science</i> , 2004, , 13-27.	1.3	0
180	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

#	ARTICLE	IF	CITATIONS
181	Interactions between <i>Lactobacillus kefiranofaciens</i> and <i>Saccharomyces cerevisiae</i> in mixed culture for kefiran production. <i>Journal of Bioscience and Bioengineering</i> , 2003, 96, 279-284.	2.2	79
182	Enhanced kefiran production by mixed culture of and. <i>Journal of Biotechnology</i> , 2003, 100, 43-53.	3.8	91
183	Nonisothermal Crystallization Kinetics of Biodegradable Random Poly(3-hydroxybutyrate-co-3-hydroxyvalerate) and Block One. <i>Journal of Chemical Engineering of Japan</i> , 2003, 36, 639-646.	0.6	8
184	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
185	Metabolic Control Analysis in Glutamate Synthetic Pathway: Experimental Sensitivity Analysis at a Key Branch Point. <i>ACS Symposium Series</i> , 2002, , 39-52.	0.5	1
186	Model predictive controller for biodegradable polyhydroxyalkanoate production in fed-batch culture. <i>Journal of Biotechnology</i> , 2002, 95, 157-169.	3.8	12
187	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
188	Classification of fermentation performance by multivariate analysis based on mean hypothesis testing. <i>Journal of Bioscience and Bioengineering</i> , 2002, 94, 251-257.	2.2	12
189	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
190	Roles of glucose and acetate as carbon sources in histidine production with <i>Brevibacterium flavum</i> FERM1564 revealed by metabolic flux analysis. <i>Biotechnology and Bioprocess Engineering</i> , 2002, 7, 171-177.	2.6	6
191	Metabolic Engineering. Integrating Methodologies of Molecular Breeding and Bioprocess Systems Engineering. <i>Journal of Bioscience and Bioengineering</i> , 2002, 94, 563-573.	2.2	2
192	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	5
193	Metabolic engineering-integrating methodologies of molecular breeding and bioprocess systems engineering. <i>Journal of Bioscience and Bioengineering</i> , 2002, 94, 563-73.	2.2	4
194	Classification of Fermentation Performance by Multivariate Analysis Based on Mean Hypothesis Testing. <i>Journal of Bioscience and Bioengineering</i> , 2002, 94, 251-257.	2.2	2
195	Quality Control of Polyhydroxyalkanoates in Fed-Batch Culture Based on a Metabolic Reaction Model. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2001, 34, 201-206.	0.4	1
196	Learning from the Wisdom of the Ecosystem: Novel Control Strategy Exploiting Microbial Interaction in Co-Culture System. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2001, 34, 189-194.	0.4	0
197	ç"Ÿç%©ãf—ãfã,»ã,1ã,ã,1ãf†ãfã-¥ã†ã"ã»£è-ã-¥ã†. <i>Nippon Nogeikagaku Kaishi</i> , 2001, 75, 678-682.	0.0	0
198	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

#	ARTICLE	IF	CITATIONS
199	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
200	Maximum virginiamycin production by optimization of cultivation conditions in batch culture with autoregulator addition. , 2000, 49, 437-444.		21
201	Mining of Biological Data I: Identifying Discriminating Features Via Mean Hypothesis Testing. <i>Metabolic Engineering</i> , 2000, 2, 218-227.	7.0	24
202	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
203	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
204	Optimization of agitation and aeration conditions for maximum virginiamycin production. <i>Applied Microbiology and Biotechnology</i> , 1999, 51, 164-169.	3.6	32
205	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
206	Maximum production strategy for biodegradable copolymer P(HB-co-HV) in fed-batch culture of <i>Alcaligenes eutrophus</i> . , 1999, 62, 518-525.		32
207	On-line monitoring of fungal cell concentration by dielectric spectroscopy. <i>Journal of Biotechnology</i> , 1999, 69, 115-123.	3.8	19
208	Maximum production strategy for biodegradable copolymer P(HB-co-HV) in fed-batch culture of <i>Alcaligenes eutrophus</i> . <i>Biotechnology and Bioengineering</i> , 1999, 62, 518-525.	3.3	1
209	Nisin Production by a Mixed-Culture System Consisting of <i>Lactococcus lactis</i> and <i>Kluyveromyces marxianus</i> . <i>Applied and Environmental Microbiology</i> , 1999, 65, 3134-3141.	3.1	84
210	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
211	Method of <i>Corynebacterium glutamicum</i> fermentation time extension with high lysine production rate by leucine addition. <i>Journal of Bioscience and Bioengineering</i> , 1998, 86, 180-184.	0.9	7
212	Experimental determination of group flux control coefficients in metabolic networks. , 1998, 58, 149-153.		24
213	Optimization of Dissolved Oxygen Supply Method for Maximum Virginiamycin Production. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 1998, 31, 193-198.	0.4	0
214	Database Mining Tools for Bioprocess Analysis. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 1998, 31, 405-410.	0.4	1
215	Optimal Production of Biodegradable Copolymer, P(HB-co-HV), in Fed-Batch Culture of <i>Alcaligenes eutrophus</i> . IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 1998, 31, 173-178.	0.4	0
216	Feeding Strategy of Required Components by Metabolic Engineering Approach in a Lysine Production Process. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 1998, 31, 375-380.	0.4	0

#	ARTICLE	IF	CITATIONS
217	Quantification of Data Clusters for Bioprocess Performance Classification via Artificial Neural Networks. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 1998, 31, 439-444.	0.4	1
218	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. Journal of Bioscience and Bioengineering, 1997, 83, 435-442.	0.9	22
219	An on-line physiological state recognition system for the lysine fermentation process based on a metabolic reaction model. , 1997, 55, 170-181.		62
220	Comparison of estimation techniques for a time-dependent parameter in a metabolic reaction model. Journal of Bioscience and Bioengineering, 1996, 81, 363-365.	0.9	3
221	Image analysis of mycelial morphology in virginiamycin production by batch culture of <i>Streptomyces virginiae</i> . Journal of Bioscience and Bioengineering, 1996, 81, 7-12.	0.9	34
222	Mole fraction control of poly(3-hydroxybutyric-co-3-hydroxyvaleric) acid in fed-batch culture of <i>Alcaligenes eutrophus</i> . Journal of Bioscience and Bioengineering, 1996, 81, 422-428.	0.9	24
223	On-line recognition of physiological state in a yeast fed-batch culture. Journal of Process Control, 1996, 6, 373-378.	3.3	6
224	Maximum virginiamycin production by optimization of cultivation conditions in batch culture with autoregulator addition. Biotechnology and Bioengineering, 1996, 49, 437-444.	3.3	8
225	On-Line Physiological State Recognition and Parameter Estimation in the Metabolic Reaction Model Using Error Vectors. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 1995, 28, 118-123.	0.4	0
226	Optimum autoregulator addition strategy for maximum virginiamycin production in batch culture of <i>Streptomyces virginiae</i> . Biotechnology and Bioengineering, 1995, 46, 437-442.	3.3	27
227	On-line state recognition in a yeast fed-batch culture using error vectors. Biotechnology and Bioengineering, 1995, 47, 165-173.	3.3	28
228	ON-LINE PHYSIOLOGICAL STATE RECOGNITION AND PARAMETER ESTIMATION IN THE METABOLIC REACTION MODEL USING ERROR VECTORS. , 1995, , 118-123.		0
229	Comparative studies of in vitro and in vivo function of three different shaped bioartificial pancreases made of agarose hydrogel. Biomaterials, 1994, 15, 113-120.	11.4	58
230	Control of Molecular Weight Distribution and Mole Fraction in Poly(-D(α)-3-hydroxyalkanoate) (PHA) Production by <i>Alcaligenes eutrophus</i> . Studies in Polymer Science, 1994, 12, 365-372.	0.2	2
231	Fuzzy control of ethanol concentration its application to maximum glutathione production in yeast fed-batch culture. Biotechnology and Bioengineering, 1993, 41, 493-501.	3.3	59
232	Calculation of optimal trajectories for fermentation processes by genetic algorithm. Journal of Bioscience and Bioengineering, 1993, 75, 474.	0.9	7
233	Kinetic study of poly-d(α)-3-hydroxybutyric acid (PHB) production and its molecular weight distribution control in a fed-batch culture of <i>Alcaligenes eutrophus</i> . Journal of Bioscience and Bioengineering, 1993, 76, 465-469.	0.9	43
234	Effect of amino acids on glutathione production by <i>Saccharomyces cerevisiae</i> . Applied Microbiology and Biotechnology, 1992, 36, 538.	3.6	67

#	ARTICLE	IF	CITATIONS
235	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
236	Agarose for a bioartificial pancreas. <i>Journal of Biomedical Materials Research Part B</i> , 1992, 26, 967-977.	3.1	137
237	Modelling, Optimization and Realization of Fed-Batch Culture using the Specific Growth Rate.. <i>Kagaku Kogaku Ronbunshu</i> , 1991, 17, 572-578.	0.3	0
238	Optimal production of glutathione by controlling the specific growth rate of yeast in fed-batch culture. <i>Biotechnology and Bioengineering</i> , 1991, 38, 196-205.	3.3	77
239	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
240	Measurement of enzyme reaction rates using advanced pH control system: Application of repetitive PF system. <i>Biotechnology and Bioengineering</i> , 1989, 34, 794-803.	3.3	4
241	Profile control of the specific growth rate in fed-batch experiments. <i>Applied Microbiology and Biotechnology</i> , 1989, 30, 276.	3.6	22
242	Bacteriocin Production Process by a Mixed Culture System. , 0, , 395-411.		1