Hiroshi Shimizu

List of Publications by Year in Descending Order

241 papers	**4,920** citations	**39** h-index	**56** g-index
255 ext. papers	**5,658** ext. citations	**4.6** avg, IF	**5.72** L-index

#	Paper	IF	Citations
241	Systems Biology of Cyanobacteria for Investigating Light Adaptive Mechanisms. *Seibutsu Butsuri*, **2022**, 62, 104-109	0	
240	Mutations in hik26 and slr1916 lead to high-light stress tolerance in Synechocystis sp. PCC6803. *Communications Biology*, **2021**, 4, 343	6.7	4
239	Random Transfer of Genes into Reveals a Complex Background of Heat Tolerance. *Journal of Fungi (Basel, Switzerland)*, **2021**, 7,	5.6	2
238	Estimation of linear and cyclic electron flows in photosynthesis based on C-metabolic flux analysis. *Journal of Bioscience and Bioengineering*, **2021**, 131, 277-282	3.3	4
237	Identification of a rate-limiting step in a metabolic pathway using the kinetic model and in vitro experiment. *Journal of Bioscience and Bioengineering*, **2021**, 131, 271-276	3.3	4
236	Role of type I NADH dehydrogenase in Synechocystis sp. PCC 6803 under phycobilisome excited red light. *Plant Science*, **2021**, 304, 110798	5.3	4
235	Thioredoxin pathway in Anabaena sp. PCC 7120: activity of NADPH-thioredoxin reductase C. *Journal of Biochemistry*, **2021**, 169, 709-719	3.1	1
234	Soft-sensor development for monitoring the lysine fermentation process. *Journal of Bioscience and Bioengineering*, **2021**, 132, 183-189	3.3	1
233	Proteome analysis of response to different spectral light irradiation in Synechocystis sp. PCC 6803. *Journal of Proteomics*, **2021**, 246, 104306	3.9	1
232	Treatment of Retinoblastoma 1-Intact Hepatocellular Carcinoma With Cyclin-Dependent Kinase 4/6 Inhibitor Combination Therapy. *Hepatology*, **2021**, 74, 1971-1993	11.2	8
231	Reactor control system in bacterial co-culture based on fluorescent proteins using an Arduino-based home-made device. *Biotechnology Journal*, **2021**, 16, e2100169	5.6	0
230	Recent advances in metabolic engineering-integration of in silico design and experimental analysis of metabolic pathways. *Journal of Bioscience and Bioengineering*, **2021**, 132, 429-436	3.3	1
229	mfapy: An open-source Python package for C-based metabolic flux analysis. *Metabolic Engineering Communications*, **2021**, 13, e00177	6.5	0
228	Flux controlling technology for central carbon metabolism for efficient microbial bio-production. *Current Opinion in Biotechnology*, **2020**, 64, 169-174	11.4	7
227	Transcription Factor ArcA is a Flux Sensor for the Oxygen Consumption Rate in Escherichia coli. *Biotechnology Journal*, **2020**, 15, e1900353	5.6	3
226	Effects of mutations of GID protein-coding genes on malate production and enzyme expression profiles in Saccharomyces cerevisiae. *Applied Microbiology and Biotechnology*, **2020**, 104, 4971-4983	5.7	4
225	Novel allosteric inhibition of phosphoribulokinase identified by ensemble kinetic modeling of sp. PCC 6803 metabolism. *Metabolic Engineering Communications*, **2020**, 11, e00153	6.5	1

224	Data science-based modeling of the lysine fermentation process. *Journal of Bioscience and Bioengineering*, **2020**, 130, 409-415	3.3	5
223	Direct and quantitative analysis of altered metabolic flux distributions and cellular ATP production pathway in fumarate hydratase-diminished cells. *Scientific Reports*, **2020**, 10, 13065	4.9	1
222	Assessment of Protein Content and Phosphorylation Level in sp. PCC 6803 under Various Growth Conditions Using Quantitative Phosphoproteomic Analysis. *Molecules*, **2020**, 25,	4.8	7
221	Comparison of metabolic profiles of yeasts based on the difference of the Crabtree positive and negative. *Journal of Bioscience and Bioengineering*, **2020**, 129, 52-58	3.3	9
220	Flux balance analysis of cyanobacteria reveals selective use of photosynthetic electron transport components under different spectral light conditions. *Photosynthesis Research*, **2020**, 143, 31-43	3.7	12
219	Prediction of Rate-Limiting Reactions for Growth-Associated Production Using a Constraint-Based Approach. *Biotechnology Journal*, **2019**, 14, e1800431	5.6	0
218	Optogenetic switch for controlling the central metabolic flux of Escherichia coli. *Metabolic Engineering*, **2019**, 55, 68-75	9.7	20
217	C-Metabolic Flux Analysis Reveals Effect of Phenol on Central Carbon Metabolism in. *Frontiers in Microbiology*, **2019**, 10, 1010	5.7	8
216	Time-resolved analysis of short term metabolic adaptation at dark transition in Synechocystis sp. PCC 6803. *Journal of Bioscience and Bioengineering*, **2019**, 128, 424-428	3.3	4
215	Theophylline-inducible riboswitch accurately regulates protein expression at low level in Escherichia coli. *Biotechnology Letters*, **2019**, 41, 743-751	3	4
214	Light-inducible flux control of triosephosphate isomerase on glycolysis in Escherichia coli. *Biotechnology and Bioengineering*, **2019**, 116, 3292-3300	4.9	7
213	High-yielding rice Takanari has superior photosynthetic response to a commercial rice Koshihikari under fluctuating light. *Journal of Experimental Botany*, **2019**, 70, 5287-5297	7	20
212	Repression of mitochondrial metabolism for cytosolic pyruvate-derived chemical production in Saccharomyces cerevisiae. *Microbial Cell Factories*, **2019**, 18, 177	6.4	3
211	Fragmentation of Dicarboxylic and Tricarboxylic Acids in the Krebs Cycle Using GC-EI-MS and GC-EI-MS/MS. *Mass Spectrometry*, **2019**, 8, A0073	1.7	4
210	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. *Metabolic Engineering*, **2019**, 51, 43-49	9.7	4
209	Effect of precise control of flux ratio between the glycolytic pathways on mevalonate production in Escherichia coli. *Biotechnology and Bioengineering*, **2019**, 116, 1080-1088	4.9	9
208	Transomics data-driven, ensemble kinetic modeling for system-level understanding and engineering of the cyanobacteria central metabolism. *Metabolic Engineering*, **2019**, 52, 273-283	9.7	20
207	Magnesium starvation improves production of malonyl-CoA-derived metabolites in Escherichia coli. *Metabolic Engineering*, **2019**, 52, 215-223	9.7	14

206	Targeted proteome analysis of microalgae under high-light conditions by optimized protein extraction of photosynthetic organisms. *Journal of Bioscience and Bioengineering*, **2019**, 127, 394-402	3.3	4
205	Application of adaptive laboratory evolution to overcome a flux limitation in an Escherichia coli production strain. *Biotechnology and Bioengineering*, **2018**, 115, 1542-1551	4.9	17
204	Metabolic flux of the oxidative pentose phosphate pathway under low light conditions in Synechocystis sp. PCC 6803. *Journal of Bioscience and Bioengineering*, **2018**, 126, 38-43	3.3	14
203	Metabolic engineering of mevalonate-producing Escherichia coli strains based on thermodynamic analysis. *Metabolic Engineering*, **2018**, 47, 1-9	9.7	15
202	Expression of Saccharomyces cerevisiae cDNAs to enhance the growth of non-ethanol-producing S. cerevisiae strains lacking pyruvate decarboxylases. *Journal of Bioscience and Bioengineering*, **2018**, 126, 317-321	3.3	1
201	Integrated Analysis of the Transcriptome and Metabolome of Corynebacterium glutamicum during Penicillin-Induced Glutamic Acid Production. *Biotechnology Journal*, **2018**, 13, e1700612	5.6	10
200	Sclerotherapy for Rectal Varices by a Small-Bore Needle Puncture Through the Greater Sciatic Foramen. *CardioVascular and Interventional Radiology*, **2018**, 41, 317-322	2.7	5
199	A pyruvate carbon flux tugging strategy for increasing 2,3-butanediol production and reducing ethanol subgeneration in the yeast. *Biotechnology for Biofuels*, **2018**, 11, 180	7.8	16
198	Transcriptome analysis of the cyanobacterium Synechocystis sp. PCC 6803 and mechanisms of photoinhibition tolerance under extreme high light conditions. *Journal of Bioscience and Bioengineering*, **2018**, 126, 596-602	3.3	15
197	Comparative analysis of fermentation and enzyme expression profiles among industrial Saccharomyces cerevisiae strains. *Applied Microbiology and Biotechnology*, **2018**, 102, 7071-7081	5.7	3
196	Optimal C-labeling of glycerol carbon source for precise flux estimation in Escherichia coli. *Journal of Bioscience and Bioengineering*, **2018**, 125, 301-305	3.3	3
195	Mass Spectrometry-Based Method to Study Inhibitor-Induced Metabolic Redirection in the Central Metabolism of Cancer Cells. *Mass Spectrometry*, **2018**, 7, A0067	1.7	4
194	Transarterial Embolization for Life-Threatening Spontaneous Hemopneumothorax. *Interventional Radiology*, **2018**, 3, 84-87	0.1	
193	Comparative Targeted Proteomics of the Central Metabolism and Photosystems in SigE Mutant Strains of sp. PCC 6803. *Molecules*, **2018**, 23,	4.8	8
192	C-metabolic flux analysis of ethanol-assimilating Saccharomyces cerevisiae for S-adenosyl-L-methionine production. *Microbial Cell Factories*, **2018**, 17, 82	6.4	9
191	Characterization of oil-producing yeast Lipomyces starkeyi on glycerol carbon source based on metabolomics and C-labeling. *Applied Microbiology and Biotechnology*, **2018**, 102, 8909-8920	5.7	7
190	Omics-Integrated Approach for Metabolic State Analysis of Microbial Processes **2017**, 213-236		
189	Control of Microbial Processes **2017**, 237-258		

188	Metabolic engineering of Synechocystis sp. PCC 6803 for enhanced ethanol production based on flux balance analysis. *Bioprocess and Biosystems Engineering*, **2017**, 40, 791-796	3.7	31
187	Metabolic impact of nutrient starvation in mevalonate-producing Escherichia coli. *Bioresource Technology*, **2017**, 245, 1634-1640	11	11
186	The RB-IL-6 axis controls self-renewal and endocrine therapy resistance by fine-tuning mitochondrial activity. *Oncogene*, **2017**, 36, 5145-5157	9.2	24
185	Heterologous expression of bacterial phosphoenol pyruvate carboxylase and Entner-Doudoroff pathway in Saccharomyces cerevisiae for improvement of isobutanol production. *Journal of Bioscience and Bioengineering*, **2017**, 124, 263-270	3.3	12
184	Prediction of Cross-resistance and Collateral Sensitivity by Gene Expression profiles and Genomic Mutations. *Scientific Reports*, **2017**, 7, 14009	4.9	21
183	Identification of alcohol stress tolerance genes of sp. PCC 6803 using adaptive laboratory evolution. *Biotechnology for Biofuels*, **2017**, 10, 307	7.8	29
182	Pulmonary Tumor Thrombotic Microangiopathy - Antemortem Diagnosis With Pulmonary Artery Wedge Blood Cell Sampling in a Recurrent Breast Cancer Patient. *Circulation Journal*, **2017**, 81, 1959-1960	2.9	6
181	Learning from quantitative data to understand central carbon metabolism. *Biotechnology Advances*, **2017**, 35, 971-980	17.8	18
180	Metabolic engineering of isopropyl alcohol-producing Escherichia coli strains with C-metabolic flux analysis. *Biotechnology and Bioengineering*, **2017**, 114, 2782-2793	4.9	15
179	Metabolic Flux Analysis of the Synechocystis sp. PCC 6803 ΔrtABCD Mutant Reveals a Mechanism for Metabolic Adaptation to Nitrogen-Limited Conditions. *Plant and Cell Physiology*, **2017**, 58, 537-545	4.9	14
178	C-metabolic flux analysis for mevalonate-producing strain of Escherichia coli. *Journal of Bioscience and Bioengineering*, **2017**, 123, 177-182	3.3	35
177	Prediction of Hopeless Peptides Unlikely to be Selected for Targeted Proteome Analysis. *Mass Spectrometry*, **2017**, 6, A0056	1.7	6
176	Targeted proteome analysis of single-gene deletion strains of Saccharomyces cerevisiae lacking enzymes in the central carbon metabolism. *PLoS ONE*, **2017**, 12, e0172742	3.7	13
175	A rare case of long-term survival with idiopathic dilatation of the pulmonary artery. *International Journal of Cardiology*, **2016**, 223, 337-339	3.2	1
174	Enhancement of 1,5-diaminopentane production in a recombinant strain of Corynebacterium glutamicum by Tween 40 addition. *Journal of General and Applied Microbiology*, **2016**, 62, 42-5	1.5	12
173	GC-MS/MS survey of collision-induced dissociation of tert-butyldimethylsilyl-derivatized amino acids and its application to (13)C-metabolic flux analysis of Escherichia coli central metabolism. *Analytical and Bioanalytical Chemistry*, **2016**, 408, 6133-40	4.4	10
172	Positive effects of proline addition on the central metabolism of wild-type and lactic acid-producing Saccharomyces cerevisiae strains. *Bioprocess and Biosystems Engineering*, **2016**, 39, 1711-6	3.7	1
171	Glutamic Acid Fermentation: Discovery of Glutamic Acid-Producing Microorganisms, Analysis of the Production Mechanism, Metabolic Engineering, and Industrial Production Process **2016**, 339-360		6

170	Metabolic Adaptation to Nutritional Stress in Human Colorectal Cancer. *Scientific Reports*, **2016**, 6, 38415	4.9	39
169	Recent advances in amino acid production by microbial cells. *Current Opinion in Biotechnology*, **2016**, 42, 133-146	11.4	75
168	Investigation of useful carbon tracers for C-metabolic flux analysis of by considering five experimentally determined flux distributions. *Metabolic Engineering Communications*, **2016**, 3, 187-195	6.5	12
167	Combinatorial deletions of glgC and phaCE enhance ethanol production in Synechocystis sp. PCC 6803. *Journal of Biotechnology*, **2016**, 239, 13-19	3.7	40
166	Metabolome analysis of Saccharomyces cerevisiae and optimization of culture medium for S-adenosyl-L-methionine production. *AMB Express*, **2016**, 6, 38	4.1	17
165	(13)C-metabolic flux analysis in S-adenosyl-L-methionine production by Saccharomyces cerevisiae. *Journal of Bioscience and Bioengineering*, **2015**, 120, 532-8	3.3	26
164	Metabolic characterization of cultured mammalian cells by mass balance analysis, tracer labeling experiments and computer-aided simulations. *Journal of Bioscience and Bioengineering*, **2015**, 120, 725-31	3.3	9
163	Enhanced dipicolinic acid production during the stationary phase in Bacillus subtilis by blocking acetoin synthesis. *Bioscience, Biotechnology and Biochemistry*, **2015**, 79, 2073-80	2.1	9
162	SSDesign: Computational metabolic pathway design based on flux variability using elementary flux modes. *Biotechnology and Bioengineering*, **2015**, 112, 759-68	4.9	9
161	Absolute quantitation of glycolytic intermediates reveals thermodynamic shifts in Saccharomyces cerevisiae strains lacking PFK1 or ZWF1 genes. *Journal of Bioscience and Bioengineering*, **2015**, 120, 280-6	3.3	22
160	Effect of malic enzyme on ethanol production by Synechocystis sp. PCC 6803. *Journal of Bioscience and Bioengineering*, **2015**, 119, 82-4	3.3	13
159	Phenotypic convergence in bacterial adaptive evolution to ethanol stress. *BMC Evolutionary Biology*, **2015**, 15, 180	3	20
158	In Silico Metabolic Pathway Design and 13C-Based Metabolic Flux Analysis for Bio-Production. *Kagaku To Seibutsu*, **2015**, 53, 455-461	0	
157	Metabolomic analysis of acid stress response in Saccharomyces cerevisiae. *Journal of Bioscience and Bioengineering*, **2015**, 120, 396-404	3.3	29
156	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 Saccharomyces cerevisiae using ultra fast mass spectrometry. *Journal of Bioscience and Bioengineering*, **2015**, 119, 117-20	3.3	12
155	C-based metabolic flux analysis of Saccharomyces cerevisiae with a reduced Crabtree effect. *Journal of Bioscience and Bioengineering*, **2015**, 120, 140-4	3.3	16
154	Construction of a Genome-Scale Metabolic Model of Arthrospira platensis NIES-39 and Metabolic Design for Cyanobacterial Bioproduction. *PLoS ONE*, **2015**, 10, e0144430	3.7	20
153	13 C-metabolic flux analysis in heterologous cellulase production by Bacillus subtilis genome-reduced strain. *Journal of Biotechnology*, **2014**, 179, 42-9	3.7	30

152	Integrated metabolic flux and omics analysis of Synechocystis sp. PCC 6803 under mixotrophic and photoheterotrophic conditions. *Plant and Cell Physiology*, **2014**, 55, 1605-12	4.9	60
151	A vector library for silencing central carbon metabolism genes with antisense RNAs in Escherichia coli. *Applied and Environmental Microbiology*, **2014**, 80, 564-73	4.8	28
150	Glutamic Acid **2014**, 473-495		3
149	Increased 3-hydroxypropionic acid production from glycerol, by modification of central metabolism in Escherichia coli. *Microbial Cell Factories*, **2014**, 13, 64	6.4	53
148	Reliable Metabolic Flux Estimation in Escherichia coli Central Carbon Metabolism Using Intracellular Free Amino Acids. *Metabolites*, **2014**, 4, 408-20	5.6	14
147	Enhanced acetic acid and succinic acid production under microaerobic conditions by Corynebacterium glutamicum harboring Escherichia coli transhydrogenase gene pntAB. *Journal of General and Applied Microbiology*, **2014**, 60, 112-8	1.5	25
146	Potential of a Saccharomyces cerevisiae recombinant strain lacking ethanol and glycerol biosynthesis pathways in efficient anaerobic bioproduction. *Bioengineered*, **2014**, 5, 123-8	5.7	4
145	Development of an automated culture system for laboratory evolution. *Journal of the Association for Laboratory Automation*, **2014**, 19, 478-82		25
144	Metabolic engineering of Saccharomyces cerevisiae to improve succinic acid production based on metabolic profiling. *Bioscience, Biotechnology and Biochemistry*, **2014**, 78, 151-9	2.1	40
143	FastPros: screening of reaction knockout strategies for metabolic engineering. *Bioinformatics*, **2014**, 30, 981-7	7.2	32
142	OpenMebius: an open source software for isotopically nonstationary 13C-based metabolic flux analysis. *BioMed Research International*, **2014**, 2014, 627014	3	72
141	Flux analysis and metabolomics for systematic metabolic engineering of microorganisms. *Biotechnology Advances*, **2013**, 31, 818-26	17.8	84
140	Utilization of Saccharomyces cerevisiae recombinant strain incapable of both ethanol and glycerol biosynthesis for anaerobic bioproduction. *Applied Microbiology and Biotechnology*, **2013**, 97, 4811-9	5.7	24
139	Genome-wide identification of the targets for genetic manipulation to improve L-lactate production by Saccharomyces cerevisiae by using a single-gene deletion strain collection. *Journal of Biotechnology*, **2013**, 168, 185-93	3.7	3
138	ArtPathDesign: rational heterologous pathway design system for the production of nonnative metabolites. *Journal of Bioscience and Bioengineering*, **2013**, 116, 524-7	3.3	5
137	Integrated transcriptomic and metabolomic analysis of the central metabolism of Synechocystis sp. PCC 6803 under different trophic conditions. *Biotechnology Journal*, **2013**, 8, 571-80	5.6	44
136	Systems metabolic engineering: the creation of microbial cell factories by rational metabolic design and evolution. *Advances in Biochemical Engineering/Biotechnology*, **2013**, 131, 1-23	1.7	14
135	In silico screening of triple reaction knockout Escherichia coli strains for overproduction of useful metabolites. *Journal of Bioscience and Bioengineering*, **2013**, 115, 221-8	3.3	20

134	Systems metabolic engineering for the production of bio-nylon precursor. *Biotechnology Journal*, **2013**, 8, 513-4	5.6	7
133	Development of a physical model-based algorithm for the detection of single-nucleotide substitutions by using tiling microarrays. *PLoS ONE*, **2013**, 8, e54571	3.7	5
132	Stable disruption of ethanol production by deletion of the genes encoding alcohol dehydrogenase isozymes in Saccharomyces cerevisiae. *Journal of Bioscience and Bioengineering*, **2012**, 113, 192-5	3.3	39
131	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, 526-8	3.3	18
130	An in silico platform for the design of heterologous pathways in nonnative metabolite production. *BMC Bioinformatics*, **2012**, 13, 93	3.6	19
129	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	6.4	40
128	Molecular mechanisms and metabolic engineering of glutamate overproduction in Corynebacterium glutamicum. *Sub-Cellular Biochemistry*, **2012**, 64, 261-81	5.5	15
127	Design of Superior Cell Factories Based on Systems Wide Omics Analysis **2012**, 57-81		3
126	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	3.3	20
125	Evaluating (13)C enrichment data of free amino acids for precise metabolic flux analysis. *Biotechnology Journal*, **2011**, 6, 1377-87	5.6	23
124	Investigation of phosphorylation status of OdhI protein during penicillin- and Tween 40-triggered glutamate overproduction by Corynebacterium glutamicum. *Applied Microbiology and Biotechnology*, **2011**, 91, 143-51	5.7	31
123	Reconstruction and verification of a genome-scale metabolic model for Synechocystis sp. PCC6803. *Applied Microbiology and Biotechnology*, **2011**, 92, 347-58	5.7	53
122	Engineering strategy of yeast metabolism for higher alcohol production. *Microbial Cell Factories*, **2011**, 10, 70	6.4	38
121	Comprehensive phenotypic analysis of single-gene deletion and overexpression strains of Saccharomyces cerevisiae. *Yeast*, **2011**, 28, 349-61	3.4	90
120	Requirement of de novo synthesis of the OdhI protein in penicillin-induced glutamate production by Corynebacterium glutamicum. *Applied Microbiology and Biotechnology*, **2010**, 86, 911-20	5.7	56
119	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	5.7	22
118	Transcriptome analysis of parallel-evolved Escherichia coli strains under ethanol stress. *BMC Genomics*, **2010**, 11, 579	4.5	104
117	Differential importance of trehalose accumulation in Saccharomyces cerevisiae in response to various environmental stresses. *Journal of Bioscience and Bioengineering*, **2010**, 109, 262-6	3.3	80

116	Genome-wide expression analysis of Saccharomyces pastorianus orthologous genes using oligonucleotide microarrays. *Journal of Bioscience and Bioengineering*, **2010**, 110, 602-7	3.3	27
115	Model-based analysis of non-specific binding for background correction of high-density oligonucleotide microarrays. *Bioinformatics*, **2009**, 25, 36-41	7.2	16
114	A model-based analysis method for detection of single-base substitution using resequencing microarrays. *Journal of Bioscience and Bioengineering*, **2009**, 108, S160	3.3	
113	Flux balance analysis of Corynebacterium glutamicum using a genome-scale metabolic model. *Journal of Bioscience and Bioengineering*, **2009**, 108, S166	3.3	
112	Analysis of adaptation to high ethanol concentration in Saccharomyces cerevisiae using DNA microarray. *Bioprocess and Biosystems Engineering*, **2009**, 32, 681-8	3.7	31
111	Effect of odhA overexpression and odhA antisense RNA expression on Tween-40-triggered glutamate production by Corynebacterium glutamicum. *Applied Microbiology and Biotechnology*, **2009**, 81, 1097-106	5.7	57
110	Investigating the effectiveness of DNA microarray analysis for identifying the genes involved in l-lactate production by Saccharomyces cerevisiae. *Applied Microbiology and Biotechnology*, **2009**, 84, 1149-59	5.7	16
109	Effect of trehalose accumulation on response to saline stress in Saccharomyces cerevisiae. *Yeast*, **2009**, 26, 17-30	3.4	53
108	Comprehensive phenotypic analysis for identification of genes affecting growth under ethanol stress in Saccharomyces cerevisiae. *FEMS Yeast Research*, **2009**, 9, 32-44	3.1	171
107	Analysis of stochasticity in promoter activation by using a dual-fluorescence reporter system. *BioSystems*, **2009**, 97, 160-4	1.9	4
106	Proteomic analysis of responses to osmotic stress in laboratory and sake-brewing strains of Saccharomyces cerevisiae. *Process Biochemistry*, **2009**, 44, 647-653	4.8	15
105	Analysis of metabolic network based on conservation of molecular structure. *BioSystems*, **2009**, 95, 175-8	1.9	5
104	Development and experimental verification of a genome-scale metabolic model for Corynebacterium glutamicum. *Microbial Cell Factories*, **2009**, 8, 43	6.4	92
103	Beer volatile compounds and their application to low-malt beer fermentation. *Journal of Bioscience and Bioengineering*, **2008**, 106, 317-23	3.3	66
102	Distinct roles of two anaplerotic pathways in glutamate production induced by biotin limitation in Corynebacterium glutamicum. *Journal of Bioscience and Bioengineering*, **2008**, 106, 51-8	3.3	69
101	Dynamic change in promoter activation during lysine biosynthesis in Escherichia coli cells. *Molecular BioSystems*, **2008**, 4, 128-34		10
100	Genome-wide analysis of the effects of location and number of stress response elements on gene expression in Saccharomyces cerevisiae. *Journal of Bioscience and Bioengineering*, **2008**, 106, 507-10	3.3	3
99	Analysis of lager brewing yeast at low temperature fermentation using DNA microarray. *Journal of Biotechnology*, **2008**, 136, S351-S352	3.7	1

98	Improvement of L-lactate production by CYB2 gene disruption in a recombinant Saccharomyces cerevisiae strain under low pH condition. *Bioscience, Biotechnology and Biochemistry*, **2008**, 72, 3063-6	2.1	15
97	Adaptation of Saccharomyces cerevisiae cells to high ethanol concentration and changes in fatty acid composition of membrane and cell size. *PLoS ONE*, **2008**, 3, e2623	3.7	57
96	An improved physico-chemical model of hybridization on high-density oligonucleotide microarrays. *Bioinformatics*, **2008**, 24, 1278-85	7.2	38
95	Characterization of new isolated Ralstonia eutropha strain A-04 and kinetic study of biodegradable copolyester poly(3-hydroxybutyrate-co-4-hydroxybutyrate) production. *Journal of Industrial Microbiology and Biotechnology*, **2008**, 35, 1205-15	4.2	38
94	Study on roles of anaplerotic pathways in glutamate overproduction of Corynebacterium glutamicum by metabolic flux analysis. *Microbial Cell Factories*, **2007**, 6, 19	6.4	65
93	Metabolic pathway recruiting through genomic data analysis for industrial application of Saccharomyces cerevisiae. *Biochemical Engineering Journal*, **2007**, 36, 28-37	4.2	4
92	Analysis of fluctuation in protein abundance without promoter regulation based on Escherichia coli continuous culture. *BioSystems*, **2007**, 90, 614-22	1.9	4
91	Kinetic modeling of kefiran production in mixed culture of Lactobacillus kefiranofaciens and Saccharomyces cerevisiae. *Process Biochemistry*, **2007**, 42, 570-579	4.8	7
90	Extracting the hidden features in saline osmotic tolerance in Saccharomyces cerevisiae from DNA microarray data using the self-organizing map: biosynthesis of amino acids. *Applied Microbiology and Biotechnology*, **2007**, 75, 415-26	5.7	20
89	Reduction of lactate production in Lactococcus lactis, a combined strategy: metabolic engineering by introducing foreign alanine dehydrogenase gene and hemin addition. *World Journal of Microbiology and Biotechnology*, **2007**, 23, 947-953	4.4	1
88	INVERSE METABOLIC ENGINEERING BY INTEGRATION OF MULTIPLE OMICS ANALYSES. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2007**, 40, 19-24		
87	3P354 Analysis of the relationship between noise in gene expression and the regulatory sturucture in amino acid biosynthesis pathway(Others,Poster Presentations). *Seibutsu Butsuri*, **2007**, 47, S291	0	
86	Identification of target genes conferring ethanol stress tolerance to Saccharomyces cerevisiae based on DNA microarray data analysis. *Journal of Biotechnology*, **2007**, 131, 34-44	3.7	158
85	Physiological analysis of yeast cells by flow cytometry during serial-repitching of low-malt beer fermentation. *Journal of Bioscience and Bioengineering*, **2007**, 103, 451-6	3.3	15
84	Analysis of hemin effect on lactate reduction in Lactococcus lactis. *Journal of Bioscience and Bioengineering*, **2007**, 103, 529-34	3.3	8
83	Production of Glutamate and Glutamate-Related Amino Acids: Molecular Mechanism Analysis and Metabolic Engineering **2006**, 1-38		21
82	Comparative analysis of transcriptional responses to saline stress in the laboratory and brewing strains of Saccharomyces cerevisiae with DNA microarray. *Applied Microbiology and Biotechnology*, **2006**, 70, 346-57	5.7	60
81	Simultaneous control of apparent extract and volatile compounds concentrations in low-malt beer fermentation. *Applied Microbiology and Biotechnology*, **2006**, 73, 549-58	5.7	14

80	Precise metabolic flux analysis of coryneform bacteria by gas chromatography-mass spectrometry and verification by nuclear magnetic resonance. *Journal of Bioscience and Bioengineering*, **2006**, 102, 413-24	3.3	21
79	Comparison of transcriptional responses to osmotic stresses induced by NaCl and sorbitol additions in Saccharomyces cerevisiae using DNA microarray. *Journal of Bioscience and Bioengineering*, **2006**, 102, 568-71	3.3	27
78	Robustness of cascade pH and dissolved oxygen control in symbiotic nisin production process system of Lactococcus lactis and Kluyveromyces marxianus. *Journal of Bioscience and Bioengineering*, **2006**, 101, 274-6	3.3	9
77	Computational prediction of impact of rerouting the carbon flux in metabolic pathway on cell growth and nisin production by Lactococcus lactis. *Biochemical Engineering Journal*, **2006**, 28, 220-230	4.2	9
76	Characterization and enzymatic degradation of microbial copolyester P(3HB-co-3HV)s produced by metabolic reaction model-based system. *Polymer Degradation and Stability*, **2006**, 91, 2941-2950	4.7	15
75	Analysis of Fluctuation in Gene Expression Based on Continuous Culture System. *Lecture Notes in Computer Science*, **2006**, 113-127	0.9	
74	Microbial Interaction in a Symbiotic Bioprocess of Lactic Acid Bacterium and Diary Yeast. *Lecture Notes in Computer Science*, **2006**, 93-106	0.9	2
73	On-Line Estimation and Control of Apparent Extract Concentration in Low-Malt Beer Fermentation. *Journal of the Institute of Brewing*, **2005**, 111, 128-136	2	6
72	Development of Co-Culture Systems of Lactic Acid Bacteria and Yeasts for Bioproduction. *Japanese Journal of Lactic Acid Bacteria*, **2005**, 16, 2-10	0	2
71	Comparative study of flux redistribution of metabolic pathway in glutamate production by two coryneform bacteria. *Metabolic Engineering*, **2005**, 7, 59-69	9.7	56
70	Application of a mathematical model and Differential Evolution algorithm approach to optimization of bacteriocin production by Lactococcus lactis C7. *Bioprocess and Biosystems Engineering*, **2005**, 28, 15-26	2.7	16
69	DNA microarray analysis onSaccharomyces cerevisiae under high carbon dioxide concentration in fermentation process. *Biotechnology and Bioprocess Engineering*, **2005**, 10, 451-461	3.1	8
68	Metabolic flux control analysis of branch points: an improved approach to obtain flux control coefficients from large perturbation data. *Metabolic Engineering*, **2004**, 6, 391-400	9.7	29
67	Simultaneous Control of Apparent Extract and Volatile Compounds Concentrations in Beer Fermentation. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2004**, 37, 451-456		
66	Analysis of Responses of Complex Bionetworks to Changes in Environmental Conditions. *Lecture Notes in Computer Science*, **2004**, 13-27	0.9	
65	Nonisothermal Crystallization Kinetics of Biodegradable Random Poly(3-hydroxybutyrate-co-3-hydroxyvalerate) and Block One. *Journal of Chemical Engineering of Japan*, **2003**, 36, 639-646	0.8	7
64	Clustering gene expression pattern and extracting relationship in gene network based on artificial neural networks. *Journal of Bioscience and Bioengineering*, **2003**, 96, 421-8	3.3	21
63	Interactions between Lactobacillus kefiranofaciens and Saccharomyces cerevisiae in mixed culture for kefiran production. *Journal of Bioscience and Bioengineering*, **2003**, 96, 279-84	3.3	63

62	Enhanced kefiran production by mixed culture of Lactobacillus kefiranofaciens and Saccharomyces cerevisiae. *Journal of Biotechnology*, **2003**, 100, 43-53	3.7	72
61	Data preprocessing and output evaluation of an autoassociative neural network model for online fault detection in virginiamycin production. *Journal of Bioscience and Bioengineering*, **2002**, 94, 70-77	3.3	12
60	Classification of fermentation performance by multivariate analysis based on mean hypothesis testing. *Journal of Bioscience and Bioengineering*, **2002**, 94, 251-257	3.3	11
59	Metabolic engineering ꞏIntegrating methodologies of molecular breeding and bioprocess systems engineering. *Journal of Bioscience and Bioengineering*, **2002**, 94, 563-573	3.3	32
58	Roles of glucose and acetate as carbon sources inl-histidine production withBrevibacterium flavum FERM1564 revealed by metabolic flux analysis. *Biotechnology and Bioprocess Engineering*, **2002**, 7, 171-177	2.1	5
57	Effect of Carbon and Nitrogen Additions on Consumption Activity of Apparent Extract of Yeast Cells in a Brewing Process. *Journal of the American Society of Brewing Chemists*, **2002**, 60, 163-169	1.9	13
56	Metabolic Control Analysis in Glutamate Synthetic Pathway: Experimental Sensitivity Analysis at a Key Branch Point. *ACS Symposium Series*, **2002**, 39-52	0.4	1
55	Model predictive controller for biodegradable polyhydroxyalkanoate production in fed-batch culture. *Journal of Biotechnology*, **2002**, 95, 157-69	3.7	10
54	Metabolic Engineering. Integrating Methodologies of Molecular Breeding and Bioprocess Systems Engineering.. *Journal of Bioscience and Bioengineering*, **2002**, 94, 563-573	3.3	1
53	Data preprocessing and output evaluation of an autoassociative neural network model for online fault detection in virginiamycin production. *Journal of Bioscience and Bioengineering*, **2002**, 94, 70-7	3.3	5
52	Metabolic engineering--integrating methodologies of molecular breeding and bioprocess systems engineering. *Journal of Bioscience and Bioengineering*, **2002**, 94, 563-73	3.3	1
51	Classification of fermentation performance by multivariate analysis based on mean hypothesis testing. *Journal of Bioscience and Bioengineering*, **2002**, 94, 251-7	3.3	1
50	Quality Control of Polyhydroxyalkanoates in Fed-Batch Culture Based on a Metabolic Reaction Model. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2001**, 34, 201-206		1
49	Learning from the Wisdom of the Ecosystem: Novel Control Strategy Exploiting Microbial Interaction in Co-Culture System. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2001**, 34, 189-194		
48	?????????????????. *Nippon Nogeikagaku Kaishi*, **2001**, 75, 678-682		
47	Modelling and optimization of environmental conditions for kefiran production by Lactobacillus kefiranofaciens. *Applied Microbiology and Biotechnology*, **2001**, 57, 639-46	5.7	33
46	Multivariable control of alcohol concentrations in the production of polyhydroxyalkanoates (PHAs) by Paracoccus denitrificans. *Biotechnology and Bioengineering*, **2001**, 74, 116-24	4.9	18
45	Mining of biological data I: identifying discriminating features via mean hypothesis testing. *Metabolic Engineering*, **2000**, 2, 218-27	9.7	20

44	Mining of biological data II: assessing data structure and class homogeneity by cluster analysis. *Metabolic Engineering*, **2000**, 2, 228-38	9.7	27
43	Maximizing yellow pigment production in fed-batch culture of Monascus sp. *Journal of Bioscience and Bioengineering*, **2000**, 90, 363-7	3.3	29
42	Optimization of agitation and aeration conditions for maximum virginiamycin production. *Applied Microbiology and Biotechnology*, **1999**, 51, 164-9	5.7	29
41	A maximum production strategy of lysine based on a simplified model derived from a metabolic reaction network. *Metabolic Engineering*, **1999**, 1, 299-308	9.7	13
40	Maximum production strategy for biodegradable copolymer P(HB-co-HV) in fed-batch culture of Alcaligenes eutrophus **1999**, 62, 518-525		28
39	On-line monitoring of fungal cell concentration by dielectric spectroscopy. *Journal of Biotechnology*, **1999**, 69, 115-123	3.7	17
38	Nisin production by a mixed-culture system consisting of Lactococcus lactis and Kluyveromyces marxianus. *Applied and Environmental Microbiology*, **1999**, 65, 3134-41	4.8	64
37	Maximum production strategy for biodegradable copolymer P(HB-co-HV) in fed-batch culture of Alcaligenes eutrophus **1999**, 62, 518		1
36	Bioprocess fault detection by nonlinear multivariate analysis: application of an artificial autoassociative neural network and wavelet filter bank. *Biotechnology Progress*, **1998**, 14, 79-87	2.8	16
35	Method of Corynebacterium glutamicum fermentation time extension with high lysine production rate by leucine addition. *Journal of Bioscience and Bioengineering*, **1998**, 86, 180-184		7
34	Experimental determination of group flux control coefficients in metabolic networks. *Biotechnology and Bioengineering*, **1998**, 58, 149-53	4.9	24
33	Optimization of Dissolved Oxygen Supply Method for Maximum Virginiamycin Production. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **1998**, 31, 193-198		
32	Database Mining Tools for Bioprocess Analysis. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **1998**, 31, 405-410		
31	Optimal Production of Biodegradable Copolymer, P(HB-co-HV), in Fed-Batch Culture of Alcaligenes eutrophus. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **1998**, 31, 173-178		
30	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		
29	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		
28	On-line fault diagnosis for optimal rice α-amylase production process of a temperature-sensitive mutant of Saccharomyces cerevisiae by an autoassociative neural network. *Journal of Bioscience and Bioengineering*, **1997**, 83, 435-442		18
27	An on-line physiological state recognition system for the lysine fermentation process based on a metabolic reaction model. *Biotechnology and Bioengineering*, **1997**, 55, 170-81	4.9	55

26	Maximum virginiamycin production by optimization of cultivation conditions in batch culture with autoregulator addition. *Biotechnology and Bioengineering*, **1996**, 49, 437-44	4.9	16
25	Comparison of estimation techniques for a time-dependent parameter in a metabolic reaction model. *Journal of Bioscience and Bioengineering*, **1996**, 81, 363-365		3
24	Image analysis of mycelial morphology in virginiamycin production by batch culture of Streptomyces virginiae. *Journal of Bioscience and Bioengineering*, **1996**, 81, 7-12		34
23	Mole fraction control of poly(3-hydroxybutyric-co-3-hydroxyvaleric) acid in fed-batch culture of Alcaligenes eutrophus. *Journal of Bioscience and Bioengineering*, **1996**, 81, 422-428		23
22	On-line recognition of physiological state in a yeast fed-batch culture. *Journal of Process Control*, **1996**, 6, 373-378	3.9	5
21	Maximum virginiamycin production by optimization of cultivation conditions in batch culture with autoregulator addition **1996**, 49, 437		8
20	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		
19	Optimum autoregulator addition strategy for maximum virginiamycin production in batch culture of Streptomyces virginiae. *Biotechnology and Bioengineering*, **1995**, 46, 437-42	4.9	22
18	On-line state recognition in a yeast fed-batch culture using error vectors. *Biotechnology and Bioengineering*, **1995**, 47, 165-73	4.9	27
17	ON-LINE PHYSIOLOGICAL STATE RECOGNITION AND PARAMETER ESTIMATION IN THE METABOLIC REACTION MODEL USING ERROR VECTORS **1995**, 118-123		
16	Comparative studies of in vitro and in vivo function of three different shaped bioartificial pancreases made of agarose hydrogel. *Biomaterials*, **1994**, 15, 113-20	15.6	53
15	Control of Molecular Weight Distribution and Mole Fraction in Poly(-D(Ī-3-hydroxyalkanoate) (PHA) Production by Alcaligenes eutrophus. *Studies in Polymer Science*, **1994**, 12, 365-372		1
14	Fuzzy control of ethanol concentration its application to maximum glutathione production in yeast fed-batch culture. *Biotechnology and Bioengineering*, **1993**, 41, 493-501	4.9	58
13	Calculation of optimal trajectories for fermentation processes by genetic algorithm. *Journal of Bioscience and Bioengineering*, **1993**, 75, 474		2
12	Kinetic study of poly-d(Ī-3-hydroxybutyric acid (PHB) production and its molecular weight distribution control in a fed-batch culture of Alcaligenes eutrophus. *Journal of Bioscience and Bioengineering*, **1993**, 76, 465-469		39
11	Effect of amino acids on glutathione production by Saccharomyces cerevisiae. *Applied Microbiology and Biotechnology*, **1992**, 36, 538	5.7	59
10	Cysteine addition strategy for maximum glutathione production in fed-batch culture of Saccharomyces cerevisiae. *Applied Microbiology and Biotechnology*, **1992**, 37, 141	5.7	57
9	Agarose for a bioartificial pancreas. *Journal of Biomedical Materials Research Part B*, **1992**, 26, 967-77		121

List of Publications

8	Modelling, Optimization and Realization of Fed-Batch Culture using the Specific Growth Rate.. *Kagaku Kogaku Ronbunshu*, **1991**, 17, 572-578	0.4	
7	Optimal production of glutathione by controlling the specific growth rate of yeast in fed-batch culture. *Biotechnology and Bioengineering*, **1991**, 38, 196-205	4.9	69
6	An algorithmic approach to constructing the on-line estimation system for the specific growth rate. *Biotechnology and Bioengineering*, **1989**, 33, 354-64	4.9	53
5	Measurement of enzyme reaction rates using advanced pH control system: application of repetitive PF system. *Biotechnology and Bioengineering*, **1989**, 34, 794-803	4.9	4
4	Profile control of the specific growth rate in fed-batch experiments. *Applied Microbiology and Biotechnology*, **1989**, 30, 276	5.7	17
3	Maximum Production of Glutathione in Fed-batch Culture of Saccharomycescerevisiae **1989**, 373-377	1	
2	Bacteriocin Production Process by a Mixed Culture System395-411	1	
1	High-throughput laboratory evolution ofEscherichia coliunder multiple stress environments	1	