

Chikara Furusawa

List of Publications by Year in descending order

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Version: 2024-02-01

150
papers

5,701
citations

76326

40
h-index

95266

68
g-index

163
all docs

163
docs citations

163
times ranked

9164
citing authors

#	ARTICLE	IF	CITATIONS
1	Experimental demonstration of operon formation catalyzed by insertion sequence. <i>Nucleic Acids Research</i> , 2022, 50, 1673-1686.	14.5	9
2	Identification of Bacterial Drug-Resistant Cells by the Convolutional Neural Network in Transmission Electron Microscope Images. <i>Frontiers in Microbiology</i> , 2022, 13, 839718.	3.5	0
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	Potential contribution of intrinsic developmental stability toward body plan conservation. <i>BMC Biology</i> , 2022, 20, 82.	3.8	6
5	Direction and Constraint in Phenotypic Evolution: Dimension Reduction and Global Proportionality in Phenotype Fluctuation and Responses. , 2021, , 35-58.		2
6	Elevated Sporulation Efficiency in Fission Yeast <i>Schizosaccharomyces japonicus</i> Strains Isolated from <i>Drosophila</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 350.	3.5	10
7	Morphological change of coiled bacterium <i>Spirosoma linguale</i> with acquisition of β -lactam resistance. <i>Scientific Reports</i> , 2021, 11, 13278.	3.3	1
8	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	12.8	11
9	Laboratory evolution of <i>Mycobacterium</i> on agar plates for analysis of resistance acquisition and drug sensitivity profiles. <i>Scientific Reports</i> , 2021, 11, 15136.	3.3	7
10	Mutational property of newly identified mutagen l-glutamic acid β -hydrazide in <i>Escherichia coli</i> . <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2021, 823, 111759.	1.0	2
11	The sixth transmembrane region of a pheromone G-protein coupled receptor, Map3, is implicated in discrimination of closely related pheromones in <i>Schizosaccharomyces pombe</i> . <i>Genetics</i> , 2021, 219, .	2.9	2
12	Decoding gut microbiota by imaging analysis of fecal samples. <i>IScience</i> , 2021, 24, 103481.	4.1	2
13	High-throughput laboratory evolution reveals evolutionary constraints in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2020, 11, 5970.	12.8	37
14	Understanding metabolic adaptation by using bacterial laboratory evolution and trans-omics analysis. <i>Biophysical Reviews</i> , 2020, 12, 677-682.	3.2	8
15	Toward understanding of evolutionary constraints: experimental and theoretical approaches. <i>Biophysical Reviews</i> , 2020, 12, 1155-1161.	3.2	9
16	Suppression of antibiotic resistance evolution by single-gene deletion. <i>Scientific Reports</i> , 2020, 10, 4178.	3.3	15
17	Toward Predicting Gene Expression and Metabolic Functions from Label-Free Raman Imaging of Living Cells. <i>Biophysical Journal</i> , 2020, 118, 347a.	0.5	0
18	Evolutionary Changes in DnaA-Dependent Chromosomal Replication in Cyanobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 786.	3.5	12

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19	Analysis of Bacterial Laboratory Evolution toward Prediction, Control, and Macroscopic State Theory of Evolution. <i>Seibutsu Butsuri</i> , 2019, 59, 262-265.	0.1	0
20	Theoretical modeling reveals that regulatory T cells increase T-cell interaction with antigen-presenting cells for stable immune tolerance. <i>International Immunology</i> , 2019, 31, 743-753.	4.0	6
21	High-throughput identification of the sensitivities of an <i>Escherichia coli</i> Δ recA mutant strain to various chemical compounds. <i>Journal of Antibiotics</i> , 2019, 72, 566-573.	2.0	13
22	Complete Genome Sequence of a Radioresistant Bacterial Strain, <i>Deinococcus grandis</i> ATCC 43672. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
23	Complete Genome Sequences of Three Star-Shaped Bacteria, <i>Stella humosa</i> , <i>Stella vacuolata</i> , and <i>Stella</i> Species ATCC 35155. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
24	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
25	Formation of dominant mode by evolution in biological systems. <i>Physical Review E</i> , 2018, 97, 042410.	2.1	38
26	Toward prediction and control of antibiotic-resistance evolution. <i>Current Opinion in Biotechnology</i> , 2018, 54, 45-49.	6.6	56
27	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
28	Understanding and engineering alcohol-tolerant bacteria using OMICS technology. <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 157.	3.6	33
29	Enhancement of Δ strategy evolution in histidine utilization using a container with compartments. <i>Genes To Cells</i> , 2018, 23, 893-903.	1.2	1
30	Macroscopic Theory for Evolving Biological Systems Akin to Thermodynamics. <i>Annual Review of Biophysics</i> , 2018, 47, 273-290.	10.0	16
31	Raman spectral signature reflects transcriptomic features of antibiotic resistance in <i>Escherichia coli</i> . <i>Communications Biology</i> , 2018, 1, 85.	4.4	62
32	Single cell analysis reveals a biophysical aspect of collective cell-state transition in embryonic stem cell differentiation. <i>Scientific Reports</i> , 2018, 8, 11965.	3.3	11
33	Time-programmable drug dosing allows the manipulation, suppression and reversal of antibiotic drug resistance in vitro. <i>Nature Communications</i> , 2017, 8, 15589.	12.8	71
34	SCODE: an efficient regulatory network inference algorithm from single-cell RNA-Seq during differentiation. <i>Bioinformatics</i> , 2017, 33, 2314-2321.	4.1	297
35	Prediction of Cross-resistance and Collateral Sensitivity by Gene Expression profiles and Genomic Mutations. <i>Scientific Reports</i> , 2017, 7, 14009.	3.3	29
36	Raman spectroscopy as a tool for ecology and evolution. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20170174.	3.4	14

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37	Improvement of isopropanol tolerance of <i>Escherichia coli</i> using adaptive laboratory evolution and omics technologies. <i>Journal of Biotechnology</i> , 2017, 255, 47-56.	3.8	36
38	Acceleration and suppression of resistance development by antibiotic combinations. <i>BMC Genomics</i> , 2017, 18, 328.	2.8	24
39	Expression Profiling of Antibiotic-Resistant Bacteria Obtained by Laboratory Evolution. <i>Methods in Molecular Biology</i> , 2017, 1520, 263-279.	0.9	1
40	Metabolic dynamics restricted by conserved carriers: Jamming and feedback. <i>PLoS Computational Biology</i> , 2017, 13, e1005847.	3.2	8
41	Phenotypic changes associated with the fitness cost in antibiotic resistant <i>Escherichia coli</i> strains. <i>Molecular BioSystems</i> , 2016, 12, 414-420.	2.9	7
42	Robust and Accurate Discrimination of Self/Non-Self Antigen Presentations by Regulatory T Cell Suppression. <i>PLoS ONE</i> , 2016, 11, e0163134.	2.5	1
43	Phenotypic convergence in bacterial adaptive evolution to ethanol stress. <i>BMC Evolutionary Biology</i> , 2015, 15, 180.	3.2	30
44	Universal Relationship in Gene-Expression Changes for Cells in Steady-Growth State. <i>Physical Review X</i> , 2015, 5, .	8.9	19
45	Global relationships in fluctuation and response in adaptive evolution. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150482.	3.4	20
46	Bacterial transcriptome reorganization in thermal adaptive evolution. <i>BMC Genomics</i> , 2015, 16, 802.	2.8	22
47	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
48	Suppression of antibiotic resistance acquisition by combined use of antibiotics. <i>Journal of Bioscience and Bioengineering</i> , 2015, 120, 467-469.	2.2	12
49	Pluripotency, Differentiation, and Reprogramming: A Gene Expression Dynamics Model with Epigenetic Feedback Regulation. <i>PLoS Computational Biology</i> , 2015, 11, e1004476.	3.2	68
50	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
51	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
52	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
53	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
54	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

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55	Prediction of antibiotic resistance by gene expression profiles. <i>Nature Communications</i> , 2014, 5, 5792.	12.8	220
56	FastPros: screening of reaction knockout strategies for metabolic engineering. <i>Bioinformatics</i> , 2014, 30, 981-987.	4.1	43
57	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
58	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
59	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
60	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
61	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
62	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
63	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
64	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
65	3P256 Laboratory evolution of antibiotic resistant <i>Escherichia coli</i> (20. Origin of life & Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 0	0.1	0
66	Development of a Physical Model-Based Algorithm for the Detection of Single-Nucleotide Substitutions by Using Tiling Microarrays. <i>PLoS ONE</i> , 2013, 8, e54571.	2.5	6
67	Epigenetic Feedback Regulation Accelerates Adaptation and Evolution. <i>PLoS ONE</i> , 2013, 8, e61251.	2.5	21
68	Universal statistical laws in replicating cellular dynamics(The 1st Award Seminar for outstanding) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 0 52, AS27.	0.1	0
69	A Dynamical-Systems View of Stem Cell Biology. <i>Science</i> , 2012, 338, 215-217.	12.6	172
70	An in silico platform for the design of heterologous pathways in nonnative metabolite production. <i>BMC Bioinformatics</i> , 2012, 13, 93.	2.6	20
71	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
72	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

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73	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
74	Adaptation to Optimal Cell Growth through Self-Organized Criticality. <i>Physical Review Letters</i> , 2012, 108, 208103.	7.8	42
75	Design of Superior Cell Factories Based on Systems Wide Omics Analysis. , 2012, , 57-81.		3
76	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
77	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
78	Fluctuation-Driven Adaptation and Symbiosis in Cellular Dynamics. <i>Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering</i> , 2012, , 238-248.	0.3	0
79	Comparison of Sequence Reads Obtained from Three Next-Generation Sequencing Platforms. <i>PLoS ONE</i> , 2011, 6, e19534.	2.5	75
80	Oscillatory Protein Expression Dynamics Endows Stem Cells with Robust Differentiation Potential. <i>PLoS ONE</i> , 2011, 6, e27232.	2.5	108
81	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
82	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
83	Investigation of phosphorylation status of Odh1 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
84	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
85	Engineering strategy of yeast metabolism for higher alcohol production. <i>Microbial Cell Factories</i> , 2011, 10, 70.	4.0	42
86	Comprehensive phenotypic analysis of single gene deletion and overexpression strains of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2011, 28, 349-361.	1.7	124
87	2SA1500 A dynamic model of cell differentiation: toward understanding of stem cell systems(2SA) Tj ETQq1 1 0.784314 rgBT /Overlook Seibutsu Butsuri, 2010, 50, S8.	0.1	0
88	<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
89	Relationship between noise characteristics in protein expressions and regulatory structures of amino acid biosynthesis pathways. <i>IET Systems Biology</i> , 2010, 4, 82-89.	1.5	6
90	Transcriptome analysis of parallel-evolved <i>Escherichia coli</i> strains under ethanol stress. <i>BMC Genomics</i> , 2010, 11, 579.	2.8	125

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91	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
92	Transition from Positive to Neutral in Mutation Fixation along with Continuing Rising Fitness in Thermal Adaptive Evolution. <i>PLoS Genetics</i> , 2010, 6, e1001164.	3.5	74
93	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
94	The cyclic gene <i>Hes1</i> contributes to diverse differentiation responses of embryonic stem cells. <i>Genes and Development</i> , 2009, 23, 1870-1875.	5.9	226
95	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
96	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
97	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
98	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
99	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
100	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
101	Analysis of stochasticity in promoter activation by using a dual-fluorescence reporter system. <i>BioSystems</i> , 2009, 97, 160-164.	2.0	4
102	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
103	Analysis of metabolic network based on conservation of molecular structure. <i>BioSystems</i> , 2009, 95, 175-178.	2.0	5
104	Global/temporal gene expression analysis of <i>Escherichia coli</i> in the early stages of symbiotic relationship development with the cellular slime mold <i>Dictyostelium discoideum</i> . <i>BioSystems</i> , 2009, 96, 141-164.	2.0	4
105	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
106	Chaotic expression dynamics implies pluripotency: when theory and experiment meet. <i>Biology Direct</i> , 2009, 4, 17.	4.6	46
107	Consistency principle in biological dynamical systems. <i>Theory in Biosciences</i> , 2008, 127, 195-204.	1.4	9
108	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

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109	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
110	Analysis of lager brewing yeast at low temperature fermentation using DNA microarray. <i>Journal of Biotechnology</i> , 2008, 136, S351-S352.	3.8	1
111	Relevance of phenotypic noise to adaptation and evolution. <i>IET Systems Biology</i> , 2008, 2, 234-246.	1.5	9
112	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
113	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
114	A Generic Mechanism for Adaptive Growth Rate Regulation. <i>PLoS Computational Biology</i> , 2008, 4, e3.	3.2	63
115	An improved physico-chemical model of hybridization on high-density oligonucleotide microarrays. <i>Bioinformatics</i> , 2008, 24, 1278-1285.	4.1	45
116	Quantitative expression analysis using oligonucleotide microarrays based on a physico-chemical model. , 2008, , .		0
117	Metabolic flux balance analysis of an industrially useful microorganism <i>Corynebacterium glutamicum</i> by a genome-scale reconstructed model. , 2008, , .		0
118	INVERSE METABOLIC ENGINEERING BY INTEGRATION OF MULTIPLE OMICS ANALYSES. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2007, 40, 19-24.	0.4	0
119	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
120	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
121	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
122	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
123	Experimental optimization of probe length to increase the sequence specificity of high-density oligonucleotide microarrays. <i>BMC Genomics</i> , 2007, 8, 373.	2.8	55
124	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
125	Insight into the sequence specificity of a probe on an Affymetrix GeneChip by titration experiments using only one oligonucleotide. <i>Biophysics (Nagoya-shi, Japan)</i> , 2007, 3, 47-56.	0.4	1
126	Universal Statistics for Chemical Abundances in a Reproducing Cell. <i>Journal of the Korean Physical Society</i> , 2007, 50, 142.	0.7	1

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127	On Compatible Condition for Morphogenetic Diversity and Recursive Production of Multicellular Organisms. <i>Seibutsu Butsuri</i> , 2007, 47, 029-035.	0.1	0
128	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
129	2P480 Relationship between Evolutionary Dynamics and Preservation of Molecular Structures in Metabolic Network(50. Non-equilibrium and complex system,Poster Session,Abstract,Meeting Program) Tj ETQq1 1o01784314rgBT /O		
130	An evolutionary relationship between genetic variation and phenotypic fluctuation. <i>Journal of Theoretical Biology</i> , 2006, 240, 78-86.	1.7	48
131	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
132	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
133	Evolutionary origin of power-laws in a biochemical reaction network: Embedding the distribution of abundance into topology. <i>Physical Review E</i> , 2006, 73, 011912.	2.1	15
134	Morphogenesis, plasticity and irreversibility. <i>International Journal of Developmental Biology</i> , 2006, 50, 223-232.	0.6	17
135	Analysis of Fluctuation in Gene Expression Based on Continuous Culture System. <i>Lecture Notes in Computer Science</i> , 2006, , 113-127.	1.3	0
136	Selection of initial conditions for recursive production of multicellular organisms. <i>Journal of Theoretical Biology</i> , 2005, 233, 501-514.	1.7	11
137	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
138	Ubiquity of log-normal distributions in intra-cellular reaction dynamics. <i>Biophysics (Nagoya-shi)</i> Tj ETQq0 0 0 rgBT /O Overlock 10 Tf 50 30	0.4	145
139	Characterization of mesendoderm: a diverging point of the definitive endoderm and mesoderm in embryonic stem cell differentiation culture. <i>Development (Cambridge)</i> , 2005, 132, 4363-4374.	2.5	410
140	UNIVERSAL STATISTICS OF CELLS WITH RECURSIVE PRODUCTION. <i>World Scientific Lecture Notes in Complex Systems</i> , 2005, , 155-176.	0.1	0
141	Global change in <i>Escherichia coli</i> gene expression in initial stage of symbiosis with <i>Dictyostelium</i> cells. <i>BioSystems</i> , 2004, 73, 163-171.	2.0	6
142	Robust development as a consequence of generated positional information. <i>Journal of Theoretical Biology</i> , 2003, 224, 413-435.	1.7	19
143	Zipf's Law in Gene Expression. <i>Physical Review Letters</i> , 2003, 90, 088102.	7.8	213
144	Origin of multicellular organisms as an inevitable consequence of dynamical systems. <i>The Anatomical Record</i> , 2002, 268, 327-342.	1.8	48

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145	Theory of Robustness of Irreversible Differentiation in a Stem Cell System: Chaos Hypothesis. <i>Journal of Theoretical Biology</i> , 2001, 209, 395-416.	1.7	91
146	Robust and irreversible development in cell society as a general consequence of intra-inter dynamics. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2000, 280, 22-33.	2.6	5
147	Complex Organization in Multicellularity as a Necessity in Evolution. <i>Artificial Life</i> , 2000, 6, 265-281.	1.3	23
148	Origin of Complexity in Multicellular Organisms. <i>Physical Review Letters</i> , 2000, 84, 6130-6133.	7.8	42
149	Emergence of Rules in Cell Society: Differentiation, Hierarchy, and Stability. <i>Bulletin of Mathematical Biology</i> , 1998, 60, 659-687.	1.9	78
150	Emergence of Multicellular Organisms with Dynamic Differentiation and Spatial Pattern. <i>Artificial Life</i> , 1998, 4, 79-93.	1.3	46