James C Liao

List of Publications by Year
in descending order

225	24,257	5574 82	8167 148
papers	citations	h-index	g-index

278	278	278	15802
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A cell-free self-replenishing CO2-fixing system. Nature Catalysis, 2022, 5, 154-162.	34.4	40
2	Metabolomics-Driven Identification of the Rate-Limiting Steps in 1-Propanol Production. Frontiers in Microbiology, 2022, 13, 871624.	3.5	4
3	Role of cyanobacterial phosphoketolase in energy regulation and glucose secretion under dark anaerobic and osmotic stress conditions. Metabolic Engineering, 2021, 65, 255-262.	7.0	19
4	Identification of COVID-19 B-cell epitopes with phage-displayed peptide library. Journal of Biomedical Science, 2021, 28, 43.	7.0	17
5	Analysis of genomic distributions of SARS-CoV-2 reveals a dominant strain type with strong allelic associations. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30679-30686.	7.1	69
6	Converting Escherichia coli to a Synthetic Methylotroph Growing Solely on Methanol. Cell, 2020, 182, 933-946.e14.	28.9	154
7	Metabolome analysis revealed the knockout of glyoxylate shunt as an effective strategy for improvement of 1-butanol production in transgenic Escherichia coli. Journal of Bioscience and Bioengineering, 2019, 127, 301-308.	2.2	17
8	Escherichia coli as a host for metabolic engineering. Metabolic Engineering, 2018, 50, 16-46.	7.0	250
9	Rearrangement of Coenzyme A-Acylated Carbon Chain Enables Synthesis of Isobutanol <i>via</i> a Novel Pathway in <i>Ralstonia eutropha</i>. ACS Synthetic Biology, 2018, 7, 794-800.	3.8	25
10	Construction and evolution of an <i>Escherichia coli</i> strain relying on nonoxidative glycolysis for sugar catabolism. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3538-3546.	7.1	87
11	A modified serine cycle in Escherichia coli coverts methanol and CO2 to two-carbon compounds. Nature Communications, 2018, 9, 3992.	12.8	106
12	Metabolic repair through emergence of new pathways in Escherichia coli. Nature Chemical Biology, 2018, 14, 1005-1009.	8.0	20
13	Synthetic methanol auxotrophy of Escherichia coli for methanol-dependent growth and production. Metabolic Engineering, 2018, 49, 257-266.	7.0	80
14	Augmenting the Calvinâ€“Bensonâ€“Bassham cycle by a synthetic malyl-CoA-glycerate carbon fixation pathway. Nature Communications, 2018, 9, 2008.	12.8	73
15	Directed strain evolution restructures metabolism for 1-butanol production in minimal media. Metabolic Engineering, 2018, 49, 153-163.	7.0	22
16	Rational engineering of diol dehydratase enables 1,4-butanediol biosynthesis from xylose. Metabolic Engineering, 2017, 40, 148-156.	7.0	73
17	Metabolic systems modeling for cell factories improvement. Current Opinion in Biotechnology, 2017, 46, 114-119.	6.6	18
18	Kinetically accessible yield (KAY) for redirection of metabolism to produce exo-metabolites. Metabolic Engineering, 2017, 41, 144-151.	7.0	4

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19	Metabolomics-driven approach to solving a CoA imbalance for improved 1-butanol production in Escherichia coli. Metabolic Engineering, 2017, 41, 135-143.	7.0	79
20	Engineering a Thermostable Keto Acid Decarboxylase Using Directed Evolution and Computationally Directed Protein Design. ACS Synthetic Biology, 2017, 6, 610-618.	3.8	24
21	Orthogonal partial least squares/projections to latent structures regression-based metabolomics approach for identification of gene targets for improvement of 1-butanol production in Escherichia coli. Journal of Bioscience and Bioengineering, 2017, 124, 498-505.	2.2	24
22	Stability of Ensemble Models Predicts Productivity of Enzymatic Systems. PLoS Computational Biology, 2016, 12, e1004800.	3.2	23
23	Sustainable biorefining in wastewater by engineered extreme alkaliphile Bacillus marmarensis. Scientific Reports, 2016, 6, 20224.	3.3	31
24	Fuelling the future: microbial engineering for the production of sustainable biofuels. Nature Reviews Microbiology, 2016, 14, 288-304.	28.6	476
25	CO ₂ -fixing one-carbon metabolism in a cellulose-degrading bacterium <i>Clostridium thermocellum</i>. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13180-13185.	7.1	48
26	Quantitative target analysis and kinetic profiling of acyl-CoAs reveal the rate-limiting step in cyanobacterial 1-butanol production. Metabolomics, 2016, 12, 26.	3.0	28
27	Characterization and evolution of an activator-independent methanol dehydrogenase from Cupriavidus necator N-1. Applied Microbiology and Biotechnology, 2016, 100, 4969-4983.	3.6	65
28	Frontiers in microbial 1-butanol and isobutanol production. FEMS Microbiology Letters, 2016, 363, fnw020.	1.8	77
29	Behavior Training Reverses Asymmetry in Hippocampal Transcriptome of the Cav3.2 Knockout Mice. PLoS ONE, 2015, 10, e0118832.	2.5	7
30	A Synthetic Anhydrotetracycline-Controllable Gene Expression System in <i>Ralstonia eutropha</i> H16. ACS Synthetic Biology, 2015, 4, 101-106.	3.8	26
31	Outlook for the Production of Butanol from Cellulolytic Strains of Clostridia. , 2015, , 291-306.		1
32	Consolidated bioprocessing of cellulose to isobutanol using Clostridium thermocellum. Metabolic Engineering, 2015, 31, 44-52.	7.0	149
33	An entropy-like index of bifurcational robustness for metabolic systems. Integrative Biology (United) Tj ETQq1 1 0.784314 rgBT /Over	1.3	6
34	Metabolic engineering of cyanobacteria for photosynthetic 3-hydroxypropionic acid production from CO2 using Synechococcus elongatus PCC 7942. Metabolic Engineering, 2015, 31, 163-170.	7.0	90
35	Integrative genomic mining for enzyme function to enable engineering of a non-natural biosynthetic pathway. Nature Communications, 2015, 6, 10005.	12.8	77
36	Mathematical modeling of the insulin signal transduction pathway for prediction of insulin sensitivity from expression data. Molecular Genetics and Metabolism, 2015, 114, 66-72.	1.1	16

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37	Comprehensive Detection of Genes Causing a Phenotype Using Phenotype Sequencing and Pathway Analysis. PLoS ONE, 2014, 9, e88072.	2.5	4
38	Isobutanol production at elevated temperatures in thermophilic Geobacillus thermoglucosidasius. Metabolic Engineering, 2014, 24, 1-8.	7.0	107
39	Engineering synergy in biotechnology. Nature Chemical Biology, 2014, 10, 319-322.	8.0	147
40	Consolidated conversion of protein waste into biofuels and ammonia using Bacillus subtilis. Metabolic Engineering, 2014, 23, 53-61.	7.0	83
41	Development of an NADPH-Dependent Homophenylalanine Dehydrogenase by Protein Engineering. ACS Synthetic Biology, 2014, 3, 13-20.	3.8	26
42	Building carbonâ€“carbon bonds using a biocatalytic methanol condensation cycle. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15928-15933.	7.1	114
43	Ensemble Modeling for Robustness Analysis in engineering non-native metabolic pathways. Metabolic Engineering, 2014, 25, 63-71.	7.0	89
44	Isobutanol production as an alternative metabolic sink to rescue the growth deficiency of the glycogen mutant of Synechococcus elongatus PCC 7942. Photosynthesis Research, 2014, 120, 301-310.	2.9	101
45	A kinetic model of Escherichia coli core metabolism satisfying multiple sets of mutant flux data. Metabolic Engineering, 2014, 25, 50-62.	7.0	160
46	Biological conversion of carbon dioxide to photosynthetic fuels and electrofuels. Energy and Environmental Science, 2013, 6, 2892.	30.8	74
47	A reverse glyoxylate shunt to build a non-native route from C4 to C2 in Escherichia coli. Metabolic Engineering, 2013, 19, 116-127.	7.0	53
48	Protein-based biorefining: metabolic engineering for production of chemicals and fuel with regeneration of nitrogen fertilizers. Applied Microbiology and Biotechnology, 2013, 97, 1397-1406.	3.6	31
49	Engineering a synthetic pathway in cyanobacteria for isopropanol production directly from carbon dioxide and light. Metabolic Engineering, 2013, 20, 101-108.	7.0	128
50	Synthetic non-oxidative glycolysis enables complete carbon conservation. Nature, 2013, 502, 693-697.	27.8	329
51	Oxygen-tolerant coenzyme A-acylating aldehyde dehydrogenase facilitates efficient photosynthetic n-butanol biosynthesis in cyanobacteria. Energy and Environmental Science, 2013, 6, 2672.	30.8	143
52	Engineering a cyanobacterium as the catalyst for the photosynthetic conversion of CO2 to 1,2-propanediol. Microbial Cell Factories, 2013, 12, 4.	4.0	104
53	Metabolic engineering of 2â€pentanone synthesis in <i>Escherichia coli</i>. AIChE Journal, 2013, 59, 3167-3175.	3.6	25
54	Toward a Biological Replacement of Petroleum. ACS Symposium Series, 2013, , 1-17.	0.5	0

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55	Protein engineering for metabolic engineering: Current and nextâ€generation tools. Biotechnology Journal, 2013, 8, 545-555.	3.5	37
56	Next generation biofuel engineering in prokaryotes. Current Opinion in Chemical Biology, 2013, 17, 462-471.	6.1	139
57	Microbial synthesis of n-butanol, isobutanol, and other higher alcohols from diverse resources. Bioresource Technology, 2013, 135, 339-349.	9.6	171
58	Optimizationâ€driven identification of genetic perturbations accelerates the convergence of model parameters in ensemble modeling of metabolic networks. Biotechnology Journal, 2013, 8, 1090-1104.	3.5	22
59	Synergy as design principle for metabolic engineering of 1-propanol production in Escherichia coli. Metabolic Engineering, 2013, 17, 12-22.	7.0	59
60	Genome Sequence of the Extreme Obligate Alkaliphile Bacillus marmarensis Strain DSM 21297. Genome Announcements, 2013, 1, .	0.8	7
61	Design and characterization of synthetic fungal-bacterial consortia for direct production of isobutanol from cellulosic biomass. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14592-14597.	7.1	391
62	A selection platform for carbon chain elongation using the CoA-dependent pathway to produce linear higher alcohols. Metabolic Engineering, 2012, 14, 504-511.	7.0	126
63	ATP drives direct photosynthetic production of 1-butanol in cyanobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6018-6023.	7.1	327
64	A Synthetic Recursive â€œ+1â€•Pathway for Carbon Chain Elongation. ACS Chemical Biology, 2012, 7, 689-697.	3.4	106
65	Toward nitrogen neutral biofuel production. Current Opinion in Biotechnology, 2012, 23, 406-413.	6.6	59
66	Energy biotechnology. Current Opinion in Biotechnology, 2012, 23, 287-289.	6.6	4
67	Photosynthetic production of 2-methyl-1-butanol from CO2 in cyanobacterium Synechococcus elongatus PCC7942 and characterization of the native acetohydroxyacid synthase. Energy and Environmental Science, 2012, 5, 9574.	30.8	99
68	Determining PTEN Functional Status by Network Component Deduced Transcription Factor Activities. PLoS ONE, 2012, 7, e31053.	2.5	10
69	Combined inactivation of the Clostridium cellulolyticum lactate and malate dehydrogenase genes substantially increases ethanol yield from cellulose and switchgrass fermentations. Biotechnology for Biofuels, 2012, 5, 2.	6.2	125
70	Integrated Electromicrobial Conversion of CO ₂ to Higher Alcohols. Science, 2012, 335, 1596-1596.	12.6	605
71	Engineering synthetic recursive pathways to generate non-natural small molecules. Nature Chemical Biology, 2012, 8, 518-526.	8.0	51
72	Metabolic ensemble modeling for strain engineers. Biotechnology Journal, 2012, 7, 343-353.	3.5	51

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73	Extending Carbon Chain Length of 1-Butanol Pathway for 1-Hexanol Synthesis from Glucose by Engineered <i>Escherichia coli</i>. Journal of the American Chemical Society, 2011, 133, 11399-11401.	13.7	131
74	Metabolic Engineering of Clostridium cellulolyticum for Production of Isobutanol from Cellulose. Applied and Environmental Microbiology, 2011, 77, 2727-2733.	3.1	274
75	Revealing the Functions of the Transketolase Enzyme Isoforms in Rhodopseudomonas palustris Using a Systems Biology Approach. PLoS ONE, 2011, 6, e28329.	2.5	10
76	Oxidized Low-Density Lipoprotein Inhibits Nitric Oxide-Mediated Coronary Arteriolar Dilation by Up-regulating Endothelial Arginase I. Microcirculation, 2011, 18, 36-45.	1.8	38
77	Conversion of proteins into biofuels by engineering nitrogen flux. Nature Biotechnology, 2011, 29, 346-351.	17.5	265
78	An evolutionary strategy for isobutanol production strain development in Escherichia coli. Metabolic Engineering, 2011, 13, 674-681.	7.0	105
79	Driving Forces Enable High-Titer Anaerobic 1-Butanol Synthesis in Escherichia coli. Applied and Environmental Microbiology, 2011, 77, 2905-2915.	3.1	572
80	High-flux isobutanol production using engineered Escherichia coli: a bioreactor study with in situ product removal. Applied Microbiology and Biotechnology, 2011, 90, 1681-1690.	3.6	214
81	Redox homeostasis phenotypes in RubisCOâ€deficient <i>Rhodobacter sphaeroides</i> via ensemble modeling. Biotechnology Progress, 2011, 27, 15-22.	2.6	13
82	Identification of transcription factors perturbed by the synthesis of high levels of a foreign protein in yeast <i>saccharomyces cerevisiae</i>. Biotechnology Progress, 2011, 27, 925-936.	2.6	3
83	Reducing the allowable kinetic space by constructing ensemble of dynamic models with the same steady-state flux. Metabolic Engineering, 2011, 13, 60-75.	7.0	52
84	Metabolic engineering of cyanobacteria for 1-butanol production from carbon dioxide. Metabolic Engineering, 2011, 13, 353-363.	7.0	352
85	Phenotype Sequencing: Identifying the Genes That Cause a Phenotype Directly from Pooled Sequencing of Independent Mutants. PLoS ONE, 2011, 6, e16517.	2.5	20
86	Bioengineering of microorganisms for C₃ to C₅ alcohols production. Biotechnology Journal, 2010, 5, 1297-1308.	3.5	35
87	Engineering the isobutanol biosynthetic pathway in Escherichia coli by comparison of three aldehyde reductase/alcohol dehydrogenase genes. Applied Microbiology and Biotechnology, 2010, 85, 651-657.	3.6	270
88	Pentanol isomer synthesis in engineered microorganisms. Applied Microbiology and Biotechnology, 2010, 85, 893-899.	3.6	125
89	3-Methyl-1-butanol production in Escherichia coli: random mutagenesis and two-phase fermentation. Applied Microbiology and Biotechnology, 2010, 86, 1155-1164.	3.6	146
90	Engineering Corynebacterium glutamicum for isobutanol production. Applied Microbiology and Biotechnology, 2010, 87, 1045-1055.	3.6	304

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91	Trimming of mammalian transcriptional networks using network component analysis. BMC Bioinformatics, 2010, 11, 511.	2.6	14
92	Improvement of isopropanol production by metabolically engineered Escherichia coli using gas stripping. Journal of Bioscience and Bioengineering, 2010, 110, 696-701.	2.2	159
93	Moonlighting function of glycerol kinase causes systems-level changes in rat hepatoma cells. Metabolic Engineering, 2010, 12, 332-340.	7.0	12
94	Systems Approaches to Unraveling Nitric Oxide Response Networks in Prokaryotes. , 2010, , 103-136.		3
95	Evolution, genomic analysis, and reconstruction of isobutanol tolerance in <i>Escherichia coli</i>. Molecular Systems Biology, 2010, 6, 449.	7.2	252
96	Expanding metabolism for total biosynthesis of the nonnatural amino acid L-homoalanine. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6234-6239.	7.1	129
97	Ensemble Modeling of Hepatic Fatty Acid Metabolism with a Synthetic Glyoxylate Shunt. Biophysical Journal, 2010, 98, 1385-1395.	0.5	17
98	Biofuels: Biomolecular Engineering Fundamentals and Advances. Annual Review of Chemical and Biomolecular Engineering, 2010, 1, 19-36.	6.8	61
99	An agar gel membrane-PDMS hybrid microfluidic device for long term single cell dynamic study. Lab on A Chip, 2010, 10, 2710.	6.0	24
100	Acetolactate Synthase from <i>Bacillus subtilis</i> Serves as a 2-Ketoisovalerate Decarboxylase for Isobutanol Biosynthesis in <i>Escherichia coli</i>. Applied and Environmental Microbiology, 2009, 75, 6306-6311.	3.1	92
101	An integrated network approach identifies the isobutanol response network of <i>Escherichia coli</i>. Molecular Systems Biology, 2009, 5, 277.	7.2	175
102	Using Network Component Analysis to Dissect Regulatory Networks Mediated by Transcription Factors in Yeast. PLoS Computational Biology, 2009, 5, e1000311.	3.2	28
103	A hidden squareâ€root boundary between growth rate and biomass yield. Biotechnology and Bioengineering, 2009, 102, 73-80.	3.3	23
104	Engineering metabolic systems for production of advanced fuels. Journal of Industrial Microbiology and Biotechnology, 2009, 36, 471-479.	3.0	93
105	Direct photosynthetic recycling of carbon dioxide to isobutyraldehyde. Nature Biotechnology, 2009, 27, 1177-1180.	17.5	769
106	Reconstruction of the archaeal isoprenoid ether lipid biosynthesis pathway in Escherichia coli through digeranylgeranylglyceryl phosphate. Metabolic Engineering, 2009, 11, 184-191.	7.0	18
107	Ensemble modeling for strain development of l-lysine-producing Escherichia coli. Metabolic Engineering, 2009, 11, 221-233.	7.0	63
108	Microbial maximal specific growth rate as a square-root function of biomass yield and two kinetic parameters. Metabolic Engineering, 2009, 11, 409-414.	7.0	2

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109	Ensemble modeling and related mathematical modeling of metabolic networks. Journal of the Taiwan Institute of Chemical Engineers, 2009, 40, 595-601.	5.3	17
110	Microbial production of advanced transportation fuels in non-natural hosts. Current Opinion in Biotechnology, 2009, 20, 307-315.	6.6	182
111	Resistance to Diet-Induced Obesity in Mice with Synthetic Glyoxylate Shunt. Cell Metabolism, 2009, 9, 525-536.	16.2	33
112	Transcriptomic and network component analysis of glycerol kinase in skeletal muscle using a mouse model of glycerol kinase deficiency. Molecular Genetics and Metabolism, 2009, 96, 106-112.	1.1	16
113	Enantioselective synthesis of pure (R,R)-2,3-butanediol in Escherichia coli with stereospecific secondary alcohol dehydrogenases. Organic and Biomolecular Chemistry, 2009, 7, 3914.	2.8	113
114	Ensemble Modeling for Aromatic Production in Escherichia coli. PLoS ONE, 2009, 4, e6903.	2.5	52
115	Production of 2-methyl-1-butanol in engineered Escherichia coli. Applied Microbiology and Biotechnology, 2008, 81, 89-98.	3.6	143
116	Metabolic engineering for advanced biofuels production from Escherichia coli. Current Opinion in Biotechnology, 2008, 19, 414-419.	6.6	275
117	Metabolic engineering of Escherichia coli for 1-butanol production. Metabolic Engineering, 2008, 10, 305-311.	7.0	764
118	Transfer of the high-GC cyclohexane carboxylate degradation pathway from Rhodopseudomonas palustris to Escherichia coli for production of biotin. Metabolic Engineering, 2008, 10, 131-140.	7.0	2
119	Metabolic engineering of Escherichia coli for 1-butanol and 1-propanol production via the keto-acid pathways. Metabolic Engineering, 2008, 10, 312-320.	7.0	350
120	Non-fermentative pathways for synthesis of branched-chain higher alcohols as biofuels. Nature, 2008, 451, 86-89.	27.8	1,696
121	Ensemble Modeling of Metabolic Networks. Biophysical Journal, 2008, 95, 5606-5617.	0.5	233
122	Interactions of nitrosylhemoglobin and carboxyhemoglobin with erythrocyte. Nitric Oxide - Biology and Chemistry, 2008, 18, 122-135.	2.7	0
123	Global metabolic effects of glycerol kinase overexpression in rat hepatoma cells. Molecular Genetics and Metabolism, 2008, 93, 145-159.	1.1	30
124	An Information Theoretic Exploratory Method for Learning Patterns of Conditional Gene Coexpression from Microarray Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 15-24.	3.0	13
125	Expanding metabolism for biosynthesis of nonnatural alcohols. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20653-20658.	7.1	372
126	Engineering of an <i>Escherichia coli</i> Strain for the Production of 3-Methyl-1-Butanol. Applied and Environmental Microbiology, 2008, 74, 5769-5775.	3.1	149

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127	Directed Evolution of <i>Methanococcus jannaschii</i> Citramalate Synthase for Biosynthesis of 1-Propanol and 1-Butanol by <i>Escherichia coli</i>. Applied and Environmental Microbiology, 2008, 74, 7802-7808.	3.1	226
128	Determination of the Escherichia coli S-Nitrosoglutathione Response Network Using Integrated Biochemical and Systems Analysis. Journal of Biological Chemistry, 2008, 283, 5148-5157.	3.4	36
129	Engineering Cellular Metabolism. FASEB Journal, 2008, 22, 529.1.	0.5	0
130	Networkâ€based identification of critical transcription regulators in the metabolic syndrome in mice. FASEB Journal, 2008, 22, 797.1.	0.5	0
131	Directed Evolution of Ribosomal Protein S1 for Enhanced Translational Efficiency of High GC Rhodopseudomonas palustris DNA in Escherichia coli. Journal of Biological Chemistry, 2007, 282, 18929-18936.	3.4	23
132	Differential Association of Hemoglobin with Proinflammatory High Density Lipoproteins in Atherogenic/Hyperlipidemic Mice. Journal of Biological Chemistry, 2007, 282, 23698-23707.	3.4	69
133	Biological network mapping and source signal deduction. Bioinformatics, 2007, 23, 1783-1791.	4.1	8
134	Integrated network analysis identifies nitric oxide response networks and dihydroxyacid dehydratase as a crucial target in Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8484-8489.	7.1	136
135	Singleâ€cell zerothâ€order protein degradation enhances the robustness of synthetic oscillator. Molecular Systems Biology, 2007, 3, 130.	7.2	67
136	Dynamic Cell and Microparticle Control via Optoelectronic Tweezers. Journal of Microelectromechanical Systems, 2007, 16, 491-499.	2.5	155
137	Glycerol kinase deficiency alters expression of genes involved in lipid metabolism, carbohydrate metabolism, and insulin signaling. European Journal of Human Genetics, 2007, 15, 646-657.	2.8	53
138	Nitric Oxide Metabolism in Adults With Cyanotic Congenital Heart Disease. American Journal of Cardiology, 2007, 99, 691-695.	1.6	11
139	Engineered Synthetic Pathway for Isopropanol Production in <i>Escherichia coli</i>. Applied and Environmental Microbiology, 2007, 73, 7814-7818.	3.1	251
140	Versatility and Connectivity Efficiency of Bipartite Transcription Networks. Biophysical Journal, 2006, 91, 2749-2759.	0.5	6
141	Rhodopseudomonas palustris CGA009 Has Two Functional ppsR Genes, Each of Which Encodes a Repressor of Photosynthesis Gene Expression. Biochemistry, 2006, 45, 14441-14451.	2.5	34
142	Targeted disruption of glycerol kinase gene in mice: expression analysis in liver shows alterations in network partners related to glycerol kinase activity. Human Molecular Genetics, 2006, 15, 405-415.	2.9	31
143	A Gibbs sampler for the identification of gene expression and network connectivity consistency. Bioinformatics, 2006, 22, 3040-3046.	4.1	18
144	Transcriptome network component analysis with limited microarray data. Bioinformatics, 2006, 22, 1886-1894.	4.1	55

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145	Transcriptional regulation and metabolism. Biochemical Society Transactions, 2005, 33, 1423.	3.4	7
146	gNCA: A framework for determining transcription factor activity based on transcriptome: identifiability and numerical implementation. Metabolic Engineering, 2005, 7, 128-141.	7.0	98
147	Determination of functional interactions among signalling pathways in Escherichia coli K-12. Metabolic Engineering, 2005, 7, 280-290.	7.0	15
148	A synthetic geneâ€“metabolic oscillator. Nature, 2005, 435, 118-122.	27.8	357
149	Inferring yeast cell cycle regulators and interactions using transcription factor activities. BMC Genomics, 2005, 6, 90.	2.8	64
150	Analysis of nitric oxide donor effectiveness in resistance vessels. American Journal of Physiology - Heart and Circulatory Physiology, 2005, 288, H2390-H2399.	3.2	8
151	Heat Shock Response of Archaeoglobus fulgidus. Journal of Bacteriology, 2005, 187, 6046-6057.	2.2	55
152	A Global Regulatory Role of Gluconeogenic Genes in Escherichia coli Revealed by Transcriptome Network Analysis. Journal of Biological Chemistry, 2005, 280, 36079-36087.	3.4	73
153	Vocabulon: a dictionary model approach for reconstruction and localization of transcription factor binding sites. Bioinformatics, 2005, 21, 922-931.	4.1	21
154	Single-Gene Disorders: What Role Could Moonlighting Enzymes Play?. American Journal of Human Genetics, 2005, 76, 911-924.	6.2	199
155	A Generalized Framework for Network Component Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 289-301.	3.0	39
156	Erythrocyte nitric oxide transport reduced by a submembrane cytoskeletal barrier. Biochimica Et Biophysica Acta - General Subjects, 2005, 1723, 135-142.	2.4	45
157	Markov Chain Modeling of Pyelonephritis-Associated Pili Expression in Uropathogenic Escherichia coli. Biophysical Journal, 2005, 88, 2541-2553.	0.5	8
158	Transcriptome-based determination of multiple transcription regulator activities in Escherichia coli by using network component analysis. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 641-646.	7.1	129
159	Custom design of metabolism. Nature Biotechnology, 2004, 22, 823-824.	17.5	7
160	Stochastic modeling of the phase-variablepap operon regulation in uropathogenicEscherichia coli. Biotechnology and Bioengineering, 2004, 88, 189-203.	3.3	14
161	Network component analysis of Saccharamyces cerevisiae stress response. , 2004, 2004, 2937-40.		1
162	Design of artificial cell-cell communication using gene and metabolic networks. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2299-2304.	7.1	151

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163	Reductive nitrosylation and S-nitrosation of hemoglobin in inhomogeneous nitric oxide solutions. Nitric Oxide - Biology and Chemistry, 2004, 10, 74-82.	2.7	8
164	A perspective of metabolic engineering strategies: moving up the systems hierarchy. Biotechnology and Bioengineering, 2003, 84, 815-821.	3.3	25
165	Analysis of Nitric Oxide Consumption by Erythrocytes in Blood Vessels using a Distributed Multicellular Model. Annals of Biomedical Engineering, 2003, 31, 294-309.	2.5	40
166	A Software Package for cDNA Microarray Data Normalization and Assessing Confidence Intervals. OMICS A Journal of Integrative Biology, 2003, 7, 227-234.	2.0	16
167	Regulation of nitric oxide consumption by hypoxic red blood cells. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12504-12509.	7.1	52
168	Network component analysis: Reconstruction of regulatory signals in biological systems. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15522-15527.	7.1	550
169	Nitric oxide is consumed, rather than conserved, by reaction with oxyhemoglobin under physiological conditions. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10341-10346.	7.1	195
170	Global Expression Profiling of Acetate-grown Escherichia coli. Journal of Biological Chemistry, 2002, 277, 13175-13183.	3.4	252
171	Co-expression pattern from DNA microarray experiments as a tool for operon prediction. Nucleic Acids Research, 2002, 30, 2886-2893.	14.5	116
172	Nitric oxide reaction with red blood cells and hemoglobin under heterogeneous conditions. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7763-7768.	7.1	94
173	A Multi-Cellular Distributed Model for Nitric Oxide Transport in the Blood. Computer Aided Chemical Engineering, 2002, , 877-882.	0.5	0
174	A memorial review of Jay Bailey's contribution in prokaryotic metabolic engineering. Biotechnology and Bioengineering, 2002, 79, 504-508.	3.3	2
175	Blood feud: Keeping hemoglobin from nixing NO. Nature Medicine, 2002, 8, 1350-1351.	30.7	12
176	Erythrocyte Consumption of Nitric Oxide: Competition Experiment and Model Analysis. Nitric Oxide - Biology and Chemistry, 2001, 5, 18-31.	2.7	78
177	Microbial pathway engineering for industrial processes: evolution, combinatorial biosynthesis and rational design. Current Opinion in Microbiology, 2001, 4, 330-335.	5.1	51
178	REVIEW: Metabolic Engineering of Isoprenoids. Metabolic Engineering, 2001, 3, 27-39.	7.0	85
179	Acetate-inducible protein overexpression from theglnAp2 promoter ofEscherichia coli. Biotechnology and Bioengineering, 2001, 75, 504-509.	3.3	3
180	Precursor Balancing for Metabolic Engineering of Lycopene Production in Escherichia coli. Biotechnology Progress, 2001, 17, 57-61.	2.6	190

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