List of Publications by Year in descending order

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IMMES CLIMO

#	Article	IF	CITATIONS
1	Non-fermentative pathways for synthesis of branched-chain higher alcohols as biofuels. Nature, 2008, 451, 86-89.	27.8	1,696
2	Direct photosynthetic recycling of carbon dioxide to isobutyraldehyde. Nature Biotechnology, 2009, 27, 1177-1180.	17.5	769
3	Metabolic engineering of Escherichia coli for 1-butanol production. Metabolic Engineering, 2008, 10, 305-311.	7.0	764
4	Integrated Electromicrobial Conversion of CO ₂ to Higher Alcohols. Science, 2012, 335, 1596-1596.	12.6	605
5	Driving Forces Enable High-Titer Anaerobic 1-Butanol Synthesis in Escherichia coli. Applied and Environmental Microbiology, 2011, 77, 2905-2915.	3.1	572
6	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
7	Issues in cDNA microarray analysis: quality filtering, channel normalization, models of variations and assessment of gene effects. Nucleic Acids Research, 2001, 29, 2549-2557.	14.5	494
8	Improving lycopene production in Escherichia coli by engineering metabolic control. Nature Biotechnology, 2000, 18, 533-537.	17.5	485
9	Fuelling the future: microbial engineering for the production of sustainable biofuels. Nature Reviews Microbiology, 2016, 14, 288-304.	28.6	476
10	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
11	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
12	A synthetic gene–metabolic oscillator. Nature, 2005, 435, 118-122.	27.8	357
13	Metabolic engineering of cyanobacteria for 1-butanol production from carbon dioxide. Metabolic Engineering, 2011, 13, 353-363.	7.0	352
14	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
15	Synthetic non-oxidative glycolysis enables complete carbon conservation. Nature, 2013, 502, 693-697.	27.8	329
16	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
17	Engineering Corynebacterium glutamicum for isobutanol production. Applied Microbiology and Biotechnology, 2010, 87, 1045-1055.	3.6	304
18	Intravascular flow decreases erythrocyte consumption of nitric oxide. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 8757-8761.	7.1	289

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19	Metabolic engineering for advanced biofuels production from Escherichia coli. Current Opinion in Biotechnology, 2008, 19, 414-419.	6.6	275
20	Metabolic Engineering of Clostridium cellulolyticum for Production of Isobutanol from Cellulose. Applied and Environmental Microbiology, 2011, 77, 2727-2733.	3.1	274
21	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
22	Conversion of proteins into biofuels by engineering nitrogen flux. Nature Biotechnology, 2011, 29, 346-351.	17.5	265
23	Global Expression Profiling of Acetate-grown Escherichia coli. Journal of Biological Chemistry, 2002, 277, 13175-13183.	3.4	252
24	Evolution, genomic analysis, and reconstruction of isobutanol tolerance in <i>Escherichia coli</i> . Molecular Systems Biology, 2010, 6, 449.	7.2	252
25	Engineered Synthetic Pathway for Isopropanol Production in <i>Escherichia coli</i> . Applied and Environmental Microbiology, 2007, 73, 7814-7818.	3.1	251
26	Escherichia coli as a host for metabolic engineering. Metabolic Engineering, 2018, 50, 16-46.	7.0	250
27	Estimation of nitric oxide production and reactionrates in tissue by use of a mathematical model. American Journal of Physiology - Heart and Circulatory Physiology, 1998, 274, H2163-H2176.	3.2	240
28	Ensemble Modeling of Metabolic Networks. Biophysical Journal, 2008, 95, 5606-5617.	0.5	233
29	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
30	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
31	Erythrocytes Possess an Intrinsic Barrier to Nitric Oxide Consumption. Journal of Biological Chemistry, 2000, 275, 2342-2348.	3.4	205
32	Single-Gene Disorders: What Role Could Moonlighting Enzymes Play?. American Journal of Human Genetics, 2005, 76, 911-924.	6.2	199
33	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
34	Precursor Balancing for Metabolic Engineering of Lycopene Production in Escherichia coli. Biotechnology Progress, 2001, 17, 57-61.	2.6	190
35	Microbial production of advanced transportation fuels in non-natural hosts. Current Opinion in Biotechnology, 2009, 20, 307-315.	6.6	182
36	An integrated network approach identifies the isobutanol response network of <i>Escherichia coli</i> . Molecular Systems Biology, 2009, 5, 277.	7.2	175

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37	Microbial synthesis of n-butanol, isobutanol, and other higher alcohols from diverse resources. Bioresource Technology, 2013, 135, 339-349.	9.6	171
38	Pathway analysis, engineering, and physiological considerations for redirecting central metabolism. , 1996, 52, 129-140.		165
39	Effective diffusion distance of nitric oxide in the microcirculation. American Journal of Physiology - Heart and Circulatory Physiology, 1998, 274, H1705-H1714.	3.2	164
40	Modulation of nitric oxide bioavailability by erythrocytes. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 11771-11776.	7.1	160
41	A kinetic model of Escherichia coli core metabolism satisfying multiple sets of mutant flux data. Metabolic Engineering, 2014, 25, 50-62.	7.0	160
42	Arginase modulates nitric oxide production in activated macrophages. American Journal of Physiology - Heart and Circulatory Physiology, 1998, 274, H342-H348.	3.2	159
43	Improvement of isopropanol production by metabolically engineered Escherichia coli using gas stripping. Journal of Bioscience and Bioengineering, 2010, 110, 696-701.	2.2	159
44	Dynamic Cell and Microparticle Control via Optoelectronic Tweezers. Journal of Microelectromechanical Systems, 2007, 16, 491-499.	2.5	155
45	Converting Escherichia coli to a Synthetic Methylotroph Growing Solely on Methanol. Cell, 2020, 182, 933-946.e14.	28.9	154
46	Engineered isoprenoid pathway enhances astaxanthin production inEscherichia coli. , 1999, 62, 235-241.		152
47	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
48	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
49	Consolidated bioprocessing of cellulose to isobutanol using Clostridium thermocellum. Metabolic Engineering, 2015, 31, 44-52.	7.0	149
50	Engineering synergy in biotechnology. Nature Chemical Biology, 2014, 10, 319-322.	8.0	147
51	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
52	Production of 2-methyl-1-butanol in engineered Escherichia coli. Applied Microbiology and Biotechnology, 2008, 81, 89-98.	3.6	143
53	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
54	Next generation biofuel engineering in prokaryotes. Current Opinion in Chemical Biology, 2013, 17, 462-471.	6.1	139

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55	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
56	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
57	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
58	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
59	Engineering a synthetic pathway in cyanobacteria for isopropanol production directly from carbon dioxide and light. Metabolic Engineering, 2013, 20, 101-108.	7.0	128
60	Gene Expression Profiling by DNA Microarrays and Metabolic Fluxes in Escherichia coli. Biotechnology Progress, 2000, 16, 278-286.	2.6	126
61	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
62	Pentanol isomer synthesis in engineered microorganisms. Applied Microbiology and Biotechnology, 2010, 85, 893-899.	3.6	125
63	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
64	Pathway engineering for production of aromatics inEscherichia coli: Confirmation of stoichiometric analysis by independent modulation of AroG, TktA, and Pps activities. Biotechnology and Bioengineering, 1995, 46, 361-370.	3.3	124
65	Co-expression pattern from DNA microarray experiments as a tool for operon prediction. Nucleic Acids Research, 2002, 30, 2886-2893.	14.5	116
66	Building carbon–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
67	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
68	Isobutanol production at elevated temperatures in thermophilic Geobacillus thermoglucosidasius. Metabolic Engineering, 2014, 24, 1-8.	7.0	107
69	Directed Evolution of Metabolically Engineered Escherichia coli for Carotenoid Production. Biotechnology Progress, 2000, 16, 922-926.	2.6	106
70	A Synthetic Recursive "+1―Pathway for Carbon Chain Elongation. ACS Chemical Biology, 2012, 7, 689-697.	3.4	106
71	A modified serine cycle in Escherichia coli coverts methanol and CO2 to two-carbon compounds. Nature Communications, 2018, 9, 3992.	12.8	106
72	An evolutionary strategy for isobutanol production strain development in Escherichia coli. Metabolic Engineering, 2011, 13, 674-681.	7.0	105

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73	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
74	Downregulation of Endothelial Constitutive Nitric Oxide Synthase Expression by Lipopolysaccharide. Biochemical and Biophysical Research Communications, 1996, 225, 1-5.	2.1	101
75	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
76	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
77	gNCA: A framework for determining transcription factor activity based on transcriptome: identifiability and numerical implementation. Metabolic Engineering, 2005, 7, 128-141.	7.0	98
78	Stimulation of glucose catabolism in Escherichia coli by a potential futile cycle. Journal of Bacteriology, 1992, 174, 7527-7532.	2.2	97
79	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
80	Engineering metabolic systems for production of advanced fuels. Journal of Industrial Microbiology and Biotechnology, 2009, 36, 471-479.	3.0	93
81	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
82	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
83	Ensemble Modeling for Robustness Analysis in engineering non-native metabolic pathways. Metabolic Engineering, 2014, 25, 63-71.	7.0	89
84	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
85	Control of gluconeogenic growth by pps and pck in Escherichia coli. Journal of Bacteriology, 1993, 175, 6939-6944.	2.2	85
86	REVIEW: Metabolic Engineering of Isoprenoids. Metabolic Engineering, 2001, 3, 27-39.	7.0	85
87	DNA Microarray Detection of Metabolic Responses to Protein Overproduction in Escherichia coli. Metabolic Engineering, 2000, 2, 201-209.	7.0	84
88	Consolidated conversion of protein waste into biofuels and ammonia using Bacillus subtilis. Metabolic Engineering, 2014, 23, 53-61.	7.0	83
89	ox <scp>LDL</scp> specifically impairs endothelium-dependent, NO-mediated dilation of coronary arterioles. American Journal of Physiology - Heart and Circulatory Physiology, 2000, 278, H175-H183.	3.2	80
90	Synthetic methanol auxotrophy of Escherichia coli for methanol-dependent growth and production. Metabolic Engineering, 2018, 49, 257-266.	7.0	80

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91	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
92	Erythrocyte Consumption of Nitric Oxide: Competition Experiment and Model Analysis. Nitric Oxide - Biology and Chemistry, 2001, 5, 18-31.	2.7	78
93	Integrative genomic mining for enzyme function to enable engineering of a non-natural biosynthetic pathway. Nature Communications, 2015, 6, 10005.	12.8	77
94	Frontiers in microbial 1-butanol and isobutanol production. FEMS Microbiology Letters, 2016, 363, fnw020.	1.8	77
95	Biological conversion of carbon dioxide to photosynthetic fuels and electrofuels. Energy and Environmental Science, 2013, 6, 2892.	30.8	74
96	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
97	Rational engineering of diol dehydratase enables 1,4-butanediol biosynthesis from xylose. Metabolic Engineering, 2017, 40, 148-156.	7.0	73
98	Augmenting the Calvin–Benson–Bassham cycle by a synthetic malyl-CoA-glycerate carbon fixation pathway. Nature Communications, 2018, 9, 2008.	12.8	73
99	Advances in metabolic control analysis. Biotechnology Progress, 1993, 9, 221-233.	2.6	70
100	Differential Association of Hemoglobin with Proinflammatory High Density Lipoproteins in Atherogenic/Hyperlipidemic Mice. Journal of Biological Chemistry, 2007, 282, 23698-23707.	3.4	69
101	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
102	Inverse Flux Analysis for Reduction of Acetate Excretion in Escherichia coli. Biotechnology Progress, 1997, 13, 361-367.	2.6	67
103	Singleâ€cell zerothâ€order protein degradation enhances the robustness of synthetic oscillator. Molecular Systems Biology, 2007, 3, 130.	7.2	67
104	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
105	Inferring yeast cell cycle regulators and interactions using transcription factor activities. BMC Genomics, 2005, 6, 90.	2.8	64
106	Ensemble modeling for strain development of l-lysine-producing Escherichia coli. Metabolic Engineering, 2009, 11, 221-233.	7.0	63
107	Biofuels: Biomolecular Engineering Fundamentals and Advances. Annual Review of Chemical and Biomolecular Engineering, 2010, 1, 19-36.	6.8	61
108	Toward nitrogen neutral biofuel production. Current Opinion in Biotechnology, 2012, 23, 406-413.	6.6	59

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109	Synergy as design principle for metabolic engineering of 1-propanol production in Escherichia coli. Metabolic Engineering, 2013, 17, 12-22.	7.0	59
110	Metabolic engineering and control analysis for production of aromatics: Role of transaldolase. , 1997, 53, 132-138.		57
111	Heat Shock Response of Archaeoglobus fulgidus. Journal of Bacteriology, 2005, 187, 6046-6057.	2.2	55
112	Transcriptome network component analysis with limited microarray data. Bioinformatics, 2006, 22, 1886-1894.	4.1	55
113	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
114	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
115	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
116	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
117	Ensemble Modeling for Aromatic Production in Escherichia coli. PLoS ONE, 2009, 4, e6903.	2.5	52
118	Microbial pathway engineering for industrial processes: evolution, combinatorial biosynthesis and rational design. Current Opinion in Microbiology, 2001, 4, 330-335.	5.1	51
119	Engineering synthetic recursive pathways to generate non-natural small molecules. Nature Chemical Biology, 2012, 8, 518-526.	8.0	51
120	Metabolic ensemble modeling for strain engineers. Biotechnology Journal, 2012, 7, 343-353.	3.5	51
121	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
122	Erythrocyte nitric oxide transport reduced by a submembrane cytoskeletal barrier. Biochimica Et Biophysica Acta - General Subjects, 2005, 1723, 135-142.	2.4	45
123	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
124	A cell-free self-replenishing CO2-fixing system. Nature Catalysis, 2022, 5, 154-162.	34.4	40
125	A Generalized Framework for Network Component Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 289-301.	3.0	39
126	Identifying rate-controlling enzymes in metabolic pathways without kinetic parameters. Biotechnology Progress, 1991, 7, 15-20.	2.6	38

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127	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
128	Alteration of Product Specificity of Rhodobacter sphaeroides Phytoene Desaturase by Directed Evolution. Journal of Biological Chemistry, 2001, 276, 41161-41164.	3.4	37
129	Protein engineering for metabolic engineering: Current and nextâ€generation tools. Biotechnology Journal, 2013, 8, 545-555.	3.5	37
130	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
131	Bioengineering of microorganisms for C ₃ to C ₅ alcohols production. Biotechnology Journal, 2010, 5, 1297-1308.	3.5	35
132	Lumping analysis of biochemical reaction systems with time scale separation. Biotechnology and Bioengineering, 1988, 31, 869-879.	3.3	34
133	Incorporating qualitative knowledge in enzyme kinetic models using fuzzy logic. , 1999, 62, 722-729.		34
134	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
135	Resistance to Diet-Induced Obesity in Mice with Synthetic Glyoxylate Shunt. Cell Metabolism, 2009, 9, 525-536.	16.2	33
136	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
137	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
138	Sustainable biorefining in wastewater by engineered extreme alkaliphile Bacillus marmarensis. Scientific Reports, 2016, 6, 20224.	3.3	31
139	Control of metabolic pathways by time-scale separation. BioSystems, 1995, 36, 55-70.	2.0	30
140	Global metabolic effects of glycerol kinase overexpression in rat hepatoma cells. Molecular Genetics and Metabolism, 2008, 93, 145-159.	1.1	30
141	Effect of ice nucleators on snow making and spray freezing. Industrial & Engineering Chemistry Research, 1990, 29, 361-366.	3.7	29
142	Using Network Component Analysis to Dissect Regulatory Networks Mediated by Transcription Factors in Yeast. PLoS Computational Biology, 2009, 5, e1000311.	3.2	28
143	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
144	Fermentation data analysis and state estimation in the presence of incomplete mass balance. Biotechnology and Bioengineering, 1989, 33, 613-622.	3.3	27

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145	Experimental determination of flux control distribution in biochemical systems: In vitro model to analyze transient metabolite concentrations. Biotechnology and Bioengineering, 1993, 41, 1121-1128.	3.3	26
146	Lipopolysaccharide Activates Endothelial Nitric Oxide Synthase through Protein Tyrosine Kinase. Biochemical and Biophysical Research Communications, 1998, 245, 33-37.	2.1	26
147	Development of an NADPH-Dependent Homophenylalanine Dehydrogenase by Protein Engineering. ACS Synthetic Biology, 2014, 3, 13-20.	3.8	26
148	A Synthetic Anhydrotetracycline-Controllable Gene Expression System in <i>Ralstonia eutropha</i> H16. ACS Synthetic Biology, 2015, 4, 101-106.	3.8	26
149	A perspective of metabolic engineering strategies: moving up the systems hierarchy. Biotechnology and Bioengineering, 2003, 84, 815-821.	3.3	25
150	Metabolic engineering of 2â€pentanone synthesis in <i>Escherichia coli</i> . AICHE Journal, 2013, 59, 3167-3175.	3.6	25
151	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
152	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
153	Engineering a Thermostable Keto Acid Decarboxylase Using Directed Evolution and Computationally Directed Protein Design. ACS Synthetic Biology, 2017, 6, 610-618.	3.8	24
154	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
155	Characteristic reaction paths of biochemical reaction systems with time scale separation. Biotechnology and Bioengineering, 1988, 31, 847-854.	3.3	23
156	Kinetic characterization of baculovirus-induced cell death in insect cell cultures. Biotechnology and Bioengineering, 1993, 41, 104-110.	3.3	23
157	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
158	A hidden squareâ€root boundary between growth rate and biomass yield. Biotechnology and Bioengineering, 2009, 102, 73-80.	3.3	23
159	Stability of Ensemble Models Predicts Productivity of Enzymatic Systems. PLoS Computational Biology, 2016, 12, e1004800.	3.2	23
160	Application of characteristic reaction paths: Rate-limiting capability of phosphofructokinase in yeast fermentation. Biotechnology and Bioengineering, 1988, 31, 855-868.	3.3	22
161	Effects of ultraviolet light irradiation in biotreatment of organophosphates. Applied Biochemistry and Biotechnology, 1996, 56, 37-47.	2.9	22
162	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

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163	Directed strain evolution restructures metabolism for 1-butanol production in minimal media. Metabolic Engineering, 2018, 49, 153-163.	7.0	22
164	Vocabulon: a dictionary model approach for reconstruction and localization of transcription factor binding sites. Bioinformatics, 2005, 21, 922-931.	4.1	21
165	Alteration of the Biochemical Valves in the Central Metabolism of <i>Escherichia coli</i> ^a . Annals of the New York Academy of Sciences, 1994, 745, 21-34.	3.8	21
166	Metabolic repair through emergence of new pathways in Escherichia coli. Nature Chemical Biology, 2018, 14, 1005-1009.	8.0	20
167	Phenotype Sequencing: Identifying the Genes That Cause a Phenotype Directly from Pooled Sequencing of Independent Mutants. PLoS ONE, 2011, 6, e16517.	2.5	20
168	Extending the quasi-steady state concept to analysis of metabolic networks. Journal of Theoretical Biology, 1987, 126, 253-273.	1.7	19
169	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
170	A Gibbs sampler for the identification of gene expression and network connectivity consistency. Bioinformatics, 2006, 22, 3040-3046.	4.1	18
171	Reconstruction of the archaeal isoprenoid ether lipid biosynthesis pathway in Escherichia coli through digeranylgeranylglyceryl phosphate. Metabolic Engineering, 2009, 11, 184-191.	7.0	18
172	Metabolic systems modeling for cell factories improvement. Current Opinion in Biotechnology, 2017, 46, 114-119.	6.6	18
173	Ensemble modeling and related mathematical modeling of metabolic networks. Journal of the Taiwan Institute of Chemical Engineers, 2009, 40, 595-601.	5.3	17
174	Ensemble Modeling of Hepatic Fatty Acid Metabolism with a Synthetic Glyoxylate Shunt. Biophysical Journal, 2010, 98, 1385-1395.	0.5	17
175	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
176	Identification of COVID-19 B-cell epitopes with phage-displayed peptide library. Journal of Biomedical Science, 2021, 28, 43.	7.0	17
177	A mutant phosphoenolpyruvate carboxykinase in Escherichia coli conferring oxaloacetate decarboxylase activity. Journal of Bacteriology, 1995, 177, 1620-1623.	2.2	16
178	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
179	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
180	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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181	Determination of functional interactions among signalling pathways in Escherichia coli K-12. Metabolic Engineering, 2005, 7, 280-290.	7.0	15
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