Christoph Wittmann

List of Publications by Year
in descending order

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200	16,374	10373	19169
papers	citations	72 h-index	118 g-index

256	256	256	12092
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	From zero to heroâ€"Design-based systems metabolic engineering of Corynebacterium glutamicum for l-lysine production. Metabolic Engineering, 2011, 13, 159-168.	3.6	528
2	A roadmap for interpreting 13 C metabolite labeling patterns from cells. Current Opinion in Biotechnology, 2015, 34, 189-201.	3.3	513
3	The yeast Kluyveromyces marxianus and its biotechnological potential. Applied Microbiology and Biotechnology, 2008, 79, 339-354.	1.7	440
4	Complete genome sequence of the myxobacterium Sorangium cellulosum. Nature Biotechnology, 2007, 25, 1281-1289.	9.4	354
5	Sampling for Metabolome Analysis of Microorganisms. Analytical Chemistry, 2007, 79, 3843-3849.	3.2	344
6	Bio-based production of chemicals, materials and fuels â€“ Corynebacterium glutamicum as versatile cell factory. Current Opinion in Biotechnology, 2012, 23, 631-640.	3.3	329
7	A field of dreams: Lignin valorization into chemicals, materials, fuels, and health-care products. Biotechnology Advances, 2019, 37, 107360.	6.0	301
8	Industrial biotechnology of Pseudomonas putida and related species. Applied Microbiology and Biotechnology, 2012, 93, 2279-2290.	1.7	290
9	Advanced Biotechnology: Metabolically Engineered Cells for the Bioâ€Based Production of Chemicals and Fuels, Materials, and Healthâ€Care Products. Angewandte Chemie - International Edition, 2015, 54, 3328-3350.	7.2	255
10	From zero to hero â€“ Production of bio-based nylon from renewable resources using engineered Corynebacterium glutamicum. Metabolic Engineering, 2014, 25, 113-123.	3.6	246
11	Top value platform chemicals: bio-based production of organic acids. Current Opinion in Biotechnology, 2015, 36, 168-175.	3.3	237
12	Fermentation of plant-based milk alternatives for improved flavour and nutritional value. Applied Microbiology and Biotechnology, 2019, 103, 9263-9275.	1.7	233
13	Impact of the cold shock phenomenon on quantification of intracellular metabolites in bacteria. Analytical Biochemistry, 2004, 327, 135-139.	1.1	225
14	From lignin to nylon: Cascaded chemical and biochemical conversion using metabolically engineered Pseudomonas putida. Metabolic Engineering, 2018, 47, 279-293.	3.6	225
15	OpenFLUX: efficient modelling software for 13C-based metabolic flux analysis. Microbial Cell Factories, 2009, 8, 25.	1.9	218
16	Correcting mass isotopomer distributions for naturally occurring isotopes. Biotechnology and Bioengineering, 2002, 80, 477-479.	1.7	213
17	Systems and synthetic metabolic engineering for amino acid production â€“ the heartbeat of industrial strain development. Current Opinion in Biotechnology, 2012, 23, 718-726.	3.3	210
18	Amplified Expression of Fructose 1,6-Bisphosphatase in Corynebacterium glutamicum Increases In Vivo Flux through the Pentose Phosphate Pathway and Lysine Production on Different Carbon Sources. Applied and Environmental Microbiology, 2005, 71, 8587-8596.	1.4	209

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19	In-Depth Profiling of Lysine-Producing Corynebacterium glutamicum by Combined Analysis of the Transcriptome, Metabolome, and Fluxome. Journal of Bacteriology, 2004, 186, 1769-1784.	1.0	200
20	Fluxome analysis using GC-MS. Microbial Cell Factories, 2007, 6, 6.	1.9	196
21	Comparative Metabolic Flux Analysis of Lysine-Producing Corynebacterium glutamicum Cultured on Glucose or Fructose. Applied and Environmental Microbiology, 2004, 70, 229-239.	1.4	184
22	Metabolically engineered Corynebacterium glutamicum for bio-based production of chemicals, fuels, materials, and healthcare products. Metabolic Engineering, 2018, 50, 122-141.	3.6	183
23	Systems-wide metabolic pathway engineering in Corynebacterium glutamicum for bio-based production of diaminopentane. Metabolic Engineering, 2010, 12, 341-351.	3.6	181
24	Integrated optical sensing of dissolved oxygen in microtiter plates: A novel tool for microbial cultivation. Biotechnology and Bioengineering, 2003, 81, 829-836.	1.7	178
25	Characterization and control of fungal morphology for improved production performance in biotechnology. Journal of Biotechnology, 2013, 163, 112-123.	1.9	175
26	Genealogy Profiling through Strain Improvement by Using Metabolic Network Analysis: Metabolic Flux Genealogy of Several Generations of Lysine-Producing Corynebacteria. Applied and Environmental Microbiology, 2002, 68, 5843-5859.	1.4	172
27	Bio-based production of the platform chemical 1,5-diaminopentane. Applied Microbiology and Biotechnology, 2011, 91, 1287-1296.	1.7	164
28	Characterization of the metabolic shift between oxidative and fermentative growth in Saccharomyces cerevisiae by comparative 13C flux analysis. Microbial Cell Factories, 2005, 4, 30.	1.9	163
29	Metabolic flux engineering of l-lysine production in Corynebacterium glutamicumâ€"over expression and modification of G6P dehydrogenase. Journal of Biotechnology, 2007, 132, 99-109.	1.9	162
30	In-silico-driven metabolic engineering of Pseudomonas putida for enhanced production of poly-hydroxyalkanoates. Metabolic Engineering, 2013, 15, 113-123.	3.6	160
31	Review: Minibioreactors. Biotechnology Letters, 2004, 26, 1-10.	1.1	159
32	Mass spectrometry for metabolic flux analysis. , 1999, 62, 739-750.		155
33	Metabolic engineering of Corynebacterium glutamicum for the production of cis, cis-muconic acid from lignin. Microbial Cell Factories, 2018, 17, 115.	1.9	150
34	Metabolic pathway analysis for rational design of L-methionine production by Escherichia coli and Corynebacterium glutamicum. Metabolic Engineering, 2006, 8, 353-369.	3.6	143
35	Improved enzyme production by bioâ€pellets of Aspergillus niger: Targeted morphology engineering using titanate microparticles. Biotechnology and Bioengineering, 2012, 109, 462-471.	1.7	139
36	Metabolic engineering of cellular transport for overproduction of the platform chemical 1,5-diaminopentane in Corynebacterium glutamicum. Metabolic Engineering, 2011, 13, 617-627.	3.6	135

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37	Morphology engineering of Aspergillus niger for improved enzyme production. Biotechnology and Bioengineering, 2010, 105, 1058-1068.	1.7	132
38	Industrial biotechnology of Pseudomonas putida: advances and prospects. Applied Microbiology and Biotechnology, 2020, 104, 7745-7766.	1.7	128
39	Metabolic engineering of Corynebacterium glutamicum for production of 1,5â€diaminopentane from hemicellulose. Biotechnology Journal, 2011, 6, 306-317.	1.8	127
40	Enabling the valorization of guaiacol-based lignin: Integrated chemical and biochemical production of cis,cis-muconic acid using metabolically engineered Amycolatopsis sp ATCC 39116. Metabolic Engineering, 2018, 45, 200-210.	3.6	125
41	Biotechnology of riboflavin. Applied Microbiology and Biotechnology, 2016, 100, 2107-2119.	1.7	123
42	Pyrazine Biosynthesis in Corynebacterium glutamicum. European Journal of Organic Chemistry, 2010, 2010, 2687-2695.	1.2	119
43	Physiology of the yeastKluyveromyces marxianusduring batch and chemostat cultures with glucose as the sole carbon source. FEMS Yeast Research, 2007, 7, 422-435.	1.1	118
44	Areal activities and stratification of hydrolytic enzymes involved in the biochemical cycles of carbon, nitrogen, sulphur and phosphorus in podsolized boreal forest soils. Soil Biology and Biochemistry, 2004, 36, 425-433.	4.2	116
45	Metabolic engineering of industrial platform microorganisms for biorefinery applications â€“ Optimization of substrate spectrum and process robustness by rational and evolutive strategies. Bioresource Technology, 2013, 135, 544-554.	4.8	115
46	Identification and Elimination of the Competing N -Acetyldiaminopentane Pathway for Improved Production of Diaminopentane by Corynebacterium glutamicum. Applied and Environmental Microbiology, 2010, 76, 5175-5180.	1.4	111
47	Systems metabolic engineering of Corynebacterium glutamicum for the production of the carbon-5 platform chemicals 5-aminovalerate and glutarate. Microbial Cell Factories, 2016, 15, 154.	1.9	109
48	Application of MALDI-TOF MS to lysine-producing Corynebacterium glutamicum. FEBS Journal, 2001, 268, 2441-2455.	0.2	108
49	Systems metabolic engineering of Escherichia coli for production of the antitumor drugs violacein and deoxyviolacein. Metabolic Engineering, 2013, 20, 29-41.	3.6	108
50	Increased lysine production by flux coupling of the tricarboxylic acid cycle and the lysine biosynthetic pathwayâ€”Metabolic engineering of the availability of succinyl-CoA in Corynebacterium glutamicum. Metabolic Engineering, 2013, 15, 184-195.	3.6	106
51	Systems metabolic engineering of xyloseâ€utilizing Corynebacterium glutamicum for production of 1,5â€diaminopentane. Biotechnology Journal, 2013, 8, 557-570.	1.8	106
52	Metabolic Engineering of the Tricarboxylic Acid Cycle for Improved Lysine Production by Corynebacterium glutamicum. Applied and Environmental Microbiology, 2009, 75, 7866-7869.	1.4	104
53	Morphology and Rheology in Filamentous Cultivations. Advances in Applied Microbiology, 2010, 72, 89-136.	1.3	100
54	Production of medium chain length polyhydroxyalkanoate in metabolic flux optimized Pseudomonas putida. Microbial Cell Factories, 2014, 13, 88.	1.9	98

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55	In vivo analysis of intracellular amino acid labelings by GC/MS. Analytical Biochemistry, 2002, 307, 379-382.	1.1	97
56	Metabolic Fluxes in Corynebacterium glutamicum during Lysine Production with Sucrose as Carbon Source. Applied and Environmental Microbiology, 2004, 70, 7277-7287.	1.4	95
57	Growth inhibition by ammonia and use of a pH-controlled feeding strategy for the effective cultivation of Mycobacterium chlorophenolicum. Applied Microbiology and Biotechnology, 1995, 44, 519-525.	1.7	93
58	Characterization and application of an optical sensor for quantification of dissolved O2 in shake-flasks. Biotechnology Letters, 2003, 25, 377-380.	1.1	90
59	Metabolic fluxes and beyondâ€”systems biology understanding and engineering of microbial metabolism. Applied Microbiology and Biotechnology, 2010, 88, 1065-1075.	1.7	90
60	GC-MS-based 13C metabolic flux analysis resolves the parallel and cyclic glucose metabolism of Pseudomonas putida KT2440 and Pseudomonas aeruginosa PAO1. Metabolic Engineering, 2019, 54, 35-53.	3.6	90
61	The Key to Acetate: Metabolic Fluxes of Acetic Acid Bacteria under Cocoa Pulp Fermentation-Simulating Conditions. Applied and Environmental Microbiology, 2014, 80, 4702-4716.	1.4	89
62	Systemsâ€wide analysis and engineering of metabolic pathway fluxes in bioâ€succinate producing Basfia succiniciproducens. Biotechnology and Bioengineering, 2013, 110, 3013-3023.	1.7	88
63	In vivo quantification of intracellular amino acids and intermediates of the methionine pathway in Corynebacterium glutamicum. Analytical Biochemistry, 2005, 340, 171-173.	1.1	87
64	Metabolic physiology of aroma-producingKluyveromyces marxianus. Yeast, 2002, 19, 1351-1363.	0.8	86
65	Metabolic responses to pyruvate kinase deletion in lysine producing Corynebacterium glutamicum. Microbial Cell Factories, 2008, 7, 8.	1.9	84
66	Systems metabolic engineering of Corynebacterium glutamicum for production of the chemical chaperone ectoine. Microbial Cell Factories, 2013, 12, 110.	1.9	84
67	Modeling and Experimental Design for Metabolic Flux Analysis of Lysine-Producing Corynebacteria by Mass Spectrometry. Metabolic Engineering, 2001, 3, 173-191.	3.6	83
68	Adaptation of <scp>B</scp>acillus subtilis carbon core metabolism to simultaneous nutrient limitation and osmotic challenge: a multiâ€omics perspective. Environmental Microbiology, 2014, 16, 1898-1917.	1.8	83
69	Polyunsaturated fatty acid production by Yarrowia lipolytica employing designed myxobacterial PUFA synthases. Nature Communications, 2019, 10, 4055.	5.8	81
70	Flux Design: In silico design of cell factories based on correlation of pathway fluxes to desired properties. BMC Systems Biology, 2009, 3, 120.	3.0	80
71	Quantification of intracellular amino acids in batch cultures of Saccharomyces cerevisiae. Applied Microbiology and Biotechnology, 2001, 56, 776-779.	1.7	79
72	Response of fluxome and metabolome to temperature-induced recombinant protein synthesis in Escherichia coli. Journal of Biotechnology, 2007, 132, 375-384.	1.9	78

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73	A bio-based route to the carbon-5 chemical glutaric acid and to bionylon-6,5 using metabolically engineeredCorynebacterium glutamicum. Green Chemistry, 2018, 20, 4662-4674.	4.6	78
74	Transcriptional and Metabolic Responses of Bacillus subtilis to the Availability of Organic Acids: Transcription Regulation Is Important but Not Sufficient To Account for Metabolic Adaptation. Applied and Environmental Microbiology, 2007, 73, 499-507.	1.4	76
75	Biochemistry, genetics and biotechnology of glycerol utilization in Pseudomonas species. Microbial Biotechnology, 2020, 13, 32-53.	2.0	76
76	Large-Scale ¹³ C Flux Profiling Reveals Conservation of the Entner-Doudoroff Pathway as a Glycolytic Strategy among Marine Bacteria That Use Glucose. Applied and Environmental Microbiology, 2015, 81, 2408-2422.	1.4	73
77	Advances in metabolic engineering of Corynebacterium glutamicum to produce high-value active ingredients for food, feed, human health, and well-being. Essays in Biochemistry, 2021, 65, 197-212.	2.1	71
78	Consequences of phosphoenolpyruvate:sugar phosphotranferase system and pyruvate kinase isozymes inactivation in central carbon metabolism flux distribution in Escherichia coli. Microbial Cell Factories, 2012, 11, 127.	1.9	70
79	Integrated analysis of gene expression and metabolic fluxes in PHA-producing Pseudomonas putida grown on glycerol. Microbial Cell Factories, 2016, 15, 73.	1.9	70
80	Metabolic network analysis of lysine producingCorynebacterium glutamicum at a miniaturized scale. Biotechnology and Bioengineering, 2004, 87, 1-6.	1.7	66
81	Response of the central metabolism of Escherichia coli to modified expression of the gene encoding the glucoseâ€6â€phosphate dehydrogenase. FEBS Letters, 2007, 581, 3771-3776.	1.3	65
82	Lysine production from the sugar alcohol mannitol: Design of the cell factory Corynebacterium glutamicum SEA-3 through integrated analysis and engineering of metabolic pathway fluxes. Metabolic Engineering, 2018, 47, 475-487.	3.6	65
83	Integration of in vivo and in silico metabolic fluxes for improvement of recombinant protein production. Metabolic Engineering, 2012, 14, 47-58.	3.6	64
84	Microbial production of polyunsaturated fatty acids â€" high-value ingredients for aquafeed, superfoods, and pharmaceuticals. Current Opinion in Biotechnology, 2021, 69, 199-211.	3.3	64
85	Derivatization of small biomolecules for optimized matrix-assisted laser desorption/ionization mass spectrometry. Journal of Mass Spectrometry, 2002, 37, 963-973.	0.7	61
86	Core Fluxome and Metafluxome of Lactic Acid Bacteria under Simulated Cocoa Pulp Fermentation Conditions. Applied and Environmental Microbiology, 2013, 79, 5670-5681.	1.4	61
87	Metabolic Engineering of Corynebacterium glutamicum for Highâ€Level Ectoine Production: Design, Combinatorial Assembly, and Implementation of a Transcriptionally Balanced Heterologous Ectoine Pathway. Biotechnology Journal, 2019, 14, e1800417.	1.8	61
88	Microbial production of extremolytes â€" high-value active ingredients for nutrition, health care, and well-being. Current Opinion in Biotechnology, 2020, 65, 118-128.	3.3	61
89	The l-Lysine Story: From Metabolic Pathways to Industrial Production. , 2007, , 39-70.		60
90	Systems Biology of Recombinant Protein Production Using Bacillus megaterium. Methods in Enzymology, 2011, 500, 165-195.	0.4	60

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91	Robustness and Plasticity of Metabolic Pathway Flux among Uropathogenic Isolates of Pseudomonas aeruginosa. PLoS ONE, 2014, 9, e88368.	1.1	60
92	MALDI-TOF MS for quantification of substrates and products in cultivations ofCorynebacterium glutamicum. Biotechnology and Bioengineering, 2001, 72, 642-647.	1.7	59
93	Dynamics of intracellular metabolites of glycolysis and TCA cycle during cell-cycle-related oscillation inSaccharomyces cerevisiae. Biotechnology and Bioengineering, 2005, 89, 839-847.	1.7	59
94	Anodic electroâ€fermentation: Anaerobic production of Lâ€Lysine by recombinant Corynebacterium glutamicum. Biotechnology and Bioengineering, 2018, 115, 1499-1508.	1.7	58
95	Appropriate sampling for intracellular amino acid analysis in five phylogenetically different yeasts. Biotechnology Letters, 2008, 30, 1993-2000.	1.1	57
96	Physiological response of Corynebacterium glutamicum to oxidative stress induced by deletion of the transcriptional repressor McbR. Microbiology (United Kingdom), 2008, 154, 3917-3930.	0.7	57
97	Contextual Flexibility in Pseudomonas aeruginosa Central Carbon Metabolism during Growth in Single Carbon Sources. MBio, 2020, 11, .	1.8	57
98	Optoregulated Drug Release from an Engineered Living Material: Selfâ€Replenishing Drug Depots for Longâ€Term, Lightâ€Regulated Delivery. Small, 2019, 15, e1804717.	5.2	56
99	Towards methionine overproduction in Corynebacterium glutamicum - methanethiol and dimethyldisulfide as reduced sulfur sources. Journal of Microbiology and Biotechnology, 2010, 20, 1196-1203.	0.9	56
100	Theoretical aspects of 13C metabolic flux analysis with sole quantification of carbon dioxide labeling. Computational Biology and Chemistry, 2005, 29, 121-133.	1.1	53
101	Optimized bioprocess for production of fructofuranosidase by recombinant Aspergillus niger. Applied Microbiology and Biotechnology, 2010, 87, 2011-2024.	1.7	53
102	Erythritol feeds the pentose phosphate pathway via three new isomerases leading to D-erythrose-4-phosphate in Brucella. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17815-17820.	3.3	53
103	The Pyruvate-Tricarboxylic Acid Cycle Node. Journal of Biological Chemistry, 2014, 289, 30114-30132.	1.6	53
104	Glycolytic Shunts Replenish the Calvinâ€“Bensonâ€“Bassham Cycle as Anaplerotic Reactions in Cyanobacteria. Molecular Plant, 2020, 13, 471-482.	3.9	53
105	Free intracellular amino acid pools during autonomous oscillations inSaccharomyces cerevisiae. Biotechnology and Bioengineering, 2003, 82, 143-151.	1.7	52
106	From systems biology to metabolically engineered cells â€” an omics perspective on the development of industrial microbes. Current Opinion in Microbiology, 2018, 45, 180-188.	2.3	52
107	Metabolic fluxes in the central carbon metabolism of Dinoroseobacter shibae and Phaeobacter gallaeciensis, two members of the marine Roseobacter clade. BMC Microbiology, 2009, 9, 209.	1.3	51
108	Filamentous fungi in good shape: Microparticles for tailor-made fungal morphology and enhanced enzyme production. Bioengineered Bugs, 2011, 2, 100-104.	2.0	51

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109	Standard reporting requirements for biological samples in metabolomics experiments: microbial and inÂvitro biology experiments. Metabolomics, 2007, 3, 189-194.	1.4	50
110	Sampling of intracellular metabolites for stationary and non-stationary 13C metabolic flux analysis in Escherichia coli. Analytical Biochemistry, 2014, 465, 38-49.	1.1	50
111	Improved riboflavin production with Ashbya gossypii from vegetable oil based on 13C metabolic network analysis with combined labeling analysis by GC/MS, LC/MS, 1D, and 2D NMR. Metabolic Engineering, 2018, 47, 357-373.	3.6	50
112	Accumulation of Homolanthionine and Activation of a Novel Pathway for Isoleucine Biosynthesis in C orynebacterium glutamicum McbR Deletion Strains. Journal of Bacteriology, 2006, 188, 609-618.	1.0	48
113	Reconciling in vivo and in silico key biological parameters of Pseudomonas putidaKT2440 during growth on glucose under carbon-limited condition. BMC Biotechnology, 2013, 13, 93.	1.7	48
114	Systems level engineering of Corynebacterium glutamicum â€“ Reprogramming translational efficiency for superior production. Engineering in Life Sciences, 2010, 10, 430-438.	2.0	47
115	Getting the big beast to workâ€”Systems biotechnology of Bacillus megaterium for novel high-value proteins. Journal of Biotechnology, 2013, 163, 87-96.	1.9	47
116	Debottlenecking recombinant protein production in Bacillus megaterium under largeâ€scale conditionsâ€”targeted precursor feeding designed from metabolomics. Biotechnology and Bioengineering, 2012, 109, 1538-1550.	1.7	46
117	Bio-based succinate from sucrose: High-resolution 13C metabolic flux analysis and metabolic engineering of the rumen bacterium Basfia succiniciproducens. Metabolic Engineering, 2017, 44, 198-212.	3.6	46
118	Respirometric 13C flux analysisâ€”Part II: In vivo flux estimation of lysine-producing Corynebacterium glutamicum. Metabolic Engineering, 2006, 8, 432-446.	3.6	44
119	Use of Single-Frequency Impedance Spectroscopy to Characterize the Growth Dynamics of Biofilm Formation in Pseudomonas aeruginosa. Scientific Reports, 2017, 7, 5223.	1.6	44
120	Microbial production of the drugs violacein and deoxyviolacein: analytical development and strain comparison. Biotechnology Letters, 2012, 34, 717-720.	1.1	41
121	Systems metabolic engineering of Escherichia coli for the heterologous production of high value molecules â€” a veteran at new shores. Current Opinion in Biotechnology, 2016, 42, 178-188.	3.3	41
122	Effect of different carbon sources on central metabolic fluxes and the recombinant production of a hydrolase from Thermobifida fusca in Bacillus megaterium. Journal of Biotechnology, 2007, 132, 385-394.	1.9	40
123	Systems metabolic engineering of Escherichia coli for gram scale production of the antitumor drug deoxyviolacein from glycerol. Biotechnology and Bioengineering, 2014, 111, 2280-2289.	1.7	40
124	Corynebacterium glutamicum for Sustainable Bioproduction: From Metabolic Physiology to Systems Metabolic Engineering. Advances in Biochemical Engineering/Biotechnology, 2016, 162, 217-263.	0.6	40
125	Analysis of 13C labeling enrichment in microbial culture applying metabolic tracer experiments using gas chromatographyâ€“combustionâ€“isotope ratio mass spectrometry. Analytical Biochemistry, 2008, 380, 202-210.	1.1	39
126	Microparticle based morphology engineering of filamentous microorganisms for industrial bio-production. Biotechnology Letters, 2012, 34, 1975-1982.	1.1	38

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127	Respirometric 13C flux analysis, Part I: Design, construction and validation of a novel multiple reactor system using on-line membrane inlet mass spectrometry. Metabolic Engineering, 2006, 8, 417-431.	3.6	37
128	High yield production of extracellular recombinant levansucrase by Bacillus megaterium. Applied Microbiology and Biotechnology, 2013, 97, 3343-3353.	1.7	36
129	Guiding stars to the field of dreams: Metabolically engineered pathways and microbial platforms for a sustainable lignin-based industry. Metabolic Engineering, 2022, 71, 13-41.	3.6	36
130	Mineralization of detritus and oxidation of methane in acid boreal coniferous forest soils: seasonal and vertical distribution and effects of clear-cut. Soil Biology and Biochemistry, 2002, 34, 1191-1200.	4.2	35
131	Towards better understanding of industrial cell factories: novel approaches for 13C metabolic flux analysis in complex nutrient environments. Current Opinion in Biotechnology, 2018, 54, 128-137.	3.3	33
132	Limited life cycle and cost assessment for the bioconversion of ligninâ€derived aromatics into adipic acid. Biotechnology and Bioengineering, 2020, 117, 1381-1393.	1.7	32
133	Metabolic flux screening of Saccharomyces cerevisiae single knockout strains on glucose and galactose supports elucidation of gene function. Journal of Biotechnology, 2007, 132, 395-404.	1.9	31
134	Oxygen supply in disposable shake-flasks: prediction of oxygen transfer rate, oxygen saturation and maximum cell concentration during aerobic growth. Biotechnology Letters, 2013, 35, 1223-1230.	1.1	31
135	Cascaded valorization of brown seaweed to produce l-lysine and value-added products using Corynebacterium glutamicum streamlined by systems metabolic engineering. Metabolic Engineering, 2021, 67, 293-307.	3.6	30
136	Comparative metabolic flux analysis of an Ashbya gossypii wild type strain and a high riboflavin-producing mutant strain. Journal of Bioscience and Bioengineering, 2015, 119, 101-106.	1.1	29
137	Metabolic flux pattern of glucose utilization by Xanthomonas campestris pv. campestris: prevalent role of the Entnerâ€“Doudoroff pathway and minor fluxes through the pentose phosphate pathway and glycolysis. Molecular BioSystems, 2014, 10, 2663-2676.	2.9	28
138	Novel Approach for High-Throughput Metabolic Screening of Whole Plants by Stable Isotopes. Plant Physiology, 2016, 171, 25-41.	2.3	27
139	Metabolic flux analysis in Ashbya gossypii using 13C-labeled yeast extract: industrial riboflavin production under complex nutrient conditions. Microbial Cell Factories, 2018, 17, 162.	1.9	27
140	Cascaded valorization of seaweed using microbial cell factories. Current Opinion in Biotechnology, 2020, 65, 102-113.	3.3	27
141	Comparative study on central metabolic fluxes of Bacillus megaterium strains in continuous culture using 13C labelled substrates. Bioprocess and Biosystems Engineering, 2006, 30, 47-59.	1.7	26
142	Transposon Mutagenesis Identified Chromosomal and Plasmid Genes Essential for Adaptation of the Marine Bacterium Dinoroseobacter shibae to Anaerobic Conditions. Journal of Bacteriology, 2013, 195, 4769-4777.	1.0	26
143	Acetate Dissimilation and Assimilation in Mycobacterium tuberculosis Depend on Carbon Availability. Journal of Bacteriology, 2015, 197, 3182-3190.	1.0	26
144	Biobased PET from lignin using an engineered cis, cis-muconate-producing Pseudomonas putida strain with superior robustness, energy and redox properties. Metabolic Engineering, 2022, 72, 337-352.	3.6	26

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145	Gene Regulatory and Metabolic Adaptation Processes of Dinoroseobacter shibae DFL12T during Oxygen Depletion. Journal of Biological Chemistry, 2014, 289, 13219-13231.	1.6	25
146	A Precise Temperature-Responsive Bistable Switch Controlling Yersinia Virulence. PLoS Pathogens, 2016, 12, e1006091.	2.1	24
147	Green pathways: Metabolic network analysis of plant systems. Metabolic Engineering, 2016, 34, 1-24.	3.6	24
148	Microparticles globallyÂreprogram Streptomyces albus toward accelerated morphogenesis, streamlined carbon core metabolism, and enhanced production of the antituberculosis polyketide pamamycin. Biotechnology and Bioengineering, 2020, 117, 3858-3875.	1.7	22
149	Metabolite profiling studies in Saccharomyces cerevisiae: an assisting tool to prioritize host targets for antiviral drug screening. Microbial Cell Factories, 2009, 8, 12.	1.9	21
150	Customization of Aspergillus niger Morphology Through Addition of Talc Micro Particles. Journal of Visualized Experiments, 2012, , .	0.2	21
151	Proteome and carbon flux analysis of PseudomonasÂaeruginosa clinical isolates from different infection sites. Proteomics, 2016, 16, 1381-1385.	1.3	21
152	A common approach for absolute quantification of short chain CoA thioesters in prokaryotic and eukaryotic microbes. Microbial Cell Factories, 2020, 19, 160.	1.9	21
153	Investigation of the central carbon metabolism of Sorangium cellulosum: metabolic network reconstruction and quantification of pathway fluxes. Journal of Microbiology and Biotechnology, 2009, 19, 23-36.	0.9	18
154	Metabolic network simulation using logical loop algorithm and Jacobian matrix. Metabolic Engineering, 2004, 6, 256-267.	3.6	17
155	Dynamic calibration and dissolved gas analysis using membrane inlet mass spectrometry for the quantification of cell respiration. Rapid Communications in Mass Spectrometry, 2003, 17, 2721-2731.	0.7	16
156	Metabolic screening of Saccharomyces cerevisiae single knockout strains reveals unexpected mobilization of metabolic potential. Process Biochemistry, 2006, 41, 2170-2179.	1.8	16
157	Production of nonâ€proteinogenic amino acids from Î±â€keto acid precursors with recombinant Corynebacterium glutamicum. Biotechnology and Bioengineering, 2013, 110, 2846-2855.	1.7	16
158	Biotechnological Production of Organic Acids from Renewable Resources. Advances in Biochemical Engineering/Biotechnology, 2017, 166, 373-410.	0.6	16
159	Metabolic physiology of Pseudomonas putida for heterologous production of myxochromide. Process Biochemistry, 2006, 41, 2146-2152.	1.8	15
160	Analysis and Engineering of Metabolic Pathway Fluxes in Corynebacterium glutamicum. , 2010, 120, 21-49.		15
161	Microparticles enhance the formation of seven major classes of natural products in native and metabolically engineered actinobacteria through accelerated morphological development. Biotechnology and Bioengineering, 2021, 118, 3076-3093.	1.7	15
162	Establishing recombinant production of pediocin PA-1 in Corynebacterium glutamicum. Metabolic Engineering, 2021, 68, 34-45.	3.6	15

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163	Functionalization of magnetic nanoparticles with high-binding capacity for affinity separation of therapeutic proteins. Journal of Nanoparticle Research, 2014, 16, 1.	0.8	14
164	Convergent evolution of zoonotic Brucella species toward the selective use of the pentose phosphate pathway. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26374-26381.	3.3	13
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