

Lars Keld Nielsen

List of Publications by Year in descending order

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267
papers

15,293
citations

17440

63
h-index

24982

109
g-index

285
all docs

285
docs citations

285
times ranked

18602
citing authors

#	ARTICLE	IF	CITATIONS
1	Perfusion culture of Chinese Hamster Ovary cells for bioprocessing applications. <i>Critical Reviews in Biotechnology</i> , 2022, 42, 1099-1115.	9.0	15
2	Soft sensors application for automated feeding control in high-throughput mammalian cell cultures. <i>Biotechnology and Bioengineering</i> , 2022, 119, 1077-1090.	3.3	5
3	Multi-omic characterisation of <i>Streptomyces hygrosopicus</i> NRRL 30439: detailed assessment of its secondary metabolic potential. <i>Molecular Omics</i> , 2022, 18, 226-236.	2.8	5
4	Modeling apoptosis resistance in CHO cells with CRISPR-mediated knockouts of Bak1, Bax, and Bok. <i>Biotechnology and Bioengineering</i> , 2022, 119, 1380-1391.	3.3	14
5	Absolute Proteome Quantification in the Gas-Fermenting Acetogen <i>Clostridium autoethanogenum</i> . <i>MSystems</i> , 2022, 7, e0002622.	3.8	10
6	Analytical tools for unravelling the metabolism of gas-fermenting Clostridia. <i>Current Opinion in Biotechnology</i> , 2022, 75, 102700.	6.6	9
7	Irritable bowel syndrome and microbiome; Switching from conventional diagnosis and therapies to personalized interventions. <i>Journal of Translational Medicine</i> , 2022, 20, 173.	4.4	19
8	Recycling carbon for sustainable protein production using gas fermentation. <i>Current Opinion in Biotechnology</i> , 2022, 76, 102723.	6.6	16
9	Engineering death resistance in CHO cells for improved perfusion culture. <i>MAbs</i> , 2022, 14, .	5.2	4
10	The topology of genome-scale metabolic reconstructions unravels independent modules and high network flexibility. <i>PLoS Computational Biology</i> , 2022, 18, e1010203.	3.2	3
11	Metabolic Modeling and Omics Data Integration: A Systems Biology Approach to Food Science. , 2021, , 396-417.		0
12	Omics driven discoveries of gene targets for apoptosis attenuation in CHO cells. <i>Biotechnology and Bioengineering</i> , 2021, 118, 481-490.	3.3	5
13	Network mapping of primary CD34+ cells by Ampliseq based whole transcriptome targeted resequencing identifies unexplored differentiation regulatory relationships. <i>PLoS ONE</i> , 2021, 16, e0246107.	2.5	0
14	multiTFA: a Python package for multi-variate thermodynamics-based flux analysis. <i>Bioinformatics</i> , 2021, 37, 3064-3066.	4.1	8
15	Towards Sustainable Bioinoculants: A Fermentation Strategy for High Cell Density Cultivation of <i>Paraburkholderia</i> sp. SOS3, a Plant Growth-Promoting Bacterium Isolated in Queensland, Australia. <i>Fermentation</i> , 2021, 7, 58.	3.0	4
16	Model-guided dynamic control of essential metabolic nodes boosts acetyl-coenzyme A dependent bioproduction in rewired <i>Pseudomonas putida</i> . <i>Metabolic Engineering</i> , 2021, 67, 373-386.	7.0	41
17	Engineering <i>Escherichia coli</i> for propionic acid production through the Wood-Werkman cycle. <i>Biotechnology and Bioengineering</i> , 2020, 117, 167-183.	3.3	20
18	Attenuating apoptosis in Chinese hamster ovary cells for improved biopharmaceutical production. <i>Biotechnology and Bioengineering</i> , 2020, 117, 1187-1203.	3.3	31

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19	A Pan-Genome Guided Metabolic Network Reconstruction of Five Propionibacterium Species Reveals Extensive Metabolic Diversity. <i>Genes</i> , 2020, 11, 1115.	2.4	18
20	SmartPeak Automates Targeted and Quantitative Metabolomics Data Processing. <i>Analytical Chemistry</i> , 2020, 92, 15968-15974.	6.5	23
21	Multicopy Targeted Integration for Accelerated Development of High-Producing Chinese Hamster Ovary Cells. <i>ACS Synthetic Biology</i> , 2020, 9, 2546-2561.	3.8	39
22	Time-course transcriptomics reveals that amino acids catabolism plays a key role in toxinogenesis and morphology in <i>Clostridium tetani</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2020, 47, 1059-1073.	3.0	6
23	Redox controls metabolic robustness in the gas-fermenting acetogen <i>Clostridium autoethanogenum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13168-13175.	7.1	54
24	Heterologous Production of 6-Deoxyerythronolide B in <i>Escherichia coli</i> through the Wood Werkman Cycle. <i>Metabolites</i> , 2020, 10, 228.	2.9	6
25	What CHO is made of: Variations in the biomass composition of Chinese hamster ovary cell lines. <i>Metabolic Engineering</i> , 2020, 61, 288-300.	7.0	46
26	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
27	Enhancing CO ₂ -Valorization Using <i>Clostridium autoethanogenum</i> for Sustainable Fuel and Chemicals Production. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 204.	4.1	79
28	Adaptation of hydroxymethylbutenyl diphosphate reductase enables volatile isoprenoid production. <i>ELife</i> , 2020, 9, .	6.0	19
29	Stoichiometric gene-to-reaction associations enhance model-driven analysis performance: Metabolic response to chronic exposure to Aldrin in prostate cancer. <i>BMC Genomics</i> , 2019, 20, 652.	2.8	12
30	A TetR-Family Protein (CAETHG_0459) Activates Transcription From a New Promoter Motif Associated With Essential Genes for Autotrophic Growth in Acetogens. <i>Frontiers in Microbiology</i> , 2019, 10, 2549.	3.5	12
31	Revisiting the Evolution and Taxonomy of Clostridia, a Phylogenomic Update. <i>Genome Biology and Evolution</i> , 2019, 11, 2035-2044.	2.5	65
32	Shedding light: The importance of reverse transcription efficiency standards in data interpretation. <i>Biomolecular Detection and Quantification</i> , 2019, 17, 100077.	7.0	29
33	Systems-level engineering and characterisation of <i>Clostridium autoethanogenum</i> through heterologous production of poly-3-hydroxybutyrate (PHB). <i>Metabolic Engineering</i> , 2019, 53, 14-23.	7.0	57
34	Engineered protein degradation of farnesyl pyrophosphate synthase is an effective regulatory mechanism to increase monoterpene production in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2018, 47, 83-93.	7.0	89
35	From reconstruction to C ₄ metabolic engineering: A case study for overproduction of polyhydroxybutyrate in bioenergy grasses. <i>Plant Science</i> , 2018, 273, 50-60.	3.6	7
36	Quantitative analysis of tetrahydrofolate metabolites from <i>clostridium autoethanogenum</i> . <i>Metabolomics</i> , 2018, 14, 35.	3.0	5

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37	Universal Alternative Splicing of Noncoding Exons. <i>Cell Systems</i> , 2018, 6, 245-255.e5.	6.2	110
38	Advances in analytical tools for high throughput strain engineering. <i>Current Opinion in Biotechnology</i> , 2018, 54, 33-40.	6.6	29
39	Toward industrial production of isoprenoids in <i>Escherichia coli</i> : Lessons learned from CRISPR-Cas9 based optimization of a chromosomally integrated mevalonate pathway. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1000-1013.	3.3	39
40	Genome-scale model guided design of <i>Propionibacterium</i> for enhanced propionic acid production. <i>Metabolic Engineering Communications</i> , 2018, 6, 1-12.	3.6	11
41	RNA-Seq Highlights High Clonal Variation in Monoclonal Antibody Producing CHO Cells. <i>Biotechnology Journal</i> , 2018, 13, e1700231.	3.5	28
42	An Expanded Heterologous <i>GAL</i> Promoter Collection for Diauxie-Inducible Expression in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 748-751.	3.8	35
43	Improving culture performance and antibody production in CHO cell culture processes by reducing the Warburg effect. <i>Biotechnology and Bioengineering</i> , 2018, 115, 2315-2327.	3.3	46
44	Multicenter European Prevalence Study of Neurocognitive Impairment and Associated Factors in HIV Positive Patients. <i>AIDS and Behavior</i> , 2018, 22, 1573-1583.	2.7	32
45	Toward Synthetic Biology Strategies for Adipic Acid Production: An <i>In Silico</i> Tool for Combined Thermodynamics and Stoichiometric Analysis of Metabolic Networks. <i>ACS Synthetic Biology</i> , 2018, 7, 490-509.	3.8	25
46	Plant genome-scale reconstruction: from single cell to multi-tissue modelling and omics analyses. <i>Current Opinion in Biotechnology</i> , 2018, 49, 42-48.	6.6	32
47	Minimizing Clonal Variation during Mammalian Cell Line Engineering for Improved Systems Biology Data Generation. <i>ACS Synthetic Biology</i> , 2018, 7, 2148-2159.	3.8	51
48	Synthetic microbe communities provide internal reference standards for metagenome sequencing and analysis. <i>Nature Communications</i> , 2018, 9, 3096.	12.8	81
49	H2 drives metabolic rearrangements in gas-fermenting <i>Clostridium autoethanogenum</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 55.	6.2	103
50	Linking genotype and phenotype in an economically viable propionic acid biosynthesis process. <i>Biotechnology for Biofuels</i> , 2018, 11, 224.	6.2	10
51	Coupling gene regulatory patterns to bioprocess conditions to optimize synthetic metabolic modules for improved sesquiterpene production in yeast. <i>Biotechnology for Biofuels</i> , 2017, 10, 43.	6.2	53
52	Arginine deiminase pathway provides ATP and boosts growth of the gas-fermenting acetogen <i>Clostridium autoethanogenum</i> . <i>Metabolic Engineering</i> , 2017, 41, 202-211.	7.0	96
53	Overexpression of the regulatory subunit of glutamate-cysteine ligase enhances monoclonal antibody production in CHO cells. <i>Biotechnology and Bioengineering</i> , 2017, 114, 1825-1836.	3.3	21
54	Maintenance of ATP Homeostasis Triggers Metabolic Shifts in Gas-Fermenting Acetogens. <i>Cell Systems</i> , 2017, 4, 505-515.e5.	6.2	128

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55	A squalene synthase protein degradation method for improved sesquiterpene production in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2017, 39, 209-219.	7.0	91
56	Functional screening in human cardiac organoids reveals a metabolic mechanism for cardiomyocyte cell cycle arrest. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8372-E8381.	7.1	361
57	Formulation, construction and analysis of kinetic models of metabolism: A review of modelling frameworks. <i>Biotechnology Advances</i> , 2017, 35, 981-1003.	11.7	128
58	Cell-free pipeline for discovery of thermotolerant xylanases and endo -1,4- β -glucanases. <i>Journal of Biotechnology</i> , 2017, 259, 191-198.	3.8	6
59	Improved production of propionic acid using genome shuffling. <i>Biotechnology Journal</i> , 2017, 12, 1600120.	3.5	23
60	Microbial Propionic Acid Production. <i>Fermentation</i> , 2017, 3, 21.	3.0	185
61	Awakening sleeping beauty: production of propionic acid in <i>Escherichia coli</i> through the sbm operon requires the activity of a methylmalonyl-CoA epimerase. <i>Microbial Cell Factories</i> , 2017, 16, 121.	4.0	15
62	Metabolic Reconstruction of <i>Setaria italica</i> : A Systems Biology Approach for Integrating Tissue-Specific Omics and Pathway Analysis of Bioenergy Grasses. <i>Frontiers in Plant Science</i> , 2016, 7, 1138.	3.6	24
63	Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals. <i>Microbiome</i> , 2016, 4, 36.	11.1	533
64	Genome Sequence of <i>Propionibacterium acidipropionici</i> ATCC 55737. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
65	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. <i>Cell Systems</i> , 2016, 3, 434-443.e8.	6.2	205
66	Systems biology and metabolic modelling unveils limitations to polyhydroxybutyrate accumulation in sugarcane leaves; lessons for C_4 engineering. <i>Plant Biotechnology Journal</i> , 2016, 14, 567-580.	8.3	17
67	A probabilistic framework for the exploration of enzymatic capabilities based on feasible kinetics and control analysis. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 576-587.	2.4	3
68	The <i>Saccharomyces cerevisiae</i> pheromone-response is a metabolically active stationary phase for bio-production. <i>Metabolic Engineering Communications</i> , 2016, 3, 142-152.	3.6	18
69	Deletion of the hypothetical protein SCO2127 of <i>Streptomyces coelicolor</i> allowed identification of a new regulator of actinorhodin production. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 9229-9237.	3.6	6
70	In vitro production of baculoviruses: identifying host and virus genes associated with high productivity. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 9239-9253.	3.6	3
71	Tetanus toxin production is triggered by the transition from amino acid consumption to peptides. <i>Anaerobe</i> , 2016, 41, 113-124.	2.1	13
72	Representing genetic variation with synthetic DNA standards. <i>Nature Methods</i> , 2016, 13, 784-791.	19.0	37

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73	Spliced synthetic genes as internal controls in RNA sequencing experiments. <i>Nature Methods</i> , 2016, 13, 792-798.	19.0	123
74	Recon 2.2: from reconstruction to model of human metabolism. <i>Metabolomics</i> , 2016, 12, 109.	3.0	243
75	Fast-SNP: a fast matrix pre-processing algorithm for efficient loopless flux optimization of metabolic models. <i>Bioinformatics</i> , 2016, 32, 3807-3814.	4.1	15
76	Construction of feasible and accurate kinetic models of metabolism: A Bayesian approach. <i>Scientific Reports</i> , 2016, 6, 29635.	3.3	72
77	Cyclic di-AMP synthesis by the diadenylate cyclase <i>CdaA</i> is modulated by the peptidoglycan biosynthesis enzyme <i>GlmM</i> in <i>actococcus lactis</i> . <i>Molecular Microbiology</i> , 2016, 99, 1015-1027.	2.5	61
78	Filling the void. <i>Current Opinion in Hematology</i> , 2016, 23, 72-77.	2.5	2
79	Genetic and biochemical characterization of genes involved in hyaluronic acid synthesis in <i>Streptococcus zooepidemicus</i> . <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 3611-3620.	3.6	15
80	Algae Genome-Scale Reconstruction, Modelling and Applications. , 2016, , 591-598.		1
81	II-ACHRB: a scalable algorithm for sampling the feasible solution space of metabolic networks. <i>Bioinformatics</i> , 2016, 32, 2330-2337.	4.1	36
82	Low carbon fuels and commodity chemicals from waste gases – systematic approach to understand energy metabolism in a model acetogen. <i>Green Chemistry</i> , 2016, 18, 3020-3028.	9.0	143
83	Multi-omics approach for comparative studies of monoclonal antibody producing CHO cells. <i>BMC Proceedings</i> , 2015, 9, .	1.6	4
84	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015, 11, 831.	7.2	68
85	Controlling heterologous gene expression in yeast cell factories on different carbon substrates and across the diauxic shift: a comparison of yeast promoter activities. <i>Microbial Cell Factories</i> , 2015, 14, 91.	4.0	161
86	Systems Biology Approaches to Understand Natural Products Biosynthesis. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 199.	4.1	6
87	Dynamic regulation of gene expression using sucrose responsive promoters and RNA interference in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2015, 14, 43.	4.0	28
88	Editorial: On the cusp of rational CHO cell engineering. <i>Biotechnology Journal</i> , 2015, 10, 929-930.	3.5	4
89	Systems analysis of methylerythritol-phosphate pathway flux in <i>E. coli</i> : insights into the role of oxidative stress and the validity of lycopene as an isoprenoid reporter metabolite. <i>Microbial Cell Factories</i> , 2015, 14, 193.	4.0	24
90	Production of Industrially Relevant Isoprenoid Compounds in Engineered Microbes. <i>Microbiology Monographs</i> , 2015, , 303-334.	0.6	20

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91	Genome-wide discovery of human splicing branchpoints. <i>Genome Research</i> , 2015, 25, 290-303.	5.5	222
92	High-Antibody-Producing Chinese Hamster Ovary Cells Up-Regulate Intracellular Protein Transport and Glutathione Synthesis. <i>Journal of Proteome Research</i> , 2015, 14, 609-618.	3.7	60
93	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. <i>Nature Methods</i> , 2015, 12, 339-342.	19.0	155
94	A multi-tissue genome-scale metabolic modeling framework for the analysis of whole plant systems. <i>Frontiers in Plant Science</i> , 2015, 6, 4.	3.6	94
95	Global dynamics of <i>Escherichia coli</i> phosphoproteome in central carbon metabolism under changing culture conditions. <i>Journal of Proteomics</i> , 2015, 126, 24-33.	2.4	18
96	A liquid chromatography-tandem mass spectrometry-based investigation of the lamellar interstitial metabolome in healthy horses and during experimental laminitis induction. <i>Veterinary Journal</i> , 2015, 206, 161-169.	1.7	12
97	Dynamic metabolic flux analysis using B-splines to study the effects of temperature shift on CHO cell metabolism. <i>Metabolic Engineering Communications</i> , 2015, 2, 46-57.	3.6	54
98	Intracellular Trafficking of Baculovirus Particles: A Quantitative Study of the <i>HearNPV/HzAM1</i> Cell and <i>AcMNPV/Sf9</i> Cell Systems. <i>Viruses</i> , 2015, 7, 2288-2307.	3.3	4
99	AllR Controls the Expression of <i>Streptomyces coelicolor</i> Allantoin Pathway Genes. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6649-6659.	3.1	3
100	A General Framework for Thermodynamically Consistent Parameterization and Efficient Sampling of Enzymatic Reactions. <i>PLoS Computational Biology</i> , 2015, 11, e1004195.	3.2	33
101	Quorum-sensing linked RNA interference for dynamic metabolic pathway control in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2015, 29, 124-134.	7.0	118
102	Effect of the peak cell density of recombinant <i>AcMNPV</i> -infected <i>Hi5</i> cells on baculovirus yields. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 1687-1700.	3.6	11
103	Evolutionary Engineering Improves Tolerance for Replacement Jet Fuels in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 3316-3325.	3.1	44
104	Decline in <i>Helicoverpa armigera</i> nucleopolyhedrovirus occlusion body yields with increasing infection cell density in vitro is strongly correlated with viral DNA levels. <i>Archives of Virology</i> , 2015, 160, 2169-2180.	2.1	4
105	The use of an acetoacetyl-CoA synthase in place of a β -ketothiolase enhances polyhydroxybutyrate production in sugarcane mesophyll cells. <i>Plant Biotechnology Journal</i> , 2015, 13, 700-707.	8.3	21
106	Metabolic Profiling and Flux Analysis of MEL-2 Human Embryonic Stem Cells during Exponential Growth at Physiological and Atmospheric Oxygen Concentrations. <i>PLoS ONE</i> , 2014, 9, e112757.	2.5	38
107	Factors affecting polyhydroxybutyrate accumulation in mesophyll cells of sugarcane and switchgrass. <i>BMC Biotechnology</i> , 2014, 14, 83.	3.3	18
108	<i>Escherichia coli</i> W shows fast, highly oxidative sucrose metabolism and low acetate formation. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 9033-9044.	3.6	27

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109	Dynamic Balancing of Isoprene Carbon Sources Reflects Photosynthetic and Photorespiratory Responses to Temperature Stress. <i>Plant Physiology</i> , 2014, 166, 2051-2064.	4.8	41
110	Control of chitin and N-acetylglucosamine utilization in <i>Saccharopolyspora erythraea</i> . <i>Microbiology (United Kingdom)</i> , 2014, 160, 1914-1928.	1.8	20
111	Extracting reaction networks from databases-opening Pandora's box. <i>Briefings in Bioinformatics</i> , 2014, 15, 973-983.	6.5	5
112	The effect of cell line, phylogenetics and medium on baculovirus budded virus yield and quality. <i>Archives of Virology</i> , 2014, 159, 91-102.	2.1	11
113	The Role of Hyaluronic Acid Precursor Concentrations in Molecular Weight Control in <i>Streptococcus zooepidemicus</i> . <i>Molecular Biotechnology</i> , 2014, 56, 147-156.	2.4	26
114	Targeted sequencing for gene discovery and quantification using RNA CaptureSeq. <i>Nature Protocols</i> , 2014, 9, 989-1009.	12.0	171
115	Plant Genome-Scale Modeling and Implementation. <i>Methods in Molecular Biology</i> , 2014, 1090, 317-332.	0.9	8
116	Concise Review: Next-Generation Cell Therapies to Prevent Infections in Neutropenic Patients. <i>Stem Cells Translational Medicine</i> , 2014, 3, 541-548.	3.3	16
117	Absolute counting of neutrophils in whole blood using flow cytometry. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2014, 85, 1057-1064.	1.5	11
118	NExT: Integration of Thermodynamic Constraints and Metabolomics Data into a Metabolic Network. <i>Methods in Molecular Biology</i> , 2014, 1191, 65-78.	0.9	8
119	Temporal Dynamics of the <i>Saccharopolyspora erythraea</i> Phosphoproteome. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1219-1230.	3.8	22
120	Network Thermodynamic Curation of Human and Yeast Genome-Scale Metabolic Models. <i>Biophysical Journal</i> , 2014, 107, 493-503.	0.5	32
121	A depth-first search algorithm to compute elementary flux modes by linear programming. <i>BMC Systems Biology</i> , 2014, 8, 94.	3.0	26
122	Production of the short peptide surfactant DAMP4 from glucose or sucrose in high cell density cultures of <i>Escherichia coli</i> BL21(DE3). <i>Microbial Cell Factories</i> , 2014, 13, 99.	4.0	9
123	Insight into hyaluronic acid molecular weight control. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 6947-6956.	3.6	43
124	Allantoin catabolism influences the production of antibiotics in <i>Streptomyces coelicolor</i> . <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 351-360.	3.6	12
125	Reducing Recon 2 for steady-state flux analysis of HEK cell culture. <i>Journal of Biotechnology</i> , 2014, 184, 172-178.	3.8	54
126	Steady-State ¹³ C Fluxomics Using OpenFLUX. <i>Methods in Molecular Biology</i> , 2014, 1191, 209-224.	0.9	9

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127	The Trehalose Phosphotransferase System (PTS) in <i>E. coli</i> W Can Transport Low Levels of Sucrose that Are Sufficient to Facilitate Induction of the <i>csc</i> Sucrose Catabolism Operon. <i>PLoS ONE</i> , 2014, 9, e88688.	2.5	10
128	Customization of ¹³ C-MFA Strategy According to Cell Culture System. <i>Methods in Molecular Biology</i> , 2014, 1191, 81-90.	0.9	2
129	Towards a Large Integrated Model of Signal Transduction and Gene Regulation Events in Mammalian Cells. , 2014, , .		0
130	<i>Saccharopolyspora erythraea</i> ™ genome is organised in high-order transcriptional regions mediated by targeted degradation at the metabolic switch. <i>BMC Genomics</i> , 2013, 14, 15.	2.8	33
131	Knock-in/Knock-out (KIKO) vectors for rapid integration of large DNA sequences, including whole metabolic pathways, onto the <i>Escherichia coli</i> chromosome at well-characterised loci. <i>Microbial Cell Factories</i> , 2013, 12, 60.	4.0	74
132	Genome scale analysis of differential mRNA expression of <i>Helicoverpa zea</i> insect cells infected with a <i>H. armigera</i> baculovirus. <i>Virology</i> , 2013, 444, 158-170.	2.4	25
133	2,2-Diphenyl-1-picrylhydrazyl as a screening tool for recombinant monoterpene biosynthesis. <i>Microbial Cell Factories</i> , 2013, 12, 76.	4.0	48
134	Dual gene expression cassette vectors with antibiotic selection markers for engineering in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2013, 12, 96.	4.0	45
135	Chemical inhibition of acetyl coenzyme <sc>A</sc> carboxylase as a strategy to increase polyhydroxybutyrate yields in transgenic sugarcane. <i>Plant Biotechnology Journal</i> , 2013, 11, 1146-1151.	8.3	17
136	Flux balance analysis of CHO cells before and after a metabolic switch from lactate production to consumption. <i>Biotechnology and Bioengineering</i> , 2013, 110, 660-666.	3.3	106
137	Engineered Quorum Sensing Using Pheromone-Mediated Cell-to-Cell Communication in <i>Saccharomyces cerevisiae</i>. <i>ACS Synthetic Biology</i> , 2013, 2, 136-149.	3.8	62
138	Decline in baculovirus-expressed recombinant protein production with increasing cell density is strongly correlated to impairment of virus replication and mRNA expression. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 5245-5257.	3.6	8
139	Technoeconomic analysis of renewable aviation fuel from microalgae, <i>Pongamia pinnata</i>, and sugarcane. <i>Biofuels, Bioproducts and Biorefining</i> , 2013, 7, 416-428.	3.7	112
140	Plant genome-scale metabolic reconstruction and modelling. <i>Current Opinion in Biotechnology</i> , 2013, 24, 271-277.	6.6	71
141	DNase Iâ€“hypersensitive exons colocalize with promoters and distal regulatory elements. <i>Nature Genetics</i> , 2013, 45, 852-859.	21.4	112
142	Enhanced Gametocyte Formation in Erythrocyte Progenitor Cells: A Site-Specific Adaptation by <i>Plasmodium falciparum</i> . <i>Journal of Infectious Diseases</i> , 2013, 208, 1170-1174.	4.0	19
143	Genome Scale Transcriptomics of Baculovirus-Insect Interactions. <i>Viruses</i> , 2013, 5, 2721-2747.	3.3	44
144	Molecular Control of Sucrose Utilization in <i>Escherichia coli</i> W, an Efficient Sucrose-Utilizing Strain. <i>Applied and Environmental Microbiology</i> , 2013, 79, 478-487.	3.1	76

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145	Physiological and Transcriptional Responses of <i>Saccharomyces cerevisiae</i> to α -Limonene Show Changes to the Cell Wall but Not to the Plasma Membrane. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3590-3600.	3.1	84
146	Non-Invasive Monitoring of Sucrose Mobilization from Culm Storage Parenchyma by Magnetic Resonance Spectroscopy. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 487-496.	1.3	5
147	Re-annotation of the <i>Saccharopolyspora erythraea</i> genome using a systems biology approach. <i>BMC Genomics</i> , 2013, 14, 699.	2.8	21
148	Bioreactor for Blood Product Production. <i>Cell Transplantation</i> , 2012, 21, 1235-1244.	2.5	6
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