

Byung-Kwan Cho

List of Publications by Year in descending order

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Version: 2024-02-01

171
papers

6,393
citations

61984

43
h-index

91884

69
g-index

174
all docs

174
docs citations

174
times ranked

7140
citing authors

#	ARTICLE	IF	CITATIONS
1	Emerging applications of bacteria as antitumor agents. <i>Seminars in Cancer Biology</i> , 2022, 86, 1014-1025.	9.6	37
2	Valorization of C1 gases to value-added chemicals using acetogenic biocatalysts. <i>Chemical Engineering Journal</i> , 2022, 428, 131325.	12.7	42
3	proChIPdb: a chromatin immunoprecipitation database for prokaryotic organisms. <i>Nucleic Acids Research</i> , 2022, 50, D1077-D1084.	14.5	9
4	Adaptive laboratory evolution of <i>Escherichia coli</i> W enhances gamma-aminobutyric acid production using glycerol as the carbon source. <i>Metabolic Engineering</i> , 2022, 69, 59-72.	7.0	12
5	Genome-scale analysis of genetic regulatory elements in <i>Streptomyces avermitilis</i> MA-4680 using transcript boundary information. <i>BMC Genomics</i> , 2022, 23, 68.	2.8	2
6	Systems Biology on Acetogenic Bacteria for Utilizing C1 Feedstocks. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2022, , 1.	1.1	0
7	System-Level Analysis of Transcriptional and Translational Regulatory Elements in <i>Streptomyces griseus</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 844200.	4.1	1
8	Synthetic 3' UTR valves for optimal metabolic flux control in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2022, 50, 4171-4186.	14.5	3
9	Poly-3-hydroxybutyrate production in acetate minimal medium using engineered <i>Methylobacterium extorquens</i> AM1. <i>Bioresource Technology</i> , 2022, 353, 127127.	9.6	13
10	Functional role of a novel algicidal compound produced by <i>Pseudoruegeria</i> sp. M32A2M on the harmful algae <i>Alexandrium catenella</i> . <i>Chemosphere</i> , 2022, 300, 134535.	8.2	14
11	Development of highly characterized genetic bioparts for efficient gene expression in CO ₂ -fixing <i>Eubacterium limosum</i> . <i>Metabolic Engineering</i> , 2022, 72, 215-226.	7.0	7
12	Comprehensive 16S rRNA and metagenomic data from the gut microbiome of aging and rejuvenation mouse models. <i>Scientific Data</i> , 2022, 9, 197.	5.3	1
13	Engineering Acetogenic Bacteria for Efficient One-Carbon Utilization. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	16
14	A genome-scale metabolic model of <i>Cupriavidus necator</i> H16 integrated with TraDIS and transcriptomic data reveals metabolic insights for biotechnological applications. <i>PLoS Computational Biology</i> , 2022, 18, e1010106.	3.2	10
15	Comparative genomic analysis of <i>Streptomyces rapamycinicus</i> NRRL 5491 and its mutant overproducing rapamycin. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
16	Development of CO gas conversion system using high CO tolerance biocatalyst. <i>Chemical Engineering Journal</i> , 2022, 449, 137678.	12.7	8
17	Photosynthetic pigment production and metabolic and lipidomic alterations in the marine cyanobacteria <i>Synechocystis</i> sp. PCC 7338 under various salinity conditions. <i>Journal of Applied Phycology</i> , 2021, 33, 197-209.	2.8	16
18	Biochemical characterization and molecular docking analysis of novel esterases from <i>Sphingobium chungbukense</i> DJ77. <i>International Journal of Biological Macromolecules</i> , 2021, 168, 403-411.	7.5	7

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19	Mini review: Enzyme-based DNA synthesis and selective retrieval for data storage. Computational and Structural Biotechnology Journal, 2021, 19, 2468-2476.	4.1	9
20	Acetogenic bacteria utilize light-driven electrons as an energy source for autotrophic growth. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	47
21	Transcriptome and translome of CO2 fixing acetogens under heterotrophic and autotrophic conditions. Scientific Data, 2021, 8, 51.	5.3	4
22	Future trends in synthetic biology in Asia. Genetics & Genomics Next, 2021, 2, e10038.	1.5	10
23	Multi-Omic Analyses Reveal Habitat Adaptation of Marine Cyanobacterium Synechocystis sp. PCC 7338. Frontiers in Microbiology, 2021, 12, 667450.	3.5	6
24	Elucidating the Regulatory Elements for Transcription Termination and Posttranscriptional Processing in the Streptomyces clavuligerus Genome. MSystems, 2021, 6, .	3.8	6
25	Unraveling the functions of uncharacterized transcription factors in <i>Escherichia coli</i> using ChIP-exo. Nucleic Acids Research, 2021, 49, 9696-9710.	14.5	30
26	Genome-Scale Analysis of Acetobacterium woodii Identifies Translational Regulation of Acetogenesis. MSystems, 2021, 6, e0069621.	3.8	8
27	RiboRid: A low cost, advanced, and ultra-efficient method to remove ribosomal RNA for bacterial transcriptomics. PLoS Genetics, 2021, 17, e1009821.	3.5	16
28	Elucidation of the Algicidal Mechanism of the Marine Bacterium Pseudoruegeria sp. M32A2M Against the Harmful Alga Alexandrium catenella Based on Time-Course Transcriptome Analysis. Frontiers in Marine Science, 2021, 8, .	2.5	4
29	Microbial production of nematicidal agents for controlling plant-parasitic nematodes. Process Biochemistry, 2021, 108, 69-79.	3.7	13
30	Improved bio-hydrogen production by overexpression of glucose-6-phosphate dehydrogenase and FeFe hydrogenase in Clostridium acetobutylicum. International Journal of Hydrogen Energy, 2021, 46, 36687-36695.	7.1	16
31	Integrating strategies for sustainable conversion of waste biomass into dark-fermentative hydrogen and value-added products. Renewable and Sustainable Energy Reviews, 2021, 150, 111491.	16.4	91
32	Systems and synthetic biology to elucidate secondary metabolite biosynthetic gene clusters encoded in <i>Streptomyces</i> genomes. Natural Product Reports, 2021, 38, 1330-1361.	10.3	35
33	A multifaceted cellular damage repair and prevention pathway promotes high-level tolerance to β -lactam antibiotics. EMBO Reports, 2021, 22, e51790.	4.5	26
34	Discovery of novel secondary metabolites encoded in actinomycete genomes through coculture. Journal of Industrial Microbiology and Biotechnology, 2021, 48, .	3.0	29
35	Engineering Bacteroides thetaiotaomicron to produce non-native butyrate based on a genome-scale metabolic model-guided design. Metabolic Engineering, 2021, 68, 174-186.	7.0	13
36	Re-classification of Streptomyces venezuelae strains and mining secondary metabolite biosynthetic gene clusters. IScience, 2021, 24, 103410.	4.1	2

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37	Streptomyces as Microbial Chassis for Heterologous Protein Expression. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 804295.	4.1	12
38	Ageing and rejuvenation models reveal changes in key microbial communities associated with healthy ageing. <i>Microbiome</i> , 2021, 9, 240.	11.1	49
39	Different Regulatory Modes of <i>Synechocystis</i> sp. PCC 6803 in Response to Photosynthesis Inhibitory Conditions. <i>MSystems</i> , 2021, 6, e0094321.	3.8	7
40	The Bitome: digitized genomic features reveal fundamental genome organization. <i>Nucleic Acids Research</i> , 2020, 48, 10157-10163.	14.5	11
41	Synthetic Biology Approaches in the Development of Engineered Therapeutic Microbes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8744.	4.1	23
42	System-level understanding of gene expression and regulation for engineering secondary metabolite production in <i>Streptomyces</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2020, 47, 739-752.	3.0	10
43	Synthetic Biology on Acetogenic Bacteria for Highly Efficient Conversion of C1 Gases to Biochemicals. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7639.	4.1	35
44	Docking Simulation and Sandwich Assay for Aptamer-Based Botulinum Neurotoxin Type C Detection. <i>Biosensors</i> , 2020, 10, 98.	4.7	9
45	A short review of the pinewood nematode, <i>Bursaphelenchus xylophilus</i> . <i>Toxicology and Environmental Health Sciences</i> , 2020, 12, 297-304.	2.1	47
46	Comparative Proteomic Profiling of Marine and Freshwater <i>Synechocystis</i> Strains Using Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Marine Science and Engineering</i> , 2020, 8, 790.	2.6	4
47	Comparative Primary Metabolic and Lipidomic Profiling of Freshwater and Marine <i>Synechocystis</i> Strains Using by GC-MS and NanoESI-MS Analyses. <i>Biotechnology and Bioprocess Engineering</i> , 2020, 25, 308-319.	2.6	11
48	Transcriptome and translome profiles of <i>Streptomyces</i> species in different growth phases. <i>Scientific Data</i> , 2020, 7, 138.	5.3	18
49	Aptamer-linked immobilized sorbent assay for detecting GMO marker, phosphinothricin acetyltransferase (PAT). <i>Molecular and Cellular Toxicology</i> , 2020, 16, 253-261.	1.7	7
50	Mini review: Genome mining approaches for the identification of secondary metabolite biosynthetic gene clusters in <i>Streptomyces</i> . <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1548-1556.	4.1	106
51	3D Printed Bioresponsive Devices with Selective Permeability Inspired by Eggshell Membrane for Effective Biochemical Conversion. <i>ACS Applied Materials & Interfaces</i> , 2020, 12, 30112-30119.	8.0	5
52	Repurposing Modular Polyketide Synthases and Non-ribosomal Peptide Synthetases for Novel Chemical Biosynthesis. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 87.	3.5	29
53	Comparative Genomics Determines Strain-Dependent Secondary Metabolite Production in <i>Streptomyces venezuelae</i> Strains. <i>Biomolecules</i> , 2020, 10, 864.	4.0	9
54	Removal of Trans-2-nonenal Using Hen Egg White Lysosomal-Related Enzymes. <i>Molecular Biotechnology</i> , 2020, 62, 380-386.	2.4	1

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55	Thirty complete <i>Streptomyces</i> genome sequences for mining novel secondary metabolite biosynthetic gene clusters. <i>Scientific Data</i> , 2020, 7, 55.	5.3	67
56	STATR: A simple analysis pipeline of Ribo-Seq in bacteria. <i>Journal of Microbiology</i> , 2020, 58, 217-226.	2.8	9
57	Iron competition triggers antibiotic biosynthesis in <i>Streptomyces coelicolor</i> during coculture with <i>Myxococcus xanthus</i> . <i>ISME Journal</i> , 2020, 14, 1111-1124.	9.8	60
58	Engineering Biology to Construct Microbial Chassis for the Production of Difficult-to-Express Proteins. <i>International Journal of Molecular Sciences</i> , 2020, 21, 990.	4.1	25
59	Adaptive Laboratory Evolution of <i>Eubacterium limosum</i> ATCC 8486 on Carbon Monoxide. <i>Frontiers in Microbiology</i> , 2020, 11, 402.	3.5	44
60	Functional cooperation of the glycine synthase-reductase and Wood-Werkman pathways for autotrophic growth of <i>Clostridium drakei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7516-7523.	7.1	88
61	Wax-printed well pads and colorimetric LAMP detection of <i>ApxIA</i> toxin gene. <i>Molecular and Cellular Toxicology</i> , 2020, 16, 263-270.	1.7	3
62	Genome-scale determination of 5' and 3' boundaries of RNA transcripts in <i>Streptomyces</i> genomes. <i>Scientific Data</i> , 2020, 7, 436.	5.3	6
63	Construction of Minimal Genomes and Synthetic Cells. , 2020, , 45-67.		0
64	Tailoring the <i>Saccharomyces cerevisiae</i> endoplasmic reticulum for functional assembly of terpene synthesis pathway. <i>Metabolic Engineering</i> , 2019, 56, 50-59.	7.0	105
65	Genome Engineering of <i>Eubacterium limosum</i> Using Expanded Genetic Tools and the CRISPR-Cas9 System. <i>ACS Synthetic Biology</i> , 2019, 8, 2059-2068.	3.8	38
66	An automated high-throughput sample preparation method using double-filtration for serum metabolite LC-MS analysis. <i>Analytical Methods</i> , 2019, 11, 4060-4065.	2.7	8
67	mRNA Engineering for the Efficient Chaperone-Mediated Co-Translational Folding of Recombinant Proteins in <i>Escherichia coli</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 3163.	4.1	4
68	The Transcription Unit Architecture of <i>Streptomyces lividans</i> TK24. <i>Frontiers in Microbiology</i> , 2019, 10, 2074.	3.5	25
69	Inactivation of a Mismatch-Repair System Diversifies Genotypic Landscape of <i>Escherichia coli</i> During Adaptive Laboratory Evolution. <i>Frontiers in Microbiology</i> , 2019, 10, 1845.	3.5	17
70	Reactivation maintains LTP at CS inputs to the lateral amygdala enabling selective fear memory persistence. <i>IBRO Reports</i> , 2019, 6, S311-S312.	0.3	0
71	Primary transcriptome and translome analysis determines transcriptional and translational regulatory elements encoded in the <i>Streptomyces clavuligerus</i> genome. <i>Nucleic Acids Research</i> , 2019, 47, 6114-6129.	14.5	49
72	Improved production of clavulanic acid by reverse engineering and overexpression of the regulatory genes in an industrial <i>Streptomyces clavuligerus</i> strain. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 1205-1215.	3.0	10

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73	Elucidation of <i>Akkermansia muciniphila</i> Probiotic Traits Driven by Mucin Depletion. <i>Frontiers in Microbiology</i> , 2019, 10, 1137.	3.5	85
74	Hierarchical Macroporous Particles for Efficient Whole-Cell Immobilization: Application in Bioconversion of Greenhouse Gases to Methanol. <i>ACS Applied Materials & Interfaces</i> , 2019, 11, 18968-18977.	8.0	57
75	Adaptive laboratory evolution of a genome-reduced <i>Escherichia coli</i> . <i>Nature Communications</i> , 2019, 10, 935.	12.8	114
76	Synthetic Biology Tools for Novel Secondary Metabolite Discovery in <i>Streptomyces</i> . <i>Journal of Microbiology and Biotechnology</i> , 2019, 29, 667-686.	2.1	64
77	Elucidation of the bacterial communities associated with the harmful microalgae <i>Alexandrium tamarense</i> and <i>Cochlodinium polykrikoides</i> using nanopore sequencing. <i>Scientific Reports</i> , 2018, 8, 5323.	3.3	43
78	Systems assessment of transcriptional regulation on central carbon metabolism by Cra and CRP. <i>Nucleic Acids Research</i> , 2018, 46, 2901-2917.	14.5	62
79	Genome-scale analysis of Methicillin-resistant <i>Staphylococcus aureus</i> USA300 reveals a tradeoff between pathogenesis and drug resistance. <i>Scientific Reports</i> , 2018, 8, 2215.	3.3	28
80	Fabrication of three-dimensional porous carbon scaffolds with tunable pore sizes for effective cell confinement. <i>Carbon</i> , 2018, 130, 814-821.	10.3	12
81	Peptide Transporter CstA Imports Pyruvate in <i>Escherichia coli</i> K-12. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	21
82	Repeated batch methanol production from a simulated biogas mixture using immobilized <i>Methylocystis bryophila</i> . <i>Energy</i> , 2018, 145, 477-485.	8.8	42
83	Synthesis of cross-linked protein-metal hybrid nanoflowers and its application in repeated batch decolorization of synthetic dyes. <i>Journal of Hazardous Materials</i> , 2018, 347, 442-450.	12.4	145
84	High-Level dCas9 Expression Induces Abnormal Cell Morphology in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 1085-1094.	3.8	147
85	Genome-scale analysis of syngas fermenting acetogenic bacteria reveals the translational regulation for its autotrophic growth. <i>BMC Genomics</i> , 2018, 19, 837.	2.8	36
86	Characterizing posttranslational modifications in prokaryotic metabolism using a multiscale workflow. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11096-11101.	7.1	44
87	Genome-scale analysis of <i>Acetobacterium bakii</i> reveals the cold adaptation of psychrotolerant acetogens by post-transcriptional regulation. <i>Rna</i> , 2018, 24, 1839-1855.	3.5	10
88	Insights into Cell-Free Conversion of CO ₂ to Chemicals by a Multienzyme Cascade Reaction. <i>ACS Catalysis</i> , 2018, 8, 11085-11093.	11.2	87
89	Selection of <i>Escherichia coli</i> Glutamate Decarboxylase Active at Neutral pH from a Focused Library. <i>Biotechnology and Bioprocess Engineering</i> , 2018, 23, 473-479.	2.6	6
90	Phycobiliproteins Production Enhancement and Lipidomic Alteration by Titanium Dioxide Nanoparticles in <i>Synechocystis</i> sp. PCC 6803 Culture. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 8522-8529.	5.2	9

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91	Applications of CRISPR/Cas System to Bacterial Metabolic Engineering. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1089.	4.1	108
92	Targeted Genome Editing Using DNA-Free RNA-Guided Cas9 Ribonucleoprotein for CHO Cell Engineering. <i>Methods in Molecular Biology</i> , 2018, 1772, 151-169.	0.9	7
93	Systematic discovery of uncharacterized transcription factors in <i>Escherichia coli</i> K-12 MG1655. <i>Nucleic Acids Research</i> , 2018, 46, 10682-10696.	14.5	65
94	Genome-wide primary transcriptome analysis of H ₂ -producing archaeon <i>Thermococcus onnurineus</i> NA1. <i>Scientific Reports</i> , 2017, 7, 43044.	3.3	32
95	Elucidation of bacterial translation regulatory networks. <i>Current Opinion in Systems Biology</i> , 2017, 2, 84-90.	2.6	5
96	Revealing genome-scale transcriptional regulatory landscape of OmpR highlights its expanded regulatory roles under osmotic stress in <i>Escherichia coli</i> K-12 MG1655. <i>Scientific Reports</i> , 2017, 7, 2181.	3.3	35
97	Enhanced production of fatty acids in three strains of microalgae using a combination of nitrogen starvation and chemical inhibitors of carbohydrate synthesis. <i>Biotechnology and Bioprocess Engineering</i> , 2017, 22, 60-67.	2.6	14
98	Genome analysis of a hyper acetone- <i>n</i> -butanol- <i>n</i> -ethanol (ABE) producing <i>Clostridium acetobutylicum</i> BKM19. <i>Biotechnology Journal</i> , 2017, 12, 1600457.	3.5	9
99	A Novel Approach for Gene Expression Optimization through Native Promoter and 5' UTR Combinations Based on RNA-seq, Ribo-seq, and TSS-seq of <i>Streptomyces coelicolor</i> . <i>ACS Synthetic Biology</i> , 2017, 6, 555-565.	3.8	29
100	Determination of the Genome and Primary Transcriptome of Syngas Fermenting <i>Eubacterium limosum</i> ATCC 8486. <i>Scientific Reports</i> , 2017, 7, 13694.	3.3	44
101	A Transcriptome Approach Toward Understanding Fruit Softening in Persimmon. <i>Frontiers in Plant Science</i> , 2017, 8, 1556.	3.6	16
102	Analysis of the Core Genome and Pan-Genome of Autotrophic Acetogenic Bacteria. <i>Frontiers in Microbiology</i> , 2016, 7, 1531.	3.5	68
103	Construction of a minimal genome as a chassis for synthetic biology. <i>Essays in Biochemistry</i> , 2016, 60, 337-346.	4.7	23
104	The dynamic transcriptional and translational landscape of the model antibiotic producer <i>Streptomyces coelicolor</i> A3(2). <i>Nature Communications</i> , 2016, 7, 11605.	12.8	201
105	Effect of Ethephon as an Ethylene-Releasing Compound on the Metabolic Profile of <i>Chlorella vulgaris</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 4807-4816.	5.2	37
106	Minimal genome: Worthwhile or worthless efforts toward being smaller?. <i>Biotechnology Journal</i> , 2016, 11, 199-211.	3.5	45
107	Genome-wide transcriptome analysis revealed organelle specific responses to temperature variations in algae. <i>Scientific Reports</i> , 2016, 6, 37770.	3.3	38
108	Analysis of the mouse gut microbiome using full-length 16S rRNA amplicon sequencing. <i>Scientific Reports</i> , 2016, 6, 29681.	3.3	178

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109	Functional elucidation of the non-coding RNAs of <i>Kluyveromyces marxianus</i> in the exponential growth phase. <i>BMC Genomics</i> , 2016, 17, 154.	2.8	2
110	Targeted Gene Deletion Using DNA-Free RNA-Guided Cas9 Nuclease Accelerates Adaptation of CHO Cells to Suspension Culture. <i>ACS Synthetic Biology</i> , 2016, 5, 1211-1219.	3.8	30
111	Effects of the timing of a culture temperature reduction on the comprehensive metabolite profiles of <i>Chlorella vulgaris</i> . <i>Journal of Applied Phycology</i> , 2016, 28, 2641-2650.	2.8	10
112	DNA-Assisted Exfoliation of Tungsten Dichalcogenides and Their Antibacterial Effect. <i>ACS Applied Materials & Interfaces</i> , 2016, 8, 1943-1950.	8.0	76
113	Reconstruction of Acetogenesis Pathway Using Short-Read Sequencing of <i>Clostridium aceticum</i> Genome. <i>Journal of Nanoscience and Nanotechnology</i> , 2015, 15, 3852-3861.	0.9	2
114	Draft Genome Sequence of <i>Acetobacterium bakii</i> DSM 8239, a Potential Psychrophilic Chemical Producer through Syngas Fermentation. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
115	Rational Protein Engineering Guided by Deep Mutational Scanning. <i>International Journal of Molecular Sciences</i> , 2015, 16, 23094-23110.	4.1	18
116	Determination of single nucleotide variants in <i>Escherichia coli</i> DH5 α by using short-read sequencing. <i>FEMS Microbiology Letters</i> , 2015, 362, .	1.8	17
117	Draft Genome Sequence of <i>Clostridium aceticum</i> DSM 1496, a Potential Butanol Producer through Syngas Fermentation. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
118	Draft Genome Sequence of Chemolithoautotrophic Acetogenic Butanol-Producing Eubacterium <i>limosum</i> ATCC 8486. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
119	Comparative Lipidomic Profiling of Two <i>Dunaliella tertiolecta</i> Strains with Different Growth Temperatures under Nitrate-Deficient Conditions. <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 880-887.	5.2	9
120	Elucidation of the growth delimitation of <i>Dunaliella tertiolecta</i> under nitrogen stress by integrating transcriptome and peptidome analysis. <i>Bioresource Technology</i> , 2015, 194, 57-66.	9.6	51
121	Genome-scale analysis reveals a role for NdgR in the thiol oxidative stress response in <i>Streptomyces coelicolor</i> . <i>BMC Genomics</i> , 2015, 16, 116.	2.8	19
122	The architecture of ArgR-DNA complexes at the genome-scale in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2015, 43, 3079-3088.	14.5	29
123	Efficient CRISPR/Cas9-mediated multiplex genome editing in CHO cells via high-level sgRNA-Cas9 complex. <i>Biotechnology and Bioprocess Engineering</i> , 2015, 20, 825-833.	2.6	14
124	Comparative Genomics Reveals the Core and Accessory Genomes of <i>Streptomyces</i> Species. <i>Journal of Microbiology and Biotechnology</i> , 2015, 25, 1599-1605.	2.1	72
125	Exploring the Functional Residues in a Flavin-Binding Fluorescent Protein Using Deep Mutational Scanning. <i>PLoS ONE</i> , 2014, 9, e97817.	2.5	13
126	Determining the Control Circuitry of Redox Metabolism at the Genome-Scale. <i>PLoS Genetics</i> , 2014, 10, e1004264.	3.5	67

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127	Draft Genome Sequence of Acid-Tolerant <i>Clostridium drakei</i> SL1 ^T , a Potential Chemical Producer through Syngas Fermentation. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
128	Draft Genome Sequence of <i>Clostridium scatologenes</i> ATCC 25775, a Chemolithoautotrophic Acetogenic Bacterium Producing 3-Methylindole and 4-Methylphenol. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
129	Proteomic analysis of <i>Synechocystis</i> sp. PCC6803 responses to low-temperature and high light conditions. <i>Biotechnology and Bioprocess Engineering</i> , 2014, 19, 629-640.	2.6	5
130	Genome-scale reconstruction of the sigma factor network in <i>Escherichia coli</i> : topology and functional states. <i>BMC Biology</i> , 2014, 12, 4.	3.8	111
131	Fatty acids and global metabolites profiling of <i>Dunaliella tertiolecta</i> by shifting culture conditions to nitrate deficiency and high light at different growth phases. <i>Process Biochemistry</i> , 2014, 49, 996-1004.	3.7	39
132	In vitro selection of sialic acid specific RNA aptamer and its application to the rapid sensing of sialic acid modified sugars. <i>Biotechnology and Bioengineering</i> , 2013, 110, 905-913.	3.3	27
133	Emerging Tools for Synthetic Genome Design. <i>Molecules and Cells</i> , 2013, 35, 359-370.	2.6	17
134	Effects of Light Intensity and Nitrogen Starvation on Glycerolipid, Glycerophospholipid, and Carotenoid Composition in <i>Dunaliella tertiolecta</i> Culture. <i>PLoS ONE</i> , 2013, 8, e72415.	2.5	53
135	Current Challenges in Bacterial Transcriptomics. <i>Genomics and Informatics</i> , 2013, 11, 76.	0.8	15
136	Comparative Analysis of Regulatory Elements between <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> by Genome-Wide Transcription Start Site Profiling. <i>PLoS Genetics</i> , 2012, 8, e1002867.	3.5	137
137	Elucidation of bacterial genome complexity using next-generation sequencing. <i>Biotechnology and Bioprocess Engineering</i> , 2012, 17, 887-899.	2.6	2
138	Characterization, stability, and pharmacokinetics of sibutramine/ β -cyclodextrin inclusion complex. <i>Journal of Industrial and Engineering Chemistry</i> , 2012, 18, 1412-1417.	5.8	19
139	A versatile PCR-based tandem epitope tagging system for <i>Streptomyces coelicolor</i> genome. <i>Biochemical and Biophysical Research Communications</i> , 2012, 424, 22-27.	2.1	4
140	Multiple-omic data analysis of <i>Klebsiella pneumoniae</i> MGH 78578 reveals its transcriptional architecture and regulatory features. <i>BMC Genomics</i> , 2012, 13, 679.	2.8	34
141	Deciphering the transcriptional regulatory logic of amino acid metabolism. <i>Nature Chemical Biology</i> , 2012, 8, 65-71.	8.0	83
142	Deciphering the regulatory codes in bacterial genomes. <i>Biotechnology Journal</i> , 2011, 6, 1052-1063.	3.5	9
143	Sensitive and accurate identification of protein-DNA binding events in ChIP-chip assays using higher order derivative analysis. <i>Nucleic Acids Research</i> , 2011, 39, 1656-1665.	14.5	5
144	The PurR regulon in <i>Escherichia coli</i> K-12 MG1655. <i>Nucleic Acids Research</i> , 2011, 39, 6456-6464.	14.5	98

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