

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	The transcription unit architecture of the <i>Escherichia coli</i> genome. <i>Nature Biotechnology</i> , 2009, 27, 1043-1049.	17.5	251
2	RNA polymerase mutants found through adaptive evolution reprogram <i>Escherichia coli</i> for optimal growth in minimal media. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20500-20505.	7.1	219
3	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
4	Analysis of the mouse gut microbiome using full-length 16S rRNA amplicon sequencing. <i>Scientific Reports</i> , 2016, 6, 29681.	3.3	178
5	Genome-scale reconstruction of the Lrp regulatory network in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 19462-19467.	7.1	169
6	Genome-wide analysis of Fis binding in <i>Escherichia coli</i> indicates a causative role for A-/AT-tracts. <i>Genome Research</i> , 2008, 18, 900-910.	5.5	164
7	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
8	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
9	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
10	Revisit of aminotransferase in the genomic era and its application to biocatalysis. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2005, 37, 47-55.	1.8	122
11	Adaptive laboratory evolution of a genome-reduced <i>Escherichia coli</i> . <i>Nature Communications</i> , 2019, 10, 935.	12.8	114
12	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
13	Applications of CRISPR/Cas System to Bacterial Metabolic Engineering. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1089.	4.1	108
14	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
15	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
16	The PurR regulon in <i>Escherichia coli</i> K-12 MG1655. <i>Nucleic Acids Research</i> , 2011, 39, 6456-6464.	14.5	98
17	α -Amino Acid:Pyruvate Transaminase from <i>Alcaligenes denitrificans</i> Y2k-2: a New Catalyst for Kinetic Resolution of l^2 -Amino Acids and Amines. <i>Applied and Environmental Microbiology</i> , 2004, 70, 2529-2534.	3.1	92
18	Integrating strategies for sustainable conversion of waste biomass into dark-fermentative hydrogen and value-added products. <i>Renewable and Sustainable Energy Reviews</i> , 2021, 150, 111491.	16.4	91

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19	Functional cooperation of the glycine synthase-reductase and Wood-Werkman pathways for autotrophic growth of <i>Clostridium drakei</i> . Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 7516-7523.	7.1	88
20	Redesigning the substrate specificity of α -amino transferase for the kinetic resolution of aliphatic chiral amines. Biotechnology and Bioengineering, 2008, 99, 275-284.	3.3	87
21	Insights into Cell-Free Conversion of CO ₂ to Chemicals by a Multienzyme Cascade Reaction. ACS Catalysis, 2018, 8, 11085-11093.	11.2	87
22	Elucidation of Akkermansia muciniphila Probiotic Traits Driven by Mucin Depletion. Frontiers in Microbiology, 2019, 10, 1137.	3.5	85
23	Deciphering the transcriptional regulatory logic of amino acid metabolism. Nature Chemical Biology, 2012, 8, 65-71.	8.0	83
24	DNA-Assisted Exfoliation of Tungsten Dichalcogenides and Their Antibacterial Effect. ACS Applied Materials & Interfaces, 2016, 8, 1943-1950.	8.0	76
25	Kinetic resolution of (R,S)-sec-butylamine using omega-transaminase from <i>Vibrio fluvialis</i> JS17 under reduced pressure. Biotechnology and Bioengineering, 2004, 87, 772-778.	3.3	75
26	Structural and operational complexity of the <i>Geobacter sulfurreducens</i> genome. Genome Research, 2010, 20, 1304-1311.	5.5	75
27	Comparative Genomics Reveals the Core and Accessory Genomes of Streptomyces Species. Journal of Microbiology and Biotechnology, 2015, 25, 1599-1605.	2.1	72
28	Cloning and Characterization of a Novel β -Transaminase from Mesorhizobium sp. Strain LUK: a New Biocatalyst for the Synthesis of Enantiomerically Pure β -Amino Acids. Applied and Environmental Microbiology, 2007, 73, 1772-1782.	3.1	70
29	Asymmetric synthesis of L-homophenylalanine by equilibrium-shift using recombinant aromatic L-amino acid transaminase. Biotechnology and Bioengineering, 2003, 83, 226-234.	3.3	68
30	Analysis of the Core Genome and Pan-Genome of Autotrophic Acetogenic Bacteria. Frontiers in Microbiology, 2016, 7, 1531.	3.5	68
31	Determining the Control Circuitry of Redox Metabolism at the Genome-Scale. PLoS Genetics, 2014, 10, e1004264.	3.5	67
32	Thirty complete Streptomyces genome sequences for mining novel secondary metabolite biosynthetic gene clusters. Scientific Data, 2020, 7, 55.	5.3	67
33	Systematic discovery of uncharacterized transcription factors in Escherichia coli K-12 MG1655. Nucleic Acids Research, 2018, 46, 10682-10696.	14.5	65
34	Synthetic Biology Tools for Novel Secondary Metabolite Discovery in Streptomyces. Journal of Microbiology and Biotechnology, 2019, 29, 667-686.	2.1	64
35	Systems assessment of transcriptional regulation on central carbon metabolism by Cra and CRP. Nucleic Acids Research, 2018, 46, 2901-2917.	14.5	62
36	Iron competition triggers antibiotic biosynthesis in <i>Streptomyces coelicolor</i> during coculture with <i>Myxococcus xanthus</i> . ISME Journal, 2020, 14, 1111-1124.	9.8	60

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37	Transcriptional regulation of the fad regulon genes of <i>Escherichia coli</i> by ArcA. <i>Microbiology (United Kingdom)</i> , 2006, 152, 2207-2219.	1.8	57
38	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
39	Simultaneous synthesis of 2-phenylethanol and L-homophenylalanine using aromatic transaminase with yeast Ehrlich pathway. <i>Biotechnology and Bioengineering</i> , 2009, 102, 1323-1329.	3.3	53
40	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
41	PCR-based tandem epitope tagging system for <i>Escherichia coli</i> genome engineering. <i>BioTechniques</i> , 2006, 40, 67-72.	1.8	52
42	Gene Expression Profiling and the Use of Genome-Scale In Silico Models of <i>Escherichia coli</i> for Analysis: Providing Context for Content. <i>Journal of Bacteriology</i> , 2009, 191, 3437-3444.	2.2	51
43	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
44	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
45	Ageing and rejuvenation models reveal changes in key microbial communities associated with healthy ageing. <i>Microbiome</i> , 2021, 9, 240.	11.1	49
46	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
47	Acetogenic bacteria utilize light-driven electrons as an energy source for autotrophic growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	47
48	Minimal genome: Worthwhile or worthless efforts toward being smaller?. <i>Biotechnology Journal</i> , 2016, 11, 199-211.	3.5	45
49	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
50	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
51	Adaptive Laboratory Evolution of <i>Eubacterium limosum</i> ATCC 8486 on Carbon Monoxide. <i>Frontiers in Microbiology</i> , 2020, 11, 402.	3.5	44
52	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
53	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
54	Valorization of C1 gases to value-added chemicals using acetogenic biocatalysts. <i>Chemical Engineering Journal</i> , 2022, 428, 131325.	12.7	42

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55	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
56	Simultaneous synthesis of enantiomerically pure (S)-amino acids and (R)-amines using coupled transaminase reactions. <i>Biotechnology and Bioengineering</i> , 2003, 81, 783-789.	3.3	38
57	Genome-wide transcriptome analysis revealed organelle specific responses to temperature variations in algae. <i>Scientific Reports</i> , 2016, 6, 37770.	3.3	38
58	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
59	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
60	Emerging applications of bacteria as antitumor agents. <i>Seminars in Cancer Biology</i> , 2022, 86, 1014-1025.	9.6	37
61	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
62	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
63	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
64	Systems and synthetic biology to elucidate secondary metabolite biosynthetic gene clusters encoded in <i>Streptomyces</i> genomes. <i>Natural Product Reports</i> , 2021, 38, 1330-1361.	10.3	35
65	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
66	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
67	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
68	Unraveling the functions of uncharacterized transcription factors in <i>Escherichia coli</i> using ChIP-exo. <i>Nucleic Acids Research</i> , 2021, 49, 9696-9710.	14.5	30
69	Microbial regulatory and metabolic networks. <i>Current Opinion in Biotechnology</i> , 2007, 18, 360-364.	6.6	29
70	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
71	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
72	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

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73	Discovery of novel secondary metabolites encoded in actinomycete genomes through coculture. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2021, 48, .	3.0	29
74	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
75	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
76	A multifaceted cellular damage repair and prevention pathway promotes high-level tolerance to β -lactam antibiotics. <i>EMBO Reports</i> , 2021, 22, e51790.	4.5	26
77	The Transcription Unit Architecture of <i>Streptomyces lividans</i> TK24. <i>Frontiers in Microbiology</i> , 2019, 10, 2074.	3.5	25
78	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
79	Construction of a minimal genome as a chassis for synthetic biology. <i>Essays in Biochemistry</i> , 2016, 60, 337-346.	4.7	23
80	Synthetic Biology Approaches in the Development of Engineered Therapeutic Microbes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8744.	4.1	23
81	Simultaneous synthesis of enantiomerically pure (S)-amino acids and (R)-amines using β -amino transferase coupling reactions with two-liquid phase reaction system. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2003, 26, 273-285.	1.8	22
82	Draft Genome Sequence of Chemolithoautotrophic Acetogenic Butanol-Producing Eubacterium <i>limosum</i> ATCC 8486. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
83	Peptide Transporter CstA Imports Pyruvate in <i>Escherichia coli</i> K-12. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	21
84	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
85	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
86	Enzymatic resolution for the preparation of enantiomerically enriched D-?-heterocyclic alanine derivatives using <i>Escherichia coli</i> aromatic L-amino acid transaminase. <i>Biotechnology and Bioengineering</i> , 2004, 88, 512-519.	3.3	18
87	Engineering aromatic L-amino acid transaminase for the asymmetric synthesis of constrained analogs of L-phenylalanine. <i>Biotechnology and Bioengineering</i> , 2006, 94, 842-850.	3.3	18
88	Rational Protein Engineering Guided by Deep Mutational Scanning. <i>International Journal of Molecular Sciences</i> , 2015, 16, 23094-23110.	4.1	18
89	Transcriptome and translome profiles of <i>Streptomyces</i> species in different growth phases. <i>Scientific Data</i> , 2020, 7, 138.	5.3	18
90	Emerging Tools for Synthetic Genome Design. <i>Molecules and Cells</i> , 2013, 35, 359-370.	2.6	17

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91	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
92	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
93	A Transcriptome Approach Toward Understanding Fruit Softening in Persimmon. <i>Frontiers in Plant Science</i> , 2017, 8, 1556.	3.6	16
94	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
95	RiboRid: A low cost, advanced, and ultra-efficient method to remove ribosomal RNA for bacterial transcriptomics. <i>PLoS Genetics</i> , 2021, 17, e1009821.	3.5	16
96	Improved bio-hydrogen production by overexpression of glucose-6-phosphate dehydrogenase and FeFe hydrogenase in <i>Clostridium acetobutylicum</i> . <i>International Journal of Hydrogen Energy</i> , 2021, 46, 36687-36695.	7.1	16
97	Engineering Acetogenic Bacteria for Efficient One-Carbon Utilization. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	16
98	Current Challenges in Bacterial Transcriptomics. <i>Genomics and Informatics</i> , 2013, 11, 76.	0.8	15
99	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
100	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
101	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
102	Exploring the Functional Residues in a Flavin-Binding Fluorescent Protein Using Deep Mutational Scanning. <i>PLoS ONE</i> , 2014, 9, e97817.	2.5	13
103	Microbial production of nematicidal agents for controlling plant-parasitic nematodes. <i>Process Biochemistry</i> , 2021, 108, 69-79.	3.7	13
104	Engineering <i>Bacteroides thetaiotaomicron</i> to produce non-native butyrate based on a genome-scale metabolic model-guided design. <i>Metabolic Engineering</i> , 2021, 68, 174-186.	7.0	13
105	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
106	Asymmetric synthesis of unnatural-amino acids using thermophilic aromatic-amino acid transaminase. <i>Biotechnology and Bioprocess Engineering</i> , 2006, 11, 299-305.	2.6	12
107	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
108	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

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109	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
110	<i>Streptomyces</i> as Microbial Chassis for Heterologous Protein Expression. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 804295.	4.1	12
111	The Bitome: digitized genomic features reveal fundamental genome organization. <i>Nucleic Acids Research</i> , 2020, 48, 10157-10163.	14.5	11
112	Comparative Primary Metabolic and Lipidomic Profiling of Freshwater and Marine <i>Synechocystis</i> Strains Using GC-MS and NanoESI-MS Analyses. <i>Biotechnology and Bioprocess Engineering</i> , 2020, 25, 308-319.	2.6	11
113	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
114	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
115	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
116	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
117	Future trends in synthetic biology in Asia. <i>Genetics & Genomics Next</i> , 2021, 2, e10038.	1.5	10
118	Genomewide Identification of Protein Binding Locations Using Chromatin Immunoprecipitation Coupled with Microarray. <i>Methods in Molecular Biology</i> , 2008, 439, 131-145.	0.9	10
119	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
120	Deciphering the regulatory codes in bacterial genomes. <i>Biotechnology Journal</i> , 2011, 6, 1052-1063.	3.5	9
121	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
122	Genome analysis of a hyper acetone-butanol-ethanol (ABE) producing <i>Clostridium acetobutylicum</i> BKM19. <i>Biotechnology Journal</i> , 2017, 12, 1600457.	3.5	9
123	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
124	Docking Simulation and Sandwich Assay for Aptamer-Based Botulinum Neurotoxin Type C Detection. <i>Biosensors</i> , 2020, 10, 98.	4.7	9
125	Comparative Genomics Determines Strain-Dependent Secondary Metabolite Production in <i>Streptomyces venezuelae</i> Strains. <i>Biomolecules</i> , 2020, 10, 864.	4.0	9
126	STATR: A simple analysis pipeline of Ribo-Seq in bacteria. <i>Journal of Microbiology</i> , 2020, 58, 217-226.	2.8	9

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127	Mini review: Enzyme-based DNA synthesis and selective retrieval for data storage. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2468-2476.	4.1	9
128	proChIPdb: a chromatin immunoprecipitation database for prokaryotic organisms. <i>Nucleic Acids Research</i> , 2022, 50, D1077-D1084.	14.5	9
129	Synthesis of Enantiopure (S)-2-Hydroxyphenylbutanoic Acid Using Novel Hydroxy Acid Dehydrogenase from <i>Enterobacter</i> sp. BK2K. <i>Biotechnology Progress</i> , 2008, 23, 606-612.	2.6	8
130	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
131	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
132	Genome-Scale Analysis of <i>Acetobacterium woodii</i> Identifies Translational Regulation of Acetogenesis. <i>MSystems</i> , 2021, 6, e0069621.	3.8	8
133	Development of CO gas conversion system using high CO tolerance biocatalyst. <i>Chemical Engineering Journal</i> , 2022, 449, 137678.	12.7	8
134	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
135	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
136	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
137	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
138	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
139	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
140	Multi-Omic Analyses Reveal Habitat Adaptation of Marine Cyanobacterium <i>Synechocystis</i> sp. PCC 7338. <i>Frontiers in Microbiology</i> , 2021, 12, 667450.	3.5	6
141	Elucidating the Regulatory Elements for Transcription Termination and Posttranscriptional Processing in the <i>Streptomyces clavuligerus</i> Genome. <i>MSystems</i> , 2021, 6, .	3.8	6
142	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
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