

Boyang Ji

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

2,124
citations

279798

23
h-index

254184

43
g-index

63
all docs

63
docs citations

63
times ranked

2932
citing authors

#	ARTICLE	IF	CITATIONS
1	Global analysis of biosynthetic gene clusters reveals vast potential of secondary metabolite production in <i>Penicillium</i> species. <i>Nature Microbiology</i> , 2017, 2, 17044.	13.3	198
2	Human gut microbiota and healthy aging: Recent developments and future prospective. <i>Nutrition and Healthy Aging</i> , 2016, 4, 3-16.	1.1	150
3	Metabolic engineering for increased lipid accumulation in <i>Yarrowia lipolytica</i> – A Review. <i>Bioresource Technology</i> , 2020, 313, 123707.	9.6	126
4	Modelling approaches for studying the microbiome. <i>Nature Microbiology</i> , 2019, 4, 1253-1267.	13.3	114
5	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021, 600, 500-505.	27.8	102
6	Microbiome and metabolome features of the cardiometabolic disease spectrum. <i>Nature Medicine</i> , 2022, 28, 303-314.	30.7	102
7	From next-generation sequencing to systematic modeling of the gut microbiome. <i>Frontiers in Genetics</i> , 2015, 6, 219.	2.3	99
8	Meta-analysis of the gut microbiota in predicting response to cancer immunotherapy in metastatic melanoma. <i>JCI Insight</i> , 2020, 5, .	5.0	85
9	Serine/Threonine Protein Kinases from Bacteria, Archaea and Eukarya Share a Common Evolutionary Origin Deeply Rooted in the Tree of Life. <i>Journal of Molecular Biology</i> , 2018, 430, 27-32.	4.2	78
10	Compositional and functional differences of the mucosal microbiota along the intestine of healthy individuals. <i>Scientific Reports</i> , 2020, 10, 14977.	3.3	78
11	Comparative genomic analysis provides insights into the evolution and niche adaptation of marine <i>Magnetospira</i> sp. QH strain. <i>Environmental Microbiology</i> , 2014, 16, 525-544.	3.8	66
12	Gut microbiota dysbiosis is associated with malnutrition and reduced plasma amino acid levels: Lessons from genome-scale metabolic modeling. <i>Metabolic Engineering</i> , 2018, 49, 128-142.	7.0	65
13	The chimeric nature of the genomes of marine magnetotactic coccoid-ovoid bacteria defines a novel group of <i>Magnetospira</i> spp. <i>Environmental Microbiology</i> , 2017, 19, 1103-1119.	3.8	60
14	Impairment of gut microbial biotin metabolism and host biotin status in severe obesity: effect of biotin and prebiotic supplementation on improved metabolism. <i>Gut</i> , 2022, 71, 2463-2480.	12.1	53
15	FMN reduces Amyloid- β toxicity in yeast by regulating redox status and cellular metabolism. <i>Nature Communications</i> , 2020, 11, 867.	12.8	50
16	The First Genomic and Proteomic Characterization of a Deep-Sea Sulfate Reducer: Insights into the Piezophilic Lifestyle of <i>Desulfovibrio piezophilus</i> . <i>PLoS ONE</i> , 2013, 8, e55130.	2.5	44
17	Metagenomic analysis of bile salt biotransformation in the human gut microbiome. <i>BMC Genomics</i> , 2019, 20, 517.	2.8	44
18	Logical transformation of genome-scale metabolic models for gene level applications and analysis. <i>Bioinformatics</i> , 2015, 31, 2324-2331.	4.1	43

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19	In vitro co-cultures of human gut bacterial species as predicted from co-occurrence network analysis. <i>PLoS ONE</i> , 2018, 13, e0195161.	2.5	41
20	Insights into the pathways of iron- and sulfur-oxidation, and biofilm formation from the chemolithotrophic acidophile <i>Acidithiobacillus ferrivorans</i> CF27. <i>Research in Microbiology</i> , 2014, 165, 753-760.	2.1	38
21	Reconstruction and analysis of a <i>Kluyveromyces marxianus</i> genome-scale metabolic model. <i>BMC Bioinformatics</i> , 2019, 20, 551.	2.6	38
22	Evolution of Bacterial Protein-Tyrosine Kinases and Their Relaxed Specificity Toward Substrates. <i>Genome Biology and Evolution</i> , 2014, 6, 800-817.	2.5	35
23	Interplay of Energetics and ER Stress Exacerbates Alzheimer's Amyloid- β^2 ($A\beta^2$) Toxicity in Yeast. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 232.	2.9	28
24	Engineering yeast metabolism for the discovery and production of polyamines and polyamine analogues. <i>Nature Catalysis</i> , 2021, 4, 498-509.	34.4	26
25	Challenges in modeling the human gut microbiome. <i>Nature Biotechnology</i> , 2018, 36, 682-686.	17.5	25
26	Bayesian genome scale modelling identifies thermal determinants of yeast metabolism. <i>Nature Communications</i> , 2021, 12, 190.	12.8	25
27	Advances in Metabolic Engineering of <i>Saccharomyces cerevisiae</i> for Cocoa Butter Equivalent Production. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 594081.	4.1	23
28	Conversion of Glycerol to 3-Hydroxypropanoic Acid by Genetically Engineered <i>Bacillus subtilis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 638.	3.5	22
29	Identification of genes involved in shea butter biosynthesis from <i>Vitellaria paradoxa</i> fruits through transcriptomics and functional heterologous expression. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3727-3736.	3.6	19
30	Metabolic Alterations in Older Women With Low Bone Mineral Density Supplemented With <i>Lactobacillus reuteri</i> . <i>JBMR Plus</i> , 2021, 5, e10478.	2.7	18
31	CODY enables quantitatively spatiotemporal predictions on in vivo gut microbial variability induced by diet intervention. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	17
32	Yeast metabolic innovations emerged via expanded metabolic network and gene positive selection. <i>Molecular Systems Biology</i> , 2021, 17, e10427.	7.2	17
33	Systems Biology of Gastric Cancer: Perspectives on the Omics-Based Diagnosis and Treatment. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 203.	3.5	16
34	Mapping of Nonhomologous End Joining-Mediated Integration Facilitates Genome-Scale Trackable Mutagenesis in <i>Yarrowia lipolytica</i> . <i>ACS Synthetic Biology</i> , 2022, 11, 216-227.	3.8	14
35	The pan-genome of <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2019, 19, .	2.3	12
36	Comparative Transcriptome Analysis Shows Conserved Metabolic Regulation during Production of Secondary Metabolites in Filamentous Fungi. <i>MSystems</i> , 2019, 4, .	3.8	12

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37	In silico screening for candidate chassis strains of free fatty acid-producing cyanobacteria. BMC Genomics, 2017, 18, 33.	2.8	11
38	Cold adaptation in drylands: transcriptomic insights into cold-stressed <i>Nostoc flagelliforme</i> and characterization of a hypothetical gene with cold and nitrogen stress tolerance. Environmental Microbiology, 2021, 23, 713-727.	3.8	11
39	Complete Genome Sequence of the Piezophilic, Mesophilic, Sulfate-Reducing Bacterium <i>Desulfovibrio hydrothermalis</i> AM13. Genome Announcements, 2013, 1, .	0.8	10
40	New insight into the gut microbiome through metagenomics. Advances in Genomics and Genetics, 0, , 77.	0.8	10
41	Carbohydrate active enzymes are affected by diet transition from milk to solid food in infant gut microbiota. FEMS Microbiology Ecology, 2019, 95, .	2.7	10
42	Performance of Regression Models as a Function of Experiment Noise. Bioinformatics and Biology Insights, 2021, 15, 117793222110203.	2.0	9
43	Suppressors of amyloid- β toxicity improve recombinant protein production in yeast by reducing oxidative stress and tuning cellular metabolism. Metabolic Engineering, 2022, 72, 311-324.	7.0	9
44	Draft Genome Sequence of the Purple Photosynthetic Bacterium <i>Phaeospirillum molischianum</i> DSM120, a Particularly Versatile Bacterium. Journal of Bacteriology, 2012, 194, 3559-3560.	2.2	8
45	Exploring Gut Microbiota in Patients with Colorectal Disease Based on 16S rRNA Gene Amplicon and Shallow Metagenomic Sequencing. Frontiers in Molecular Biosciences, 2021, 8, 703638.	3.5	8
46	Genome-scale insights into the metabolic versatility of <i>Limosilactobacillus reuteri</i> . BMC Biotechnology, 2021, 21, 46.	3.3	8
47	Integrated Metabolic Modeling, Culturing, and Transcriptomics Explain Enhanced Virulence of <i>Vibrio cholerae</i> during Coinfection with Enterotoxigenic <i>Escherichia coli</i> . MSystems, 2020, 5, .	3.8	8
48	Profiling of Small Molecular Metabolites in <i>Nostoc flagelliforme</i> during Periodic Desiccation. Marine Drugs, 2019, 17, 298.	4.6	7
49	Advances in the Relationships Between Cow's Milk Protein Allergy and Gut Microbiota in Infants. Frontiers in Microbiology, 2021, 12, 716667.	3.5	6
50	Genome Analysis of the Psychrotolerant Acidophile <i>Acidithiobacillus ferrivorans</i> CF27. Advanced Materials Research, 2013, 825, 145-148.	0.3	4
51	Microbial profiling identifies potential key drivers in gastric cancer patients. Biotechnology and Biotechnological Equipment, 2021, 35, 496-503.	1.3	4
52	Editorial: Engineering Yeast to Produce Plant Natural Products. Frontiers in Bioengineering and Biotechnology, 2021, 9, 798097.	4.1	4
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54	Microbial community dynamics revisited. Nature Computational Science, 2021, 1, 640-641.	8.0	2

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55	Developments in Fatty Acid-Derived Insect Pheromone Production Using Engineered Yeasts. <i>Frontiers in Microbiology</i> , 2021, 12, 759975.	3.5	2
56	Draft Genome Sequences of Five Fungal Strains Isolated from Kefir. <i>Microbiology Resource Announcements</i> , 2021, 10, e0019521.	0.6	1
57	Characterization of two β -galactosidases LacZ and WspA1 from <i>Nostoc flagelliforme</i> with focus on the latter's central active region. <i>Scientific Reports</i> , 2021, 11, 18448.	3.3	1
58	Dataset for suppressors of amyloid- β toxicity and their functions in recombinant protein production in yeast. <i>Data in Brief</i> , 2022, 42, 108322.	1.0	0