

Qiyu Bao

List of Publications by Year in descending order

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83
papers

4,809
citations

304743

22
h-index

95266

68
g-index

91
all docs

91
docs citations

91
times ranked

6629
citing authors

#	ARTICLE	IF	CITATIONS
1	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. <i>indica</i>). Science, 2002, 296, 79-92.	12.6	3,146
2	A Complete Sequence of the <i>T. tengcongensis</i> Genome. Genome Research, 2002, 12, 689-700.	5.5	209
3	The genome sequence of <i>Salmonella enterica</i> serovar <i>Choleraesuis</i> , a highly invasive and resistant zoonotic pathogen. Nucleic Acids Research, 2005, 33, 1690-1698.	14.5	193
4	Complete genome sequence of bacteriophage T5. Virology, 2005, 332, 45-65.	2.4	106
5	Sequencing and Genetic Variation of Multidrug Resistance Plasmids in <i>Klebsiella pneumoniae</i> . PLoS ONE, 2010, 5, e10141.	2.5	52
6	<i>ampG</i> Gene of <i>Pseudomonas aeruginosa</i> and Its Role in β -Lactamase Expression. Antimicrobial Agents and Chemotherapy, 2010, 54, 4772-4779.	3.2	48
7	Molecular Characterization and Antimicrobial Susceptibility of Nasal <i>Staphylococcus aureus</i> Isolates from a Chinese Medical College Campus. PLoS ONE, 2011, 6, e27328.	2.5	47
8	MagicViewer: integrated solution for next-generation sequencing data visualization and genetic variation detection and annotation. Nucleic Acids Research, 2010, 38, W732-W736.	14.5	45
9	Effects of curcumin on levels of nitric oxide synthase and AQP-4 in a rat model of hypoxia-induced ischemic brain damage. Brain Research, 2012, 1475, 88-95.	2.2	44
10	Genome-wide analysis of restriction-modification system in unicellular and filamentous cyanobacteria. Physiological Genomics, 2006, 24, 181-190.	2.3	37
11	Analysis of Resistance to Florfenicol and the Related Mechanism of Dissemination in Different Animal-Derived Bacteria. Frontiers in Cellular and Infection Microbiology, 2020, 10, 369.	3.9	37
12	Codon usage patterns and adaptive evolution of marine unicellular cyanobacteria <i>Synechococcus</i> and <i>Prochlorococcus</i> . Molecular Phylogenetics and Evolution, 2012, 62, 206-213.	2.7	35
13	Bioinformatic analysis of the <i>Acinetobacter baumannii</i> phage AB1 genome. Gene, 2012, 507, 125-134.	2.2	33
14	SuhB Regulates the Motile-Sessile Switch in <i>Pseudomonas aeruginosa</i> through the Gac/Rsm Pathway and c-di-GMP Signaling. Frontiers in Microbiology, 2017, 8, 1045.	3.5	33
15	<i>Spirulina</i> phycocyanin induces differential protein expression and apoptosis in SKOV-3 cells. International Journal of Biological Macromolecules, 2015, 81, 951-959.	7.5	32
16	Identification of differentially expressed proteins of <i>Arthrospira (Spirulina) plantensis</i> -YZ under salt-stress conditions by proteomics and qRT-PCR analysis. Proteome Science, 2013, 11, 6.	1.7	30
17	Whole genomic DNA sequencing and comparative genomic analysis of <i>Arthrospira plantensis</i> : high genome plasticity and genetic diversity. DNA Research, 2016, 23, 325-338.	3.4	30
18	Sequence Analysis of pKF3-70 in <i>Klebsiella pneumoniae</i> : Probable Origin from R100-Like Plasmid of <i>Escherichia coli</i> . PLoS ONE, 2010, 5, e8601.	2.5	29

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19	The Effect of Sodium Fluoride on Cell Apoptosis and the Mechanism of Human Lung BEAS-2B Cells In Vitro. <i>Biological Trace Element Research</i> , 2017, 179, 59-69.	3.5	29
20	cTFbase: a database for comparative genomics of transcription factors in cyanobacteria. <i>BMC Genomics</i> , 2007, 8, 104.	2.8	28
21	Spread of the florfenicol resistance floR gene among clinical <i>Klebsiella pneumoniae</i> isolates in China. <i>Antimicrobial Resistance and Infection Control</i> , 2018, 7, 127.	4.1	28
22	Transcriptome analysis of phycocyanin inhibitory effects on SKOV-3 cell proliferation. <i>Gene</i> , 2016, 585, 58-64.	2.2	26
23	The β -Lactamase Gene Profile and a Plasmid-Carrying Multiple Heavy Metal Resistance Genes of <i>Enterobacter cloacae</i> . <i>International Journal of Genomics</i> , 2018, 2018, 1-12.	1.6	25
24	AmrZ Regulates Swarming Motility Through Cyclic di-GMP-Dependent Motility Inhibition and Controlling Pel Polysaccharide Production in <i>Pseudomonas aeruginosa</i> PA14. <i>Frontiers in Microbiology</i> , 2019, 10, 1847.	3.5	25
25	ArchaeaTF: An integrated database of putative transcription factors in Archaea. <i>Genomics</i> , 2008, 91, 102-107.	2.9	22
26	Codon Usage Patterns in <i>Corynebacterium glutamicum</i> : Mutational Bias, Natural Selection and Amino Acid Conservation. <i>Comparative and Functional Genomics</i> , 2010, 2010, 1-7.	2.0	21
27	Characterisation of a class 1 integron associated with the formation of quadruple bla _{GES-5} cassettes from an IncP-1 β group plasmid in <i>Pseudomonas aeruginosa</i> . <i>International Journal of Antimicrobial Agents</i> , 2018, 52, 485-491.	2.5	20
28	OXA-830, a Novel Chromosomally Encoded Extended-Spectrum Class D β -Lactamase in <i>Aeromonas simiae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2732.	3.5	19
29	Comparative proteomic analysis revealed metabolic changes and the translational regulation of Cry protein synthesis in <i>Bacillus thuringiensis</i> . <i>Journal of Proteomics</i> , 2012, 75, 1235-1246.	2.4	17
30	Molecular Epidemiology and Characterization of Genotypes of <i>Acinetobacter baumannii</i> ; Isolates from Regions of South China. <i>Japanese Journal of Infectious Diseases</i> , 2016, 69, 180-185.	1.2	17
31	Determining the Genetic Characteristics of Resistance and Virulence of the <i>Staphylococcus epidermidis</i> Cluster Group Through Pan-Genome Analysis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 274.	3.9	16
32	Phenotypic and Molecular Characteristics of Carbapenem-Non-Susceptible Enterobacteriaceae from a Teaching Hospital in Wenzhou, Southern China. <i>Japanese Journal of Infectious Diseases</i> , 2013, 66, 96-102.	1.2	15
33	Characterization of florfenicol resistance genes in the coagulase-negative <i>Staphylococcus</i> (CoNS) isolates and genomic features of a multidrug-resistant <i>Staphylococcus lentus</i> strain H29. <i>Antimicrobial Resistance and Infection Control</i> , 2021, 10, 9.	4.1	14
34	Molecular Characterization of a Multidrug-Resistant <i>Klebsiella pneumoniae</i> Strain R46 Isolated from a Rabbit. <i>International Journal of Genomics</i> , 2019, 2019, 1-12.	1.6	13
35	Genomic Analysis of <i>Delftia tsuruhatensis</i> Strain TR1180 Isolated From A Patient From China With In4-Like Integron-Associated Antimicrobial Resistance. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 663933.	3.9	12
36	Gene Signature Associated With Bromodomain Genes Predicts the Prognosis of Kidney Renal Clear Cell Carcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 643935.	2.3	12

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37	Distribution of β -Lactamase Genes and Genetic Context of blaKPC-2 in Clinical Carbapenemase-Producing <i>Klebsiella pneumoniae</i> Isolates. <i>Infection and Drug Resistance</i> , 2021, Volume 14, 237-247.	2.7	11
38	Molecular and Functional Characterization of a Novel Plasmid-Borne blaNDM-Like Gene, blaAFM-1, in a Clinical Strain of <i>Aeromonas hydrophila</i> . <i>Infection and Drug Resistance</i> , 2021, Volume 14, 1613-1622.	2.7	11
39	PGA4genomics for comparative genome assembly based on genetic algorithm optimization. <i>Genomics</i> , 2009, 94, 284-286.	2.9	10
40	Insights into the evolution of gene organization and multidrug resistance from <i>Klebsiella pneumoniae</i> plasmid pKF3-140. <i>Gene</i> , 2013, 519, 60-66.	2.2	10
41	Effects of phycoerythrin from <i>Gracilaria lemaneiformis</i> in proliferation and apoptosis of SW480 cells. <i>Oncology Reports</i> , 2016, 36, 3536-3544.	2.6	10
42	Florfenicol Resistance in Enterobacteriaceae and Whole-Genome Sequence Analysis of Florfenicol-Resistant <i>Leclercia adecarboxylata</i> Strain R25. <i>International Journal of Genomics</i> , 2019, 2019, 1-10.	1.6	10
43	Lineage-Specific Domain Fusion in the Evolution of Purine Nucleotide Cyclases in Cyanobacteria. <i>Journal of Molecular Evolution</i> , 2008, 67, 85-94.	1.8	9
44	Comparative genomics analysis of pKF3-94 in <i>Klebsiella pneumoniae</i> reveals plasmid compatibility and horizontal gene transfer. <i>Frontiers in Microbiology</i> , 2015, 6, 831.	3.5	9
45	Prevalence of Aminoglycoside Resistance Genes and Molecular Characterization of a Novel Gene, <i>aac(3)-Ilg</i> , among Clinical Isolates of the <i>Enterobacter cloacae</i> Complex from a Chinese Teaching Hospital. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	9
46	Structure-Function Analysis of the Transmembrane Protein AmpG from <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2016, 11, e0168060.	2.5	9
47	Effects of SNPs (CYP1B1*2 G355T, CYP1B1*3 C4326G, and CYP2E1*5 G-1293C), Smoking, and Drinking on Susceptibility to Laryngeal Cancer among Han Chinese. <i>PLoS ONE</i> , 2014, 9, e106580.	2.5	8
48	Molecular characteristics and comparative genomics analysis of a clinical <i>Enterococcus casseliflavus</i> with a resistance plasmid. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 2159-2167.	2.7	8
49	Genomic and functional characterization of fecal sample strains of <i>Proteus cibarius</i> carrying two floR antibiotic resistance genes and a multiresistance plasmid-encoded cfr gene. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2020, 69, 101427.	1.6	8
50	High-Level Aminoglycoside Resistance in Human Clinical <i>Klebsiella pneumoniae</i> Complex Isolates and Characteristics of armA-Carrying IncHI5 Plasmids. <i>Frontiers in Microbiology</i> , 2021, 12, 636396.	3.5	8
51	Characterization of Two Macrolide Resistance-Related Genes in Multidrug-Resistant <i>Pseudomonas aeruginosa</i> Isolates. <i>Polish Journal of Microbiology</i> , 2020, 69, 349-356.	1.7	8
52	Evidence of Extensive Homologous Recombination in the Core Genome of <i>Rickettsia</i> . <i>Comparative and Functional Genomics</i> , 2009, 2009, 1-5.	2.0	7
53	Molecular Variation and Horizontal Gene Transfer of the Homocysteine Methyltransferase Gene <i>mmuM</i> and its Distribution in Clinical Pathogens. <i>International Journal of Biological Sciences</i> , 2015, 11, 11-21.	6.4	7
54	Transcriptional network in ovarian cancer cell line SKOV3 treated with <i>Pinellia pedatisecta</i> Schott extract. <i>Oncology Reports</i> , 2016, 36, 462-470.	2.6	7

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55	Characterization of a Novel bla _{KLUC} Variant With Reduced \hat{I}^2 -Lactam Resistance From an IncA/C Group Plasmid in a Clinical <i>Klebsiella pneumoniae</i> Isolate. <i>Frontiers in Microbiology</i> , 2018, 9, 1908.	3.5	7
56	Comparative Genomic Analysis of <i>Rhodococcus equi</i> : An Insight into Genomic Diversity and Genome Evolution. <i>International Journal of Genomics</i> , 2019, 2019, 1-14.	1.6	7
57	In Vitro Susceptibility and Florfenicol Resistance in <i>Citrobacter</i> Isolates and Whole-Genome Analysis of Multidrug-Resistant <i>Citrobacter freundii</i> . <i>International Journal of Genomics</i> , 2019, 2019, 1-15.	1.6	6
58	<p>PAU-1, a Novel Plasmid-Encoded Ambler Class A \hat{I}^2 -Lactamase Identified in a Clinical <i>Pseudomonas aeruginosa</i> Isolate</p>. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 3827-3834.	2.7	6
59	Identification and Characterization of Two Novel bla _{KLUC} Resistance Genes through Large-Scale Resistance Plasmids Sequencing. <i>PLoS ONE</i> , 2012, 7, e47197.	2.5	6
60	Downregulation of <i>NCL</i> attenuates tumor formation and growth in <i>HeLa</i> cells by targeting the <i>PI3K</i> / <i>AKT</i> pathway. <i>Cancer Medicine</i> , 2022, 11, 1454-1464.	2.8	6
61	CSCDB: The cAMP and cGMP signaling components database. <i>Genomics</i> , 2008, 92, 60-64.	2.9	5
62	PlasmoGF: an integrated system for comparative genomics and phylogenetic analysis of <i>Plasmodium</i> gene families. <i>Bioinformatics</i> , 2008, 24, 1217-1220.	4.1	5
63	The Structure of <i>fampG</i> Gene in <i>Pseudomonas aeruginosa</i> and Its Effect on Drug Resistance. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2018, 2018, 1-7.	1.9	5
64	Comparative genomics analysis of <i>Raoultella planticola</i> S25 isolated from duck in China, with florfenicol resistance. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2020, 68, 101398.	1.6	5
65	Identification of <i>floR</i> Variants Associated With a Novel Tn4371-Like Integrative and Conjugative Element in Clinical <i>Pseudomonas aeruginosa</i> Isolates. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 685068.	3.9	5
66	Identification and characteristics of a novel aminoglycoside phosphotransferase, APH(3 \hat{A})-IIId, from an MDR clinical isolate of <i>Brucella intermedia</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 2787-2794.	3.0	5
67	Identification and molecular characterization of <i>Escherichia coli</i> bla _{SHV} genes in a Chinese teaching hospital. <i>Gene</i> , 2017, 600, 29-35.	2.2	4
68	Characterization of a Novel Chromosomal Class C \hat{I}^2 -Lactamase, YOC-1, and Comparative Genomics Analysis of a Multidrug Resistance Plasmid in <i>Yokenella regensburgei</i> W13. <i>Frontiers in Microbiology</i> , 2020, 11, 2021.	3.5	4
69	Characterization of an IncR Plasmid with Two Copies of ISCR-Linked <i>qnrB6</i> from ST968 <i>Klebsiella pneumoniae</i> . <i>International Journal of Genomics</i> , 2020, 2020, 1-8.	1.6	4
70	Molecular Mechanism of the \hat{I}^2 -Lactamase Mediated \hat{I}^2 -Lactam Antibiotic Resistance of <i>Pseudomonas aeruginosa</i> Isolated From a Chinese Teaching Hospital. <i>Frontiers in Microbiology</i> , 2022, 13, 855961.	3.5	4
71	Transcriptionomic Study on Apoptosis of SKOV-3 Cells Induced by Phycoerythrin from <i>Gracilaria lemaneiformis</i> . <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2021, 21, 1240-1249.	1.7	3
72	Identification and Characterization of a Novel Chromosomal Aminoglycoside 2 \hat{A} -N-Acetyltransferase, AAC(2 \hat{A})-IIc, From an Isolate of a Novel <i>Providencia</i> Species, <i>Providencia wenzhouensis</i> R33. <i>Frontiers in Microbiology</i> , 2021, 12, 711037.	3.5	3

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73	Early predictors of lung necrosis severity in children with community-acquired necrotizing pneumonia. <i>Pediatric Pulmonology</i> , 2022, 57, 2172-2179.	2.0	3
74	FlyPhy: a phylogenomic analysis platform for <i>Drosophila</i> genes and gene families. <i>BMC Bioinformatics</i> , 2009, 10, 123.	2.6	2
75	proTF: a comprehensive data and phylogenomics resource for prokaryotic transcription factors. <i>Bioinformatics</i> , 2010, 26, 2493-2495.	4.1	2
76	Transcriptomic Analysis of <i>Thermoanaerobacter tengcongensis</i> Grown at Different Temperatures by RNA Sequencing. <i>Journal of Genetics and Genomics</i> , 2015, 42, 335-338.	3.9	2
77	Comparative Genomics Analysis of Plasmid pPV989-94 from a Clinical Isolate of <i>Pantoea vagans</i> PV989. <i>International Journal of Genomics</i> , 2018, 2018, 1-9.	1.6	2
78	Characterization of a Novel Chromosome-Encoded AmpC β -Lactamase Gene, blaPRC β 1, in an Isolate of a Newly Classified <i>Pseudomonas</i> Species, <i>Pseudomonas wenzhouensis</i> A20, From Animal Farm Sewage. <i>Frontiers in Microbiology</i> , 2021, 12, 732932.	3.5	2
79	Proteomic analysis and qRT-PCR verification of <i>Arthrospira platensis</i> strain YZ under dark stress. <i>Phycologia</i> , 2013, 52, 538-549.	1.4	1
80	Analysis of the promoter region of the RuBisCO gene of <i>Arthrospira (Spirulina) platensis</i> . <i>Journal of Applied Phycology</i> , 2014, 26, 199-207.	2.8	0
81	Identification of Three Clf-Sdr Subfamily Proteins in <i>Staphylococcus warneri</i> , and Comparative Genomics Analysis of a Locus Encoding CWA Proteins in <i>Staphylococcus</i> Species. <i>Frontiers in Microbiology</i> , 2021, 12, 691087.	3.5	0
82	Characterization and identification of SFDC β 1, a novel AmpC β -type β -lactamase in <i>Serratia fonticola</i> . <i>Environmental Microbiology</i> , 2021, , .	3.8	0
83	Identification and Characterization of a Novel Aminoglycoside 3'-Nucleotidyltransferase, ANT(3')-IId, From <i>Acinetobacter lwoffii</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 728216.	3.5	0