Dongsheng Zhou

List of Publications by Year
in descending order

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211 papers	7,573 citations	53789 45 h-index	82542 72 g-index
219 all docs	219 docs citations	219 times ranked	7434 citing authors

#	Article	IF	Citations
1	A Thermostable mRNA Vaccine against COVID-19. Cell, 2020, 182, 1271-1283.e16.	28.9	485
2	Historical variations in mutation rate in an epidemic pathogen, Yersinia pestis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 577-582.	7.1	373
3	Molecular pathogenesis of Klebsiella pneumoniae. Future Microbiology, 2014, 9, 1071-1081.	2.0	247
4	Complete Genome Sequence of Yersinia pestis Strain 91001, an Isolate Avirulent to Humans. DNA Research, 2004, 11, 179-197.	3.4	241
5	Genetics of Metabolic Variations between Yersinia pestis Biovars and the Proposal of a New Biovar, microtus. Journal of Bacteriology, 2004, 186, 5147-5152.	2.2	200
6	Biofilm-associated infections: antibiotic resistance and novel therapeutic strategies. Future Microbiology, 2013, 8, 877-886.	2.0	156
7	Antibody responses to individual proteins of SARS coronavirus and their neutralization activities. Microbes and Infection, 2005, 7, 882-889.	1.9	146
8	Mapping and role of T cell response in SARS-CoV-2â€“infected mice. Journal of Experimental Medicine, 2021, 218, .	8.5	132
9	DNA Microarray Analysis of Genome Dynamics in Yersinia pestis: Insights into Bacterial Genome Microevolution and Niche Adaptation. Journal of Bacteriology, 2004, 186, 5138-5146.	2.2	109
10	The Iron-Responsive Fur Regulon in Yersinia pestis. Journal of Bacteriology, 2008, 190, 3063-3075.	2.2	107
11	Microarray Analysis of Temperatureâ€Induced Transcriptome of Yersinia pestis. Microbiology and Immunology, 2004, 48, 791-805.	1.4	106
12	Ultrasmall Fe-doped carbon dots nanozymes for photoenhanced antibacterial therapy and wound healing. Bioactive Materials, 2022, 12, 246-256.	15.6	101
13	Epidemic Clones, Oceanic Gene Pools, and Eco-LD in the Free Living Marine Pathogen Vibrio parahaemolyticus. Molecular Biology and Evolution, 2015, 32, 1396-1410.	8.9	98
14	Protein Microarray for Profiling Antibody Responses to Yersinia pestis Live Vaccine. Infection and Immunity, 2005, 73, 3734-3739.	2.2	88
15	The Cyclic AMP Receptor Protein, CRP, Is Required for Both Virulence and Expression of the Minimal CRP Regulon in Yersinia pestis Biovar microtus. Infection and Immunity, 2008, 76, 5028-5037.	2.2	88
16	AphA is required for biofilm formation, motility, and virulence in pandemic Vibrio parahaemolyticus. International Journal of Food Microbiology, 2013, 160, 245-251.	4.7	87
17	Dissemination of IMP-4-encoding pIMP-HZ1-related plasmids among Klebsiella pneumoniae and Pseudomonas aeruginosa in a Chinese teaching hospital. Scientific Reports, 2016, 6, 33419.	3.3	78
18	A novel enzyme-linked immunosorbent assay for detection of Escherichia coli O157:H7 using immunomagnetic and beacon gold nanoparticles. Gut Pathogens, 2014, 6, 14.	3.4	76

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19	Coexistence of a novel KPC-2-encoding MDR plasmid and an NDM-1-encoding pNDM-HN380-like plasmid in a clinical isolate ofCitrobacter freundii. Journal of Antimicrobial Chemotherapy, 2015, 70, 2987-2991.	3.0	75
20	Global analysis of iron assimilation and fur regulation in Yersinia pestis. FEMS Microbiology Letters, 2006, 258, 9-17.	1.8	74
21	NDM-1 encoded by a pNDM-BJ01-like plasmid p3SP-NDM in clinical Enterobacter aerogenes. Frontiers in Microbiology, 2015, 6, 294.	3.5	73
22	Transcriptional Regulation of opaR, qrr2â€“4 and aphA by the Master Quorum-Sensing Regulator OpaR in Vibrio parahaemolyticus. PLoS ONE, 2012, 7, e34622.	2.5	72
23	Comparative and evolutionary genomics of. Microbes and Infection, 2004, 6, 1226-1234.	1.9	71
24	Molecular and physiological insights into plague transmission, virulence and etiology. Microbes and Infection, 2006, 8, 273-284.	1.9	65
25	Different Region Analysis for Genotyping Yersinia pestis Isolates from China. PLoS ONE, 2008, 3, e2166.	2.5	65
26	DNA microarray analysis of the heat- and cold-shock stimulons in Yersinia pestis. Microbes and Infection, 2005, 7, 335-348.	1.9	62
27	Involvement of cAMP receptor protein in biofilm formation, fimbria production, capsular polysaccharide biosynthesis and lethality in mouse of Klebsiella pneumoniae serotype K1 causing pyogenic liver abscess. Journal of Medical Microbiology, 2017, 66, 1-7.	1.8	62
28	Transcriptome analysis of the Mg2+-responsive PhoP regulator inYersinia pestis. FEMS Microbiology Letters, 2005, 250, 85-95.	1.8	61
29	Regulatory effects of cAMP receptor protein (CRP) on porin genes and its own gene in Yersinia pestis. BMC Microbiology, 2011, 11, 40.	3.3	61
30	Characterization of Zur-dependent genes and direct Zur targets in Yersinia pestis. BMC Microbiology, 2009, 9, 128.	3.3	60
31	Sequencing and comparative genomics analysis of the IncHI2 plasmids pT5282-mphA and p112298-catA and the IncHI5 plasmid pYNKP001-dfrA. International Journal of Antimicrobial Agents, 2017, 49, 709-718.	2.5	60
32	Antigenicity Analysis of Different Regions of the Severe Acute Respiratory Syndrome Coronavirus Nucleocapsid Protein. Clinical Chemistry, 2004, 50, 988-995.	3.2	59
33	Molecular Darwinian Evolution of Virulence in Yersinia pestis. Infection and Immunity, 2009, 77, 2242-2250.	2.2	58
34	Determination of sRNA Expressions by RNA-seq in Yersinia pestis Grown In Vitro and during Infection. PLoS ONE, 2013, 8, e74495.	2.5	58
35	Analysis of the Three Yersinia pestis CRISPR Loci Provides New Tools for Phylogenetic Studies and Possibly for the Investigation of Ancient DNA. Advances in Experimental Medicine and Biology, 2007, 603, 327-338.	1.6	55
36	Phenotypic and transcriptional analysis of the osmotic regulator OmpR in Yersinia pestis. BMC Microbiology, 2011, 11, 39.	3.3	52

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37	Emergence of a Multidrug-Resistant Hypervirulent Klebsiella pneumoniae Sequence Type 23 Strain with a Rare bla _{CTX-M-24} -Harboring Virulence Plasmid. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	52
38	Fur Is a Repressor of Biofilm Formation in Yersinia pestis. PLoS ONE, 2012, 7, e52392.	2.5	52
39	H-NS is a repressor of major virulence gene loci in Vibrio parahaemolyticus. Frontiers in Microbiology, 2014, 5, 675.	3.5	51
40	Comparative transcriptome analysis of Yersinia pestis in response to hyperosmotic and high-salinity stress. Research in Microbiology, 2005, 156, 403-415.	2.1	50
41	Genome plasticity of Vibrio parahaemolyticus: microevolution of the 'pandemic group'. BMC Genomics, 2008, 9, 570.	2.8	50
42	Molecular Characterization of Direct Target Genes and cis-Acting Consensus Recognized by Quorum-Sensing Regulator AphA in Vibrio parahaemolyticus. PLoS ONE, 2012, 7, e44210.	2.5	50
43	Production of plasmid-encoding NDM-1 in clinical Raoultella ornithinolytica and Leclercia adecarboxylata from China. Frontiers in Microbiology, 2015, 6, 458.	3.5	50
44	Complete sequences of KPC-2-encoding plasmid p628-KPC and CTX-M-55-encoding p628-CTXM coexisted in Klebsiella pneumoniae. Frontiers in Microbiology, 2015, 6, 838.	3.5	50
45	The IncP-6 Plasmid p10265-KPC from Pseudomonas aeruginosa Carries a Novel Î”ISEc33-Associated blaKPC-2 Gene Cluster. Frontiers in Microbiology, 2016, 7, 310.	3.5	50
46	Global analysis of gene transcription regulation in prokaryotes. Cellular and Molecular Life Sciences, 2006, 63, 2260-2290.	5.4	49
47	Live-attenuatedYersinia pestisvaccines. Expert Review of Vaccines, 2013, 12, 677-686.	4.4	49
48	Circular RNA profiling provides insights into their subcellular distribution and molecular characteristics in HepG2 cells. RNA Biology, 2019, 16, 220-232.	3.1	48
49	Formation and regulation of Yersinia biofilms. Protein and Cell, 2011, 2, 173-179.	11.0	47
50	RcsAB is a major repressor of Yersinia biofilm development through directly acting on hmsCDE, hmsT and hmsHFRS. Scientific Reports, 2015, 5, 9566.	3.3	47
51	Degradable Pseudo Conjugated Polymer Nanoparticles with NIRâ€Ⅱ Photothermal Effect and Cationic Quaternary Phosphonium Structural Bacteriostasis for Antiâ€Infection Therapy. Advanced Science, 2022, 9, e2200732.	11.2	46
52	Transcriptional Regulation of the Type VI Secretion System 1 Genes by Quorum Sensing and ToxR in Vibrio parahaemolyticus. Frontiers in Microbiology, 2017, 8, 2005.	3.5	44
53	Cold-induced gene expression profiles ofVibrio parahaemolyticus: a time-course analysis. FEMS Microbiology Letters, 2009, 291, 50-58.	1.8	43
54	Autoregulation of PhoP/PhoQ and Positive Regulation of the Cyclic AMP Receptor Protein-Cyclic AMP Complex by PhoP in Yersinia pestis. Journal of Bacteriology, 2013, 195, 1022-1030.	2.2	43

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55	Survey and rapid detection of Klebsiella pneumoniae in clinical samples targeting the rcsA gene in Beijing, China. Frontiers in Microbiology, 2015, 6, 519.	3.5	43
56	Outer Membrane Proteins Ail and OmpF of Yersinia pestis Are Involved in the Adsorption of T7-Related Bacteriophage Yep-phi. Journal of Virology, 2013, 87, 12260-12269.	3.4	42
57	Extended MLST-based population genetics and phylogeny of Vibrio parahaemolyticus with high levels of recombination. International Journal of Food Microbiology, 2011, 145, 106-112.	4.7	41
58	Plasmid and chromosomal integration of four novel blaIMP-carrying transposons from Pseudomonas aeruginosa, Klebsiella pneumoniae and an Enterobacter sp.. Journal of Antimicrobial Chemotherapy, 2018, 73, 3005-3015.	3.0	41
59	Recent mixing of Vibrio parahaemolyticus populations. ISME Journal, 2019, 13, 2578-2588.	9.8	41
60	Ambient Stable Quantitative PCR Reagents for the Detection of Yersinia pestis. PLoS Neglected Tropical Diseases, 2010, 4, e629.	3.0	38
61	Use of recombinant porcine Î²-defensin 2 as a medicated feed additive for weaned piglets. Scientific Reports, 2016, 6, 26790.	3.3	36
62	Co-occurrence of 3 different resistance plasmids in a multi-drug resistant Cronobacter sakazakii isolate causing neonatal infections. Virulence, 2018, 9, 110-120.	4.4	36
63	Pseudogene accumulation might promote the adaptive microevolution of Yersinia pestis. Journal of Medical Microbiology, 2005, 54, 259-268.	1.8	35
64	Genetic characterization of two fully sequenced multi-drug resistant plasmids pP10164-2 and pP10164-3 from Leclercia adecarboxylata. Scientific Reports, 2016, 6, 33982.	3.3	35
65	Transcriptional profiling of a mice plague model: insights into interaction between Yersinia pestis and its host. Journal of Basic Microbiology, 2009, 49, 92-99.	3.3	34
66	IL-17A Produced by Neutrophils Protects against Pneumonic Plague through Orchestrating IFN-Î³â€“Activated Macrophage Programming. Journal of Immunology, 2014, 192, 704-713.	0.8	34
67	Mitochondrial complex I bridges a connection between regulation of carbon flexibility and gastrointestinal commensalism in the human fungal pathogen Candida albicans. PLoS Pathogens, 2017, 13, e1006414.	4.7	34
68	Quorum sensing modulates transcription of cpsQ-mfpABC and mfpABC in Vibrio parahaemolyticus. International Journal of Food Microbiology, 2013, 166, 458-463.	4.7	33
69	The type I-E CRISPR-Cas system influences the acquisition of bla _{KPC} -IncF plasmid in Klebsiella pneumonia. Emerging Microbes and Infections, 2020, 9, 1011-1022.	6.5	33
70	Molecular Characterization of Transcriptional Regulation of rovA by PhoP and RovA in Yersinia pestis. PLoS ONE, 2011, 6, e25484.	2.5	32
71	Autoregulation of ToxR and Its Regulatory Actions on Major Virulence Gene Loci in Vibrio parahaemolyticus. Frontiers in Cellular and Infection Microbiology, 2018, 8, 291.	3.9	32
72	Identification of tick-borne pathogens by metagenomic next-generation sequencing in Dermacentor nuttalli and Ixodes persulcatus in Inner Mongolia, China. Parasites and Vectors, 2021, 14, 287.	2.5	32

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73	Comparative transcriptomics in Yersinia pestis: a global view of environmental modulation of gene expression. BMC Microbiology, 2007, 7, 96.	3.3	31
74	Inhalable MOFâ€Derived Nanoparticles for Sonodynamic Therapy of Bacterial Pneumonia. Advanced Functional Materials, 2022, 32, .	14.9	31
75	Identification and characterization of PhoP regulon members in Yersinia pestis biovar Microtus. BMC Genomics, 2008, 9, 143.	2.8	30
76	Biosafety and biosecurity. Journal of Biosafety and Biosecurity, 2019, 1, 15-18.	2.8	30
77	Comparative analysis of KPC-2-encoding chimera plasmids with multi-replicon IncR:Inc_{pA1763-KPC}:IncN1 or IncFII_{pHN7A8}:Inc_{pA1763-KPC}: IncN1 . Infection and Drug Resistance, 2019, Volume 12, 285-296.	2.7	30
78	QsvR integrates into quorum sensing circuit to control <scp>Vibrio parahaemolyticus</scp> virulence. Environmental Microbiology, 2019, 21, 1054-1067.	3.8	30
79	Sequencing and Genomic Diversity Analysis of IncHI5 Plasmids. Frontiers in Microbiology, 2018, 9, 3318.	3.5	30
80	Innate immune responses against the fungal pathogen Candida auris. Nature Communications, 2022, 13, .	12.8	30
81	The low-salt stimulon in Vibrio parahaemolyticus. International Journal of Food Microbiology, 2010, 137, 49-54.	4.7	29
82	Cell Density- and Quorum Sensing-Dependent Expression of Type VI Secretion System 2 in VibrioÂparahaemolyticus. PLoS ONE, 2013, 8, e73363.	2.5	29
83	Genetic characterization of a novelbla_{DIM-2}-carrying megaplasmid p12969-DIM from clinicalPseudomonas putida. Journal of Antimicrobial Chemotherapy, 2016, 71, 909-912.	3.0	29
84	Identification of Signature Genes for Rapid and Specific Characterization of Yersinia pestis. Microbiology and Immunology, 2004, 48, 263-269.	1.4	28
85	Direct and negative regulation of the sycO-ypkA-ypoJ operon by cyclic AMP receptor protein (CRP) in Yersinia pestis. BMC Microbiology, 2009, 9, 178.	3.3	28
86	Genetic variations of live attenuated plague vaccine strains (Yersinia pestis EV76 lineage) during laboratory passages in different countries. Infection, Genetics and Evolution, 2014, 26, 172-179.	2.3	28
87	Surface Wettability of Nanoparticle Modulated Sonothrombolysis. Advanced Materials, 2021, 33, e2007073.	21.0	28
88	â€œRoarâ€•of blaNDM-1 and â€œsilenceâ€•of blaOXA-58 co-exist in Acinetobacter pittii. Scientific Reports, 2015, 5, 8976.	3.3	27
89	Whole-cell biotransformation systems for reduction of prochiral carbonyl compounds to chiral alcohol in Escherichia coli. Scientific Reports, 2014, 4, 6750.	3.3	27
90	Enhanced protection against Q fever in BALB/c mice elicited by immunization of chloroform-methanol residue of Coxiella burnetii via intratracheal inoculation. Vaccine, 2019, 37, 6076-6084.	3.8	27

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91	Quorum sensing regulates the transcription of lateral flagellar genes in Vibrio parahaemolyticus. Future Microbiology, 2019, 14, 1043-1053.	2.0	27
92	T6SS translocates a micropeptide to suppress STING-mediated innate immunity by sequestering manganese. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	27
93	Dissemination of KPC-2-Encoding IncX6 Plasmids Among Multiple Enterobacteriaceae Species in a Single Chinese Hospital. Frontiers in Microbiology, 2018, 9, 478.	3.5	26
94	Antibody profiling in plague patients by protein microarray. Microbes and Infection, 2008, 10, 45-51.	1.9	25
95	A novel PCR-based genotyping scheme for clinical Klebsiella pneumoniae. Future Microbiology, 2014, 9, 21-32.	2.0	25
96	IMP-1 encoded by a novel Tn402-like class 1 integron in clinical Achromobacter xylosoxidans, China. Scientific Reports, 2014, 4, 7212.	3.3	25
97	Genome-wide transcriptional response of Yersinia pestis to stressful conditions simulating phagolysosomal environments. Microbes and Infection, 2006, 8, 2669-2678.	1.9	23
98	Transcriptional regulation of cpsQâ€mfp<scp>ABC</scp> and mfp<scp>ABC</scp> by CalRÂin Vibrio parahaemolyticus. MicrobiologyOpen, 2017, 6, e00470.	3.0	23
99	Genomic characterization of novel IncFII-type multidrug resistant plasmids p0716-KPC and p12181-KPC from Klebsiella pneumoniae. Scientific Reports, 2017, 7, 5830.	3.3	23
100	The epidemic of Q fever in 2018 to 2019 in Zhuhai city of China determined by metagenomic next-generation sequencing. PLoS Neglected Tropical Diseases, 2021, 15, e0009520.	3.0	23
101	Plasmid-encoding extended-spectrum Î²-lactamase CTX-M-55 in a clinical Shigella sonnei strain, China. Future Microbiology, 2014, 9, 1143-1150.	2.0	22
102	HmsB enhances biofilm formation in Yersinia pestis. Frontiers in Microbiology, 2014, 5, 685.	3.5	22
103	Reciprocal regulation of Yersinia pestis biofilm formation and virulence by RovM and RovA. Open Biology, 2016, 6, 150198.	3.6	22
104	CalR is required for the expression of T6SS2 and the adhesion of Vibrio parahaemolyticus to HeLa cells. Archives of Microbiology, 2017, 199, 931-938.	2.2	22
105	Sequencing of blaIMP-Carrying IncN2 Plasmids, and Comparative Genomics of IncN2 Plasmids Harboring Class 1 Integrons. Frontiers in Cellular and Infection Microbiology, 2017, 7, 102.	3.9	22
106	Regulatory actions of ToxR and CalR on their own genes and type III secretion system 1 in Vibrio parahaemolyticus. Oncotarget, 2017, 8, 65809-65822.	1.8	22
107	Global gene expression profile of Yersinia pestis induced by streptomycin. FEMS Microbiology Letters, 2005, 243, 489-496.	1.8	21
108	CRP Is an Activator of Yersinia pestis Biofilm Formation that Operates via a Mechanism Involving gmhA and waaAE-coaD. Frontiers in Microbiology, 2016, 7, 295.	3.5	21

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109	Defining the genome content of live plague vaccines by use of whole-genome DNA microarray. Vaccine, 2004, 22, 3367-3374.	3.8	20
110	Genomic comparison of Yersinia pestis and Yersinia pseudotuberculosis by combination of suppression subtractive hybridization and DNA microarray. Archives of Microbiology, 2006, 186, 151-159.	2.2	20
111	Vibrio parahaemolyticus CalR down regulates the thermostable direct hemolysin (TDH) gene transcription and thereby inhibits hemolytic activity. Gene, 2017, 613, 39-44.	2.2	20
112	Comparative analysis of bla _{KPC-2}- and rmtB-carrying IncFII-family pKPC-LK30/pHN7A8 hybrid plasmids from Klebsiella pneumoniae CG258 strains disseminated among multiple Chinese hospitals. Infection and Drug Resistance, 2018, Volume 11, 1783-1793.	2.7	20
113	Replicon-Based Typing of IncI-Complex Plasmids, and Comparative Genomics Analysis of IncÎ³/K1 Plasmids. Frontiers in Microbiology, 2019, 10, 48.	3.5	20
114	Microarray expression profiling ofYersinia pestisin response to chloramphenicol. FEMS Microbiology Letters, 2006, 263, 26-31.	1.8	19
115	Expression of the Type VI Secretion System 1 Component Hcp1 Is Indirectly Repressed by OpaR inVibrio parahaemolyticus. Scientific World Journal, The, 2012, 2012, 1-7.	2.1	19
116	Plasmids of novel incompatibility group IncpRBL16 from Pseudomonas species. Journal of Antimicrobial Chemotherapy, 2020, 75, 2093-2100.	3.0	19
117	Detection of microbial aerosols in hospital wards and molecular identification and dissemination of drug resistance of Escherichia coli. Environment International, 2020, 137, 105479.	10.0	19
118	OpaR Controls the Metabolism of c-di-GMP in Vibrio parahaemolyticus. Frontiers in Microbiology, 2021, 12, 676436.	3.5	19
119	Reciprocal regulation of pH 6 antigen gene loci by PhoP and RovA inYersinia pestisbiovarMicrotus. Future Microbiology, 2013, 8, 271-280.	2.0	18
120	Rapid Degradation of Hfq-Free RyhB inYersinia pestisby PNPase Independent of Putative Ribonucleolytic Complexes. BioMed Research International, 2014, 2014, 1-7.	1.9	18
121	Structural genomics of pNDM-BTR harboring In191 and Tn6360, and otherbla_{NDM}-carrying IncN1 plasmids. Future Microbiology, 2017, 12, 1271-1281.	2.0	18
122	pSY153-MDR, a p12969-DIM-related mega plasmid carryingblaIMP-45 andarmA, from clinicalPseudomonas putida. Oncotarget, 2017, 8, 68439-68447.	1.8	18
123	Coexistence of two novel resistance plasmids, bla_{KPC-2}-carrying p14057A and tetA(A) -carrying p14057B, in Pseudomonas aeruginosa. Virulence, 2018, 9, 306-311.	4.4	18
124	Physiological and Regulatory Characterization of KatA and KatY inYersinia pestis. DNA and Cell Biology, 2008, 27, 453-462.	1.9	17
125	Regulation of pathogenicity by noncoding RNAs in bacteria. Future Microbiology, 2013, 8, 579-591.	2.0	17
126	The first report of detecting the bla SIM-2 gene and determining the complete sequence of the SIM-encoding plasmid. Clinical Microbiology and Infection, 2016, 22, 347-351.	6.0	17

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127	The type VI secretion system 2 of Vibrio parahaemolyticus is regulated by QsvR. Microbial Pathogenesis, 2020, 149, 104579.	2.9	17
128	Self-resetting molecular probes for nucleic acids detection enabled by fuel dissipative systems. Nano Today, 2021, 41, 101308.	11.9	17
129	Gene expression profiling of Yersinia pestis with deletion of lcrG, a known negative regulator for Yop secretion of type III secretion system. International Journal of Medical Microbiology, 2009, 299, 355-366.	3.6	16
130	MLST-based inference of genetic diversity and population structure of clinical Klebsiella pneumoniae, China. Scientific Reports, 2015, 5, 7612.	3.3	16
131	Plasmid pPCP1-derived sRNA HmsA promotes biofilm formation of Yersinia pestis. BMC Microbiology, 2016, 16, 176.	3.3	16
132	Real time monitoring of <scp>Aeromonas salmonicida</scp> evolution in response to successive antibiotic therapies in a commercial fish farm. Environmental Microbiology, 2019, 21, 1113-1123.	3.8	16
133	Identification of different regions among strains of Yersinia pestis by suppression subtractive hybridization. Research in Microbiology, 2005, 156, 785-789.	2.1	15
134	Quorum sensing affects virulence-associated proteins F1, LcrV, KatY and pH6 etc. of Yersinia pestis as revealed by protein microarray-based antibody profiling. Microbes and Infection, 2006, 8, 2501-2508.	1.9	15
135	Comparative genomics of five different resistance plasmids coexisting in a clinical multi-drug resistant Citrobacter freundii isolate. Infection and Drug Resistance, 2018, Volume 11, 1447-1460.	2.7	15
136	Type 1, 2, and 1/2-Hybrid IncC Plasmids From China. Frontiers in Microbiology, 2019, 10, 2508.	3.5	15
137	Novel Chromosome-Borne Accessory Genetic Elements Carrying Multiple Antibiotic Resistance Genes in Pseudomonas aeruginosa. Frontiers in Cellular and Infection Microbiology, 2021, 11, 638087.	3.9	15
138	Transcriptional regulation of the virulence genes and the biofilm formation associated operons in Vibrio parahaemolyticus. Gut Pathogens, 2021, 13, 15.	3.4	15
139	Transcriptional regulation of the waaAE-coaD operon by PhoP and RcsAB in Yersinia pestis biovar Microtus. Protein and Cell, 2014, 5, 940-944.	11.0	14
140	Genomic diversification of IncR plasmids from China. Journal of Global Antimicrobial Resistance, 2019, 19, 358-364.	2.2	14
141	The quorum sensing regulator OpaR is a repressor of polar flagellum genes in Vibrio parahaemolyticus. Journal of Microbiology, 2021, 59, 651-657.	2.8	14
142	Acquisition of Maternal Antibodies both from the Placenta and by Lactation Protects Mouse Offspring from Yersinia pestis Challenge. Vaccine Journal, 2012, 19, 1746-1750.	3.1	13
143	Altered Transcriptome of the B. melitensis Vaccine Candidate 16MÎ”vjbR, Implications for Development of Genetically Marked Live Vaccine. Indian Journal of Microbiology, 2012, 52, 575-580.	2.7	13
144	Omics strategies for revealing Yersinia pestis virulence. Frontiers in Cellular and Infection Microbiology, 2012, 2, 157.	3.9	13

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145	Sequencing of pT5282-CTXM, p13190-KPC and p30860-NR, and comparative genomics analysis of IncX8 plasmids. International Journal of Antimicrobial Agents, 2018, 52, 210-217.	2.5	13
146	Genetic Characterization of a blaVIMâ€“24-Carrying IncP-7Î² Plasmid p1160-VIM and a blaVIMâ€“4-Harboring Integrative and Conjugative Element Tn6413 From Clinical Pseudomonas aeruginosa. Frontiers in Microbiology, 2019, 10, 213.	3.5	13
147	Precision Methylome and In Vivo Methylation Kinetics Characterization of Klebsiella pneumoniae. Genomics, Proteomics and Bioinformatics, 2022, 20, 418-434.	6.9	13
148	Quorum sensing regulates transcription of the pilin gene mshA1 of MSHA pilus in Vibrio parahaemolyticus. Gene, 2022, 807, 145961.	2.2	13
149	Genomic Epidemiology of Carbapenemase-producing Klebsiella pneumoniae in China. Genomics, Proteomics and Bioinformatics, 2022, 20, 1154-1167.	6.9	13
150	The First Report of a Fully Sequenced Resistance Plasmid from Shigella boydii. Frontiers in Microbiology, 2016, 7, 1579.	3.5	12
151	Chromosomal Integration of Huge and Complex blaNDM-Carrying Genetic Elements in Enterobacteriaceae. Frontiers in Cellular and Infection Microbiology, 2021, 11, 690799.	3.9	12
152	Identification of Gene Clusters Associated with Host Adaptation and Antibiotic Resistance in Chinese Staphylococcus aureus Isolates by Microarray-Based Comparative Genomics. PLoS ONE, 2013, 8, e53341.	2.5	12
153	A proteinâ€“protein interaction map reveals that the Coxiella burnetii effector CirB inhibits host proteasome activity. PLoS Pathogens, 2022, 18, e1010660.	4.7	12
154	Comparative genomics of type 1 IncC plasmids from China. Future Microbiology, 2017, 12, 1511-1522.	2.0	11
155	A novel genotyping scheme for Vibrio parahaemolyticus with combined use of large variably-presented gene clusters (LVPCs) and variable-number tandem repeats (VNTRs). International Journal of Food Microbiology, 2011, 149, 143-151.	4.7	10
156	Cyclic AMP receptor protein is a repressor of adenylyl cyclase genecyaAinYersinia pestis. Canadian Journal of Microbiology, 2013, 59, 304-310.	1.7	10
157	H-NS represses transcription of the flagellin gene lafA of lateral flagella in Vibrio parahaemolyticus. Canadian Journal of Microbiology, 2018, 64, 69-74.	1.7	10
158	First Report of Liver Abscess Caused by Salmonella enterica Serovar Dublin. Journal of Clinical Microbiology, 2013, 51, 3140-3142.	3.9	9
159	Kinetics of Memory <scp>B</scp> Cell and Plasma Cell Responses in the Mice Immunized with Plague Vaccines. Scandinavian Journal of Immunology, 2014, 79, 157-162.	2.7	9
160	Genetic diversity and virulence of novel sequence types of Streptococcus suis from diseased and healthy pigs in China. Frontiers in Microbiology, 2015, 6, 173.	3.5	9
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