

Ruiting Lan

List of Publications by Year in descending order

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192
papers

8,616
citations

61984

43
h-index

60623

81
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205
all docs

205
docs citations

205
times ranked

8092
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid Surface Shaving for Proteomic Identification of Novel Surface Antigens for Vaccine Development. <i>Methods in Molecular Biology</i> , 2022, 2414, 47-62.	0.9	1
2	Metagenomics combined with comprehensive validation as a public health risk assessment tool for urban and agricultural run-off. <i>Water Research</i> , 2022, 209, 117941.	11.3	9
3	Horizontal transfer of antibiotic resistance genes within the bacterial communities in aquacultural environment. <i>Science of the Total Environment</i> , 2022, 820, 153286.	8.0	9
4	Genomic dissection of the microevolution of Australian epidemic <i>Bordetella pertussis</i> . <i>Emerging Microbes and Infections</i> , 2022, 11, 1460-1473.	6.5	4
5	Dissecting <i>Listeria monocytogenes</i> Persistent Contamination in a Retail Market Using Whole-Genome Sequencing. <i>Microbiology Spectrum</i> , 2022, 10, e0018522.	3.0	4
6	Beta- and Novel Delta-Coronaviruses Are Identified from Wild Animals in the Qinghai-Tibetan Plateau, China. <i>Virologica Sinica</i> , 2021, 36, 402-411.	3.0	20
7	<i>Citrobacter freundii</i> Activation of NLRP3 Inflammasome via the Type VI Secretion System. <i>Journal of Infectious Diseases</i> , 2021, 223, 2174-2185.	4.0	11
8	Population Structure and Multidrug Resistance of Non-O1/Non-O139 <i>Vibrio cholerae</i> in Freshwater Rivers in Zhejiang, China. <i>Microbial Ecology</i> , 2021, 82, 319-333.	2.8	5
9	Development and comparison of novel multiple cross displacement amplification (MCDA) assays with other nucleic acid amplification methods for SARS-CoV-2 detection. <i>Scientific Reports</i> , 2021, 11, 1873.	3.3	13
10	Establishment and Application of Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry for Detection of <i>Shewanella</i> Genus. <i>Frontiers in Microbiology</i> , 2021, 12, 625821.	3.5	8
11	Continuous Genomic Surveillance Monitored the <i>In Vivo</i> Evolutionary Trajectories of <i>Vibrio parahaemolyticus</i> and Identified a New Virulent Genotype. <i>MSystems</i> , 2021, 6, .	3.8	6
12	Comparative Phosphoproteomics of Classical <i>Bordetella</i> Elucidates the Potential Role of Serine, Threonine and Tyrosine Phosphorylation in <i>Bordetella</i> Biology and Virulence. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 660280.	3.9	4
13	Elucidation of global and national genomic epidemiology of <i>Salmonella enterica</i> serovar Enteritidis through multilevel genome typing. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
14	Antimicrobial Resistance and Molecular Characterization of <i>Citrobacter</i> spp. Causing Extraintestinal Infections. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 737636.	3.9	18
15	Multilevel Genome Typing Describes Short- and Long-Term <i>Vibrio cholerae</i> Molecular Epidemiology. <i>MSystems</i> , 2021, 6, e0013421.	3.8	6
16	Evolutionary genomics of recent clinical <i>Bordetella pertussis</i> isolates from Iran: wide circulation of multiple ptxP3 lineages and report of the first ptxP3 filamentous hemagglutinin-negative <i>B. pertussis</i> . <i>Infection, Genetics and Evolution</i> , 2021, 93, 104970.	2.3	3
17	Enhancing genomics-based outbreak detection of endemic <i>Salmonella enterica</i> serovar Typhimurium using dynamic thresholds. <i>Microbial Genomics</i> , 2021, 7, .	2.0	16
18	Improved Genomic Identification, Clustering, and Serotyping of Shiga Toxin-Producing <i>Escherichia coli</i> Using Cluster/Serotype-Specific Gene Markers. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 772574.	3.9	9

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19	Cluster-specific gene markers enhance <i>Shigella</i> and enteroinvasive <i>Escherichia coli</i> in silico serotyping. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
20	Comparative genomics of Chinese and international isolates of <i>Escherichia albertii</i> : population structure and evolution of virulence and antimicrobial resistance. <i>Microbial Genomics</i> , 2021, 7, .	2.0	7
21	National Safety Survey of Animal-use Commercial Probiotics and Their Spillover Effects From Farm to Humans: An Emerging Threat to Public Health. <i>Clinical Infectious Diseases</i> , 2020, 70, 2386-2395.	5.8	23
22	Surfaceome analysis of Australian epidemic <i>Bordetella pertussis</i> reveals potential vaccine antigens. <i>Vaccine</i> , 2020, 38, 539-548.	3.8	12
23	Early termination of the Shiga toxin transcript generates a regulatory small RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25055-25065.	7.1	16
24	Comparison of xMAP <i>Salmonella</i> Serotyping Assay With Traditional Serotyping and Discordance Resolution by Whole Genome Sequencing. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 452.	3.9	0
25	Nonsynonymous Polymorphism Counts in Bacterial Genomes: a Comparative Examination. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	3.1	3
26	A Nosocomial Respiratory Infection Outbreak of Carbapenem-Resistant <i>Escherichia coli</i> ST131 With Multiple Transmissible blaKPC α 2 Carrying Plasmids. <i>Frontiers in Microbiology</i> , 2020, 11, 2068.	3.5	18
27	Horizontal Plasmid Transfer Promotes the Dissemination of Asian Acute Hepatopancreatic Necrosis Disease and Provides a Novel Mechanism for Genetic Exchange and Environmental Adaptation. <i>MSystems</i> , 2020, 5, .	3.8	21
28	Emergence of pertactin-deficient pertussis strains in Australia can be explained by models of vaccine escape. <i>Epidemics</i> , 2020, 31, 100388.	3.0	9
29	Lineage, Antimicrobial Resistance and Virulence of <i>Citrobacter</i> spp. <i>Pathogens</i> , 2020, 9, 195.	2.8	21
30	Highly Sensitive and Specific Detection and Serotyping of Five Prevalent <i>Salmonella</i> Serovars by Multiple Cross-Displacement Amplification. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 708-719.	2.8	9
31	Analysis of complete <i>Campylobacter concisus</i> genomes identifies genomospecies features, secretion systems and novel plasmids and their association with severe ulcerative colitis. <i>Microbial Genomics</i> , 2020, 6, .	2.0	13
32	Multilevel genome typing: genomics-guided scalable resolution typing of microbial pathogens. <i>Eurosurveillance</i> , 2020, 25, .	7.0	12
33	Carriage and potential long distance transmission of <i>Listeria monocytogenes</i> by migratory black-headed gulls in Dianchi Lake, Kunming. <i>Emerging Microbes and Infections</i> , 2019, 8, 1195-1204.	6.5	10
34	Whole-Genome Sequencing Reveals a Prolonged and Persistent Intrahospital Transmission of <i>Corynebacterium striatum</i> , an Emerging Multidrug-Resistant Pathogen. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	23
35	Genomic and molecular characterisation of <i>Escherichia marmotae</i> from wild rodents in Qinghai-Tibet plateau as a potential pathogen. <i>Scientific Reports</i> , 2019, 9, 10619.	3.3	24
36	In silico Identification of Serovar-Specific Genes for <i>Salmonella</i> Serotyping. <i>Frontiers in Microbiology</i> , 2019, 10, 835.	3.5	18

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37	Long-distance transmission of pathogenic <i>Vibrio</i> species by migratory waterbirds: a potential threat to the public health. <i>Scientific Reports</i> , 2019, 9, 16303.	3.3	23
38	Beyond a Ribosomal RNA Methyltransferase, the Wider Role of <i>MraW</i> in DNA Methylation, Motility and Colonization in <i>Escherichia coli</i> O157:H7. <i>Frontiers in Microbiology</i> , 2019, 10, 2520.	3.5	8
39	Case report: whole genome sequencing based investigation of maternal-neonatal listeriosis in Sichuan, China. <i>BMC Infectious Diseases</i> , 2019, 19, 893.	2.9	15
40	Genomic Epidemiology of <i>Streptococcus suis</i> Sequence Type 7 Sporadic Infections in the Guangxi Zhuang Autonomous Region of China. <i>Pathogens</i> , 2019, 8, 187.	2.8	15
41	Genomic epidemiology of Iranian <i>Bordetella pertussis</i> : 50 years after the implementation of whole cell vaccine. <i>Emerging Microbes and Infections</i> , 2019, 8, 1416-1427.	6.5	23
42	Pertactin-Negative and Filamentous Hemagglutinin-Negative <i>Bordetella pertussis</i> , Australia, 2013–2017. <i>Emerging Infectious Diseases</i> , 2019, 25, 1196-1199.	4.3	29
43	Genomic epidemiology of erythromycin-resistant <i>Bordetella pertussis</i> in China. <i>Emerging Microbes and Infections</i> , 2019, 8, 461-470.	6.5	46
44	Genomic dissection of the most prevalent <i>Listeria monocytogenes</i> clone, sequence type ST87, in China. <i>BMC Genomics</i> , 2019, 20, 1014.	2.8	25
45	A novel multilocus variable-number tandem repeat analysis for <i>Bordetella parapertussis</i> . <i>Journal of Medical Microbiology</i> , 2019, 68, 1671-1676.	1.8	0
46	Proteomic Adaptation of Australian Epidemic <i>Bordetella pertussis</i> . <i>Proteomics</i> , 2018, 18, e1700237.	2.2	29
47	Genomic analysis of oral <i>Campylobacter concisus</i> strains identified a potential bacterial molecular marker associated with active Crohn's disease. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-14.	6.5	25
48	Comparison of the Whole Cell Proteome and Secretome of Epidemic <i>Bordetella pertussis</i> Strains From the 2008–2012 Australian Epidemic Under Sulfate-Modulating Conditions. <i>Frontiers in Microbiology</i> , 2018, 9, 2851.	3.5	12
49	Genetic Diversity, Multidrug Resistance, and Virulence of <i>Citrobacter freundii</i> From Diarrheal Patients and Healthy Individuals. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 233.	3.9	48
50	Risk Factors and Level of <i>Listeria monocytogenes</i> Contamination of Raw Pork in Retail Markets in China. <i>Frontiers in Microbiology</i> , 2018, 9, 1090.	3.5	21
51	Novel <i>Salmonella enterica</i> Serovar Typhimurium Genotype Levels as Herald of Seasonal Salmonellosis Epidemics. <i>Emerging Infectious Diseases</i> , 2018, 24, 1079-1082.	4.3	6
52	Novel multiplex PCR assay for identification and subtyping of enteroinvasive <i>Escherichia coli</i> and differentiation from <i>Shigella</i> based on target genes selected by comparative genomics. <i>Journal of Medical Microbiology</i> , 2018, 67, 1257-1264.	1.8	12
53	Vaccine-driven selection and the changing molecular epidemiology of <i>Bordetella pertussis</i> . , 2018, , 166-181.		3
54	A 12-month longitudinal study of <i>Listeria monocytogenes</i> contamination and persistence in pork retail markets in China. <i>Food Control</i> , 2017, 76, 66-73.	5.5	31

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55	Population and evolutionary dynamics of Shiga toxin producing <i>Escherichia coli</i> O157 in a beef herd: A longitudinal study. <i>Environmental Microbiology</i> , 2017, 19, 1836-1844.	3.8	3
56	Characterisation of the <i>Bordetella pertussis</i> secretome under different media. <i>Journal of Proteomics</i> , 2017, 158, 43-51.	2.4	34
57	Whole-genome sequencing and comparative genomic analysis of <i>Bordetella pertussis</i> isolates from the 2007–2008 epidemic in Israel. <i>Journal of Infection</i> , 2017, 74, 204-207.	3.3	8
58	Isolation and characterization of <i>Listeria</i> species from rodents in natural environments in China. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-6.	6.5	44
59	Genomic heterogeneity of <i>Salmonella enterica</i> serovar Typhimurium bacteriuria from chronic infection. <i>Infection, Genetics and Evolution</i> , 2017, 51, 17-20.	2.3	2
60	Comparative genomics of Australian and international isolates of <i>Salmonella</i> Typhimurium: correlation of core genome evolution with CRISPR and prophage profiles. <i>Scientific Reports</i> , 2017, 7, 9733.	3.3	26
61	Shiga Toxin-Producing <i>Escherichia coli</i> O157 Shedding Dynamics in an Australian Beef Herd. <i>Frontiers in Veterinary Science</i> , 2017, 4, 200.	2.2	4
62	Prevalence and Molecular Characteristics of Extended-Spectrum β -Lactamase Genes in <i>Escherichia coli</i> Isolated from Diarrheic Patients in China. <i>Frontiers in Microbiology</i> , 2017, 8, 144.	3.5	24
63	Antimicrobial Resistance and Cytotoxicity of <i>Citrobacter</i> spp. in Maanshan Anhui Province, China. <i>Frontiers in Microbiology</i> , 2017, 8, 1357.	3.5	42
64	Detection of Multiple Parallel Transmission Outbreak of <i>Streptococcus suis</i> Human Infection by Use of Genome Epidemiology, China, 2005. <i>Emerging Infectious Diseases</i> , 2017, 23, 204-211.	4.3	25
65	<i>Streptococcus himalayensis</i> sp. nov., isolated from the respiratory tract of <i>Marmota himalayana</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 256-261.	1.7	19
66	Detection and dissemination of the colistin resistance gene, <i>mcr-1</i> , from isolates and faecal samples in China. <i>Journal of Medical Microbiology</i> , 2017, 66, 119-125.	1.8	28
67	Evolution of Variable Number Tandem Repeats and Its Relationship with Genomic Diversity in <i>Salmonella</i> Typhimurium. <i>Frontiers in Microbiology</i> , 2016, 7, 2002.	3.5	8
68	Whole genome sequencing of <i>Salmonella</i> Typhimurium illuminates distinct outbreaks caused by an endemic multi-locus variable number tandem repeat analysis type in Australia, 2014. <i>BMC Microbiology</i> , 2016, 16, 211.	3.3	29
69	Genome analysis of <i>Campylobacter concisus</i> strains from patients with inflammatory bowel disease and gastroenteritis provides new insights into pathogenicity. <i>Scientific Reports</i> , 2016, 6, 38442.	3.3	31
70	Insights into the evolution of pathogenicity of <i>Escherichia coli</i> from genomic analysis of intestinal <i>E. coli</i> of <i>Marmota himalayana</i> in Qinghai–Tibet plateau of China. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-9.	6.5	31
71	Population structure and minimum core genome typing of <i>Legionella pneumophila</i> . <i>Scientific Reports</i> , 2016, 6, 21356.	3.3	28
72	High resolution melting curve analysis with MATLAB-based program. Measurement: Journal of the International Measurement Confederation, 2016, 90, 178-186.	5.0	5

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73	Novel Capsular Polysaccharide Loci and New Diagnostic Tools for High-Throughput Capsular Gene Typing in <i>Streptococcus suis</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 7102-7112.	3.1	31
74	SnpFilt: A pipeline for reference-free assembly-based identification of SNPs in bacterial genomes. <i>Computational Biology and Chemistry</i> , 2016, 65, 178-184.	2.3	19
75	Zonula occludens toxins and their prophages in <i>Campylobacter</i> species. <i>Gut Pathogens</i> , 2016, 8, 43.	3.4	30
76	Better colonisation of newly emerged <i>Bordetella pertussis</i> in the co-infection mouse model study. <i>Vaccine</i> , 2016, 34, 3967-3971.	3.8	40
77	Genomic dissection of Australian <i>Bordetella pertussis</i> isolates from the 2008–2012 epidemic. <i>Journal of Infection</i> , 2016, 72, 468-477.	3.3	52
78	US Gulf-like toxigenic O1 <i>Vibrio cholerae</i> causing sporadic cholera outbreaks in China. <i>Journal of Infection</i> , 2016, 72, 564-572.	3.3	12
79	The relationship between <i>Bordetella pertussis</i> genotype and clinical severity in Australian children with pertussis. <i>Journal of Infection</i> , 2016, 72, 171-178.	3.3	32
80	Infection by and dissemination of NDM-5-producing <i>Escherichia coli</i> in China: Table A1.. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 563-565.	3.0	46
81	<i>Streptococcus halotolerans</i> sp. nov. isolated from the respiratory tract of <i>Marmota himalayana</i> in Qinghai-Tibet Plateau of China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4211-4217.	1.7	16
82	<i>Streptococcus marmotae</i> sp. nov., isolated from the respiratory tract of <i>Marmota himalayana</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4315-4322.	1.7	15
83	Virulence variations in <i>Shigella</i> and enteroinvasive <i>Escherichia coli</i> using the <i>Caenorhabditis elegans</i> model. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-5.	1.8	7
84	Eight Novel Capsular Polysaccharide Synthesis Gene Loci Identified in Nontypeable <i>Streptococcus suis</i> Isolates. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4111-4119.	3.1	31
85	Multiple Endonuclease Restriction Real-Time Loop-Mediated Isothermal Amplification. <i>Journal of Molecular Diagnostics</i> , 2015, 17, 392-401.	2.8	54
86	Defining the Core Genome of <i>Salmonella enterica</i> Serovar Typhimurium for Genomic Surveillance and Epidemiological Typing. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2530-2538.	3.9	29
87	<i>Escherichia marmotae</i> sp. nov., isolated from faeces of <i>Marmota himalayana</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2130-2134.	1.7	75
88	The Type VI Secretion System Modulates Flagellar Gene Expression and Secretion in <i>Citrobacter freundii</i> and Contributes to Adhesion and Cytotoxicity to Host Cells. <i>Infection and Immunity</i> , 2015, 83, 2596-2604.	2.2	36
89	Delineating Community Outbreaks of <i>Salmonella enterica</i> Serovar Typhimurium by Use of Whole-Genome Sequencing: Insights into Genomic Variability within an Outbreak. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1063-1071.	3.9	76
90	Characterization of a large novel phage-like plasmid in <i>Salmonella enterica</i> serovar Typhimurium. <i>FEMS Microbiology Letters</i> , 2015, 362, fnv044.	1.8	20

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91	A preliminary stochastic model for managing microorganisms in a recirculating aquaculture system. <i>Annals of Microbiology</i> , 2015, 65, 1119-1129.	2.6	5
92	Pertactin negative <i>Bordetella pertussis</i> demonstrates higher fitness under vaccine selection pressure in a mixed infection model. <i>Vaccine</i> , 2015, 33, 6277-6281.	3.8	93
93	Characterization of <i>Listeria monocytogenes</i> isolated from human Listeriosis cases in China. <i>Emerging Microbes and Infections</i> , 2015, 4, 1-3.	6.5	45
94	Genomic Variability of Serial Human Isolates of <i>Salmonella enterica</i> Serovar Typhimurium Associated with Prolonged Carriage. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3507-3514.	3.9	23
95	<i>Shigella</i> and Shigellosis. , 2015, , 1147-1168.		3
96	Genotypic characterization of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 isolates in food products from china between 2005 and 2010. <i>Food Control</i> , 2015, 50, 209-214.	5.5	15
97	Delineation of genetic relatedness and population structure of oral and enteric <i>Campylobacter concisus</i> strains by analysis of housekeeping genes. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1600-1612.	1.8	22
98	Prevalence of <i>Salmonella</i> Isolates from Chicken and Pig Slaughterhouses and Emergence of Ciprofloxacin and Cefotaxime Co-Resistant <i>S. enterica</i> Serovar Indiana in Henan, China. <i>PLoS ONE</i> , 2015, 10, e0144532.	2.5	71
99	Genomic Portrait of the Evolution and Epidemic Spread of a Recently Emerged Multidrug-Resistant <i>Shigella flexneri</i> Clone in China. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1119-1126.	3.9	21
100	Identification of an O -Acyltransferase Gene (<i>oacB</i>) That Mediates 3- and 4-O-Acetylation of Rhamnose III in <i>Shigella flexneri</i> O Antigens. <i>Journal of Bacteriology</i> , 2014, 196, 1525-1531.	2.2	19
101	Rapid Increase in Pertactin-deficient <i>Bordetella pertussis</i> Isolates, Australia. <i>Emerging Infectious Diseases</i> , 2014, 20, 626-33.	4.3	151
102	Global Population Structure and Evolution of <i>Bordetella pertussis</i> and Their Relationship with Vaccination. <i>MBio</i> , 2014, 5, e01074.	4.1	257
103	Serotype-Converting Bacteriophage SfII Encodes an Acyltransferase Protein That Mediates 6-O-Acetylation of GlcNAc in <i>Shigella flexneri</i> O-Antigens, Conferring on the Host a Novel O-Antigen Epitope. <i>Journal of Bacteriology</i> , 2014, 196, 3656-3666.	2.2	23
104	Investigating genome reduction of <i>Bordetella pertussis</i> using a multiplex PCR-based reverse line blot assay (mPCR/RLB). <i>BMC Research Notes</i> , 2014, 7, 727.	1.4	10
105	Genetic and structural identification of an O-acyltransferase gene (<i>oacC</i>) responsible for the 3/4-O-acetylation on rhamnose III in <i>Shigella flexneri</i> serotype 6. <i>BMC Microbiology</i> , 2014, 14, 266.	3.3	13
106	Dissemination and serotype modification potential of pSFxv_2, an O-antigen PETn modification plasmid in <i>Shigella flexneri</i> . <i>Glycobiology</i> , 2014, 24, 305-313.	2.5	14
107	Examination of the Anaerobic Growth of <i>Campylobacter concisus</i> Strains. <i>International Journal of Microbiology</i> , 2014, 2014, 1-7.	2.3	32
108	Characterization of Shiga toxin-producing <i>Escherichia coli</i> isolated from healthy pigs in China. <i>BMC Microbiology</i> , 2014, 14, 5.	3.3	71

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109	Serological Identification and Prevalence of a Novel O-Antigen Epitope Linked to 3- and 4- <i>O</i> -Acetylated Rhamnose III of Lipopolysaccharide in <i>Shigella flexneri</i> . <i>Journal of Clinical Microbiology</i> , 2014, 52, 2033-2038.	3.9	9
110	Population structure and virulence content of avian pathogenic <i>Escherichia coli</i> isolated from outbreaks in Sri Lanka. <i>Veterinary Microbiology</i> , 2014, 168, 403-412.	1.9	62
111	Population Analysis of <i>Streptococcus suis</i> Isolates from Slaughtered Swine by Use of Minimum Core Genome Sequence Typing. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3568-3572.	3.9	24
112	The Family Enterobacteriaceae. , 2014, , 225-286.		50
113	Comparative Genomic Hybridization Identifies Virulence Differences in <i>Streptococcus suis</i> . <i>PLoS ONE</i> , 2014, 9, e87866.	2.5	15
114	Sequential Isolation in a Patient of <i>Raoultella planticola</i> and <i>Escherichia coli</i> Bearing a Novel ISCR1 Element Carrying blaNDM-1. <i>PLoS ONE</i> , 2014, 9, e89893.	2.5	68
115	Molecular analysis of non-O1/non-O139 <i>Vibrio cholerae</i> isolated from hospitalised patients in China. <i>BMC Microbiology</i> , 2013, 13, 52.	3.3	50
116	Isolation and genomic characterization of Sfl, a serotype-converting bacteriophage of <i>Shigella flexneri</i> . <i>BMC Microbiology</i> , 2013, 13, 39.	3.3	43
117	SNP genotyping of enterohemorrhagic <i>Escherichia coli</i> O157:H7 isolates from China and genomic identity of the 1999 Xuzhou outbreak. <i>Infection, Genetics and Evolution</i> , 2013, 16, 275-281.	2.3	6
118	Genomic diversity and adaptation of <i>Salmonella enterica</i> serovar Typhimurium from analysis of six genomes of different phage types. <i>BMC Genomics</i> , 2013, 14, 718.	2.8	34
119	Structure of the O-antigen of a novel <i>Shigella flexneri</i> serotype, 1d (I: 7,8). <i>Carbohydrate Research</i> , 2013, 373, 93-96.	2.3	10
120	Minimum Core Genome Sequence Typing of Bacterial Pathogens: a Unified Approach for Clinical and Public Health Microbiology. <i>Journal of Clinical Microbiology</i> , 2013, 51, 2582-2591.	3.9	84
121	O-antigen structure of <i>Shigella flexneri</i> serotype Yv and effect of the <i>lpt-O</i> gene variation on phosphoethanolamine modification of <i>S. flexneri</i> O-antigens. <i>Glycobiology</i> , 2013, 23, 475-485.	2.5	22
122	Shiga Toxin-Producing <i>Escherichia coli</i> in Yaks (<i>Bos grunniens</i>) from the Qinghai-Tibetan Plateau, China. <i>PLoS ONE</i> , 2013, 8, e65537.	2.5	32
123	Identification and Characterization of a Novel <i>Shigella flexneri</i> Serotype Yv in China. <i>PLoS ONE</i> , 2013, 8, e70238.	2.5	45
124	Development of Multiplex PCR Assays for the Identification of the 33 Serotypes of <i>Streptococcus suis</i> . <i>PLoS ONE</i> , 2013, 8, e72070.	2.5	70
125	The Prevalence and Polymorphisms of Zonula Occluden Toxin Gene in Multiple <i>Campylobacter concisus</i> Strains Isolated from Saliva of Patients with Inflammatory Bowel Disease and Controls. <i>PLoS ONE</i> , 2013, 8, e75525.	2.5	39
126	An O Island 172 Encoded RNA Helicase Regulates the Motility of <i>Escherichia coli</i> O157:H7. <i>PLoS ONE</i> , 2013, 8, e64211.	2.5	46

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127	Population Structure and Evolution of Non-O1/Non-O139 <i>Vibrio cholerae</i> by Multilocus Sequence Typing. PLoS ONE, 2013, 8, e65342.	2.5	77
128	Global Transcriptional and Phenotypic Analyses of <i>Escherichia coli</i> O157:H7 Strain Xuzhou21 and Its pO157_Sal Cured Mutant. PLoS ONE, 2013, 8, e65466.	2.5	11
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