

Chen Chen

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

88
papers

2,959
citations

25
h-index

53
g-index

94
ext. papers

3,572
ext. citations

6.6
avg, IF

4.62
L-index

#	Paper	IF	Citations
88	Alteration of microbiota and immune response of mice gavaged with <i>Klebsiella oxytoca</i> .. <i>Microbes and Infection</i> , 2022 , 104977	9.3	
87	Two-step fitness selection for intra-host variations in SARS-CoV-2.. <i>Cell Reports</i> , 2021 , 110205	10.6	9
86	High alcohol-producing causes fatty liver disease through 2,3-butanediol fermentation pathway. <i>Gut Microbes</i> , 2021 , 13, 1979883	8.8	1
85	Specific Redistribution of Severe Acute Respiratory Syndrome Coronavirus 2 Variants in the Respiratory System and Intestinal Tract. <i>Clinical Infectious Diseases</i> , 2021 , 73, e2814-e2817	11.6	6
84	Dynamics of HIV-1 quasispecies diversity of participants on long-term antiretroviral therapy based on intrahost single-nucleotide variations. <i>International Journal of Infectious Diseases</i> , 2021 , 104, 306-314	10.5	3
83	Early and consecutive RT-PCR tests with both oropharyngeal swabs and sputum could improve testing yield for patients with COVID-19: An observation cohort study in China. <i>International Journal of Infectious Diseases</i> , 2021 , 107, 242-246	10.5	2
82	Partial recovery of disturbed V-J pairing profiles of T-cell receptor in people living with HIV receiving long-term antiretroviral therapy. <i>Science China Life Sciences</i> , 2021 , 64, 152-161	8.5	0
81	COVID-19 reinfection in the presence of neutralizing antibodies. <i>National Science Review</i> , 2021 , 8, nwab0068	10.6	14
80	MINERVA: A Facile Strategy for SARS-CoV-2 Whole-Genome Deep Sequencing of Clinical Samples. <i>Molecular Cell</i> , 2020 , 80, 1123-1134.e4	17.6	8
79	Crosstalk of MicroRNAs and Oxidative Stress in the Pathogenesis of Cancer. <i>Oxidative Medicine and Cellular Longevity</i> , 2020 , 2020, 2415324	6.7	25
78	Metachronous primary lung adenocarcinomas harboring distinct KRAS mutations. <i>Thoracic Cancer</i> , 2020 , 11, 2018-2022	3.2	
77	Safe management of bodies of deceased persons with suspected or confirmed COVID-19: a rapid systematic review. <i>BMJ Global Health</i> , 2020 , 5,	6.6	29
76	A Comprehensive Review on Schisandrin B and Its Biological Properties. <i>Oxidative Medicine and Cellular Longevity</i> , 2020 , 2020, 2172740	6.7	21
75	ELISA and Chemiluminescent Enzyme Immunoassay for Sensitive and Specific Determination of Lead (II) in Water, Food and Feed Samples. <i>Foods</i> , 2020 , 9,	4.9	8
74	Ultrasensitive DNA hypermethylation detection using plasma for early detection of NSCLC: a study in Chinese patients with very small nodules. <i>Clinical Epigenetics</i> , 2020 , 12, 39	7.7	17
73	. <i>IEEE Access</i> , 2020 , 8, 59100-59113	3.5	5
72	Single-cell RNA-seq unveils critical regulators of human FOXP3+ regulatory T cell stability. <i>Science Bulletin</i> , 2020 , 65, 1114-1124	10.6	5

71	An APETALA2/ethylene responsive factor, OsEBP89 knockout enhances adaptation to direct-seeding on wet land and tolerance to drought stress in rice. <i>Molecular Genetics and Genomics</i> , 2020 , 295, 941-956	3.1	8
70	Ultrasmall NiFe layered double hydroxide strongly coupled on atomically dispersed FeCo-NC nanoflowers as efficient bifunctional catalyst for rechargeable Zn-air battery. <i>Science China Materials</i> , 2020 , 63, 1182-1195	7.1	22
69	Mapping and validation of sex-linked SNP markers in the swimming crab <i>Portunus trituberculatus</i> . <i>Aquaculture</i> , 2020 , 524, 735228	4.4	6
68	Genetic characterization and functional implications of the gene cluster for selective protein transport to extracellular membrane vesicles of <i>Shewanella vesiculosa</i> HM13. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 526, 525-531	3.4	5
67	Bioinformatics Methods for Mass Spectrometry-Based Proteomics Data Analysis. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	46
66	SARS-CoV-2-Positive Sputum and Feces After Conversion of Pharyngeal Samples in Patients With COVID-19. <i>Annals of Internal Medicine</i> , 2020 , 172, 832-834	8	137
65	Genomic surveillance of COVID-19 cases in Beijing. <i>Nature Communications</i> , 2020 , 11, 5503	17.4	16
64	Shedding light on autophagy coordinating with cell wall integrity signaling to govern pathogenicity of. <i>Autophagy</i> , 2020 , 16, 900-916	10.2	19
63	Lenticulostriate arteries appearance before thrombectomy predicts good outcome in acute middle cerebral artery occlusion. <i>BMC Neurology</i> , 2020 , 20, 139	3.1	2
62	Report on 153 sequential three-incision robotic-assisted pulmonary resections by a single surgeon: technical details and learning curve. <i>Journal of Thoracic Disease</i> , 2020 , 12, 741-748	2.6	0
61	Fatty Liver Disease Caused by High-Alcohol-Producing <i>Klebsiella pneumoniae</i> . <i>Cell Metabolism</i> , 2019 , 30, 675-688.e7	24.6	148
60	GPA: A Microbial Genetic Polymorphisms Assignments Tool in Metagenomic Analysis by Bayesian Estimation. <i>Genomics, Proteomics and Bioinformatics</i> , 2019 , 17, 106-117	6.5	4
59	Emergence of carbapenem-resistant hypervirulent <i>Klebsiella pneumoniae</i> . <i>Lancet Infectious Diseases, The</i> , 2018 , 18, 23-24	25.5	25
58	Phylogenomic analysis unravels evolution of yellow fever virus within hosts. <i>PLoS Neglected Tropical Diseases</i> , 2018 , 12, e0006738	4.8	16
57	A survey on cellular RNA editing activity in response to <i>Candida albicans</i> infections. <i>BMC Genomics</i> , 2018 , 19, 43	4.5	1
56	Genomic study of the Type IVC secretion system in <i>Clostridium difficile</i> : understanding <i>C. difficile</i> evolution via horizontal gene transfer. <i>Genome</i> , 2017 , 60, 8-16	2.4	3
55	Intra-host dynamics of Ebola virus during 2014. <i>Nature Microbiology</i> , 2016 , 1, 16151	26.6	54
54	Nosocomial transmission of <i>Clostridium difficile</i> ribotype 027 in a Chinese hospital, 2012-2014, traced by whole genome sequencing. <i>BMC Genomics</i> , 2016 , 17, 405	4.5	26

53	Identification of cardiac-related circulating microRNA profile in human chronic heart failure. <i>Oncotarget</i> , 2016 , 7, 33-45	3.3	53
52	Structural Modulation of Gut Microbiota in Rats with Allergic Bronchial Asthma Treated with Recuperating Lung Decoction. <i>Biomedical and Environmental Sciences</i> , 2016 , 29, 574-583	1.1	11
51	Genomic Characteristics of Chinese <i>Borrelia burgdorferi</i> Isolates. <i>PLoS ONE</i> , 2016 , 11, e0153149	3.7	2
50	Predictive value of the composition of the vaginal microbiota in bacterial vaginosis, a dynamic study to identify recurrence-related flora. <i>Scientific Reports</i> , 2016 , 6, 26674	4.9	29
49	Analyses of the mitochondrial mutations in the Chinese patients with sporadic Creutzfeldt-Jakob disease. <i>European Journal of Human Genetics</i> , 2015 , 23, 86-91	5.3	9
48	Phylogenetic study of clonal complex (CC)198 capsule null locus (cni) genomes: A distinctive group within the species <i>Neisseria meningitidis</i> . <i>Infection, Genetics and Evolution</i> , 2015 , 34, 372-7	4.5	7
47	Overexpression of Protein Kinase M̄n the Prelimbic Cortex Enhances the Formation of Long-Term Fear Memory. <i>Neuropsychopharmacology</i> , 2015 , 40, 2146-56	8.7	23
46	Rapid and Sensitive <i>Salmonella Typhi</i> Detection in Blood and Fecal Samples Using Reverse Transcription Loop-Mediated Isothermal Amplification. <i>Foodborne Pathogens and Disease</i> , 2015 , 12, 778-86	2.8	13
45	Genome sequence of <i>Bacillus anthracis</i> attenuated vaccine strain A16R used for human in China. <i>Journal of Biotechnology</i> , 2015 , 210, 15-6	3.7	7
44	TCRklass: a new K-string-based algorithm for human and mouse TCR repertoire characterization. <i>Journal of Immunology</i> , 2015 , 194, 446-54	5.3	29
43	Detection of <i>Clostridium difficile</i> toxin genes by PCR: sequence variation may cause false-negative results. <i>Journal of Medical Microbiology</i> , 2015 , 64, 195-197	3.2	2
42	Use of genome sequencing to assess nucleotide structure variation of <i>Staphylococcus aureus</i> strains cultured in spaceflight on Shenzhou-X, under simulated microgravity and on the ground. <i>Microbiological Research</i> , 2015 , 170, 61-8	5.3	10
41	microRNA-299-3p inhibits laryngeal cancer cell growth by targeting human telomerase reverse transcriptase mRNA. <i>Molecular Medicine Reports</i> , 2015 , 11, 4645-9	2.9	18
40	Comparative analysis of microbiome between accurately identified 16S rDNA and quantified bacteria in simulated samples. <i>Journal of Medical Microbiology</i> , 2014 , 63, 433-440	3.2	8
39	Sequence variation in <i>tcdA</i> and <i>tcdB</i> of <i>Clostridium difficile</i> : ST37 with truncated <i>tcdA</i> is a potential epidemic strain in China. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 3264-70	9.7	38
38	Evaluation of 16SpathDB 2.0, an automated 16S rRNA gene sequence database, using 689 complete bacterial genomes. <i>Diagnostic Microbiology and Infectious Disease</i> , 2014 , 78, 105-15	2.9	14
37	Conserved alanine rich protein Rv3878 in <i>Mycobacterium tuberculosis</i> contains sequence polymorphisms. <i>Tuberculosis</i> , 2014 , 94, 245-51	2.6	1
36	The purifying trend in the chromosomal integron in <i>Vibrio cholerae</i> strains during the seventh pandemic. <i>Infection, Genetics and Evolution</i> , 2014 , 26, 241-9	4.5	1

35	Whole-genome sequence comparison as a method for improving bacterial species definition. <i>Journal of General and Applied Microbiology</i> , 2014 , 60, 75-8	1.5	28
34	Rapid Identification of Bacterial Species Associated with Bronchiectasis via Metagenomic Approach. <i>Biomedical and Environmental Sciences</i> , 2014 , 27, 898-901	1.1	11
33	Dynamics of fecal microbial communities in children with diarrhea of unknown etiology and genomic analysis of associated <i>Streptococcus lutetiensis</i> . <i>BMC Microbiology</i> , 2013 , 13, 141	4.5	46
32	Genetic diversity of antigens Rv2945c and Rv0309 in <i>Mycobacterium tuberculosis</i> strains may reflect ongoing immune evasion. <i>FEMS Microbiology Letters</i> , 2013 , 347, 77-82	2.9	7
31	Comparative analysis of gene expression profiles between cortex and thalamus in Chinese fatal familial insomnia patients. <i>Molecular Neurobiology</i> , 2013 , 48, 36-48	6.2	23
30	The genome of VP3, a T7-like phage used for the typing of <i>Vibrio cholerae</i> . <i>Archives of Virology</i> , 2013 , 158, 1865-76	2.6	6
29	Reducing exposure to avian influenza H7N9. <i>Lancet, The</i> , 2013 , 381, 1815-6	4.0	29
28	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, 2582-91	9.7	64
27	Polymorphism of antigen MPT64 in <i>Mycobacterium tuberculosis</i> strains. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 1558-62	9.7	17
26	Silent geographical spread of the H7N9 virus by online knowledge analysis of the live bird trade with a distributed focused crawler. <i>Emerging Microbes and Infections</i> , 2013 , 2, e89	18.9	6
25	Global transcriptional profiling of the postmortem brain of a patient with G114V genetic Creutzfeldt-Jakob disease. <i>International Journal of Molecular Medicine</i> , 2013 , 31, 676-88	4.4	11
24	Comparative genomic analysis of <i>Brucella melitensis</i> vaccine strain M5 provides insights into virulence attenuation. <i>PLoS ONE</i> , 2013 , 8, e70852	3.7	12
23	Global transcriptional and phenotypic analyses of <i>Escherichia coli</i> O157:H7 strain Xuzhou21 and its pO157_Sal cured mutant. <i>PLoS ONE</i> , 2013 , 8, e65466	3.7	10
22	T4SP: a novel tool and database for type IV secretion systems in bacterial genomes. <i>Biomedical and Environmental Sciences</i> , 2013 , 26, 614-7	1.1	2
21	pstS1 polymorphisms of <i>Mycobacterium tuberculosis</i> strains may reflect ongoing immune evasion. <i>Tuberculosis</i> , 2013 , 93, 475-81	2.6	11
20	Genome of <i>Helicobacter pylori</i> strain XZ274, an isolate from a tibetan patient with gastric cancer in China. <i>Journal of Bacteriology</i> , 2012 , 194, 4146-7	3.5	11
19	Comparative genomic analysis of <i>Escherichia coli</i> O104:H4 stx2 prophage reveals a potential new method to identify virulence factors. <i>Genome</i> , 2012 , 55, 697-700	2.4	1
18	Type-IVC secretion system: a novel subclass of type IV secretion system (T4SS) common existing in gram-positive genus <i>Streptococcus</i> . <i>PLoS ONE</i> , 2012 , 7, e46390	3.7	35

17	All-optical virtual private network and ONUs communication in optical OFDM-based PON system. <i>Optics Express</i> , 2011 , 19, 24816-21	3.3	22
16	Identification of genes and genomic islands correlated with high pathogenicity in <i>Streptococcus suis</i> using whole genome tiling microarrays. <i>PLoS ONE</i> , 2011 , 6, e17987	3.7	23
15	Genome sequencing reveals unique mutations in characteristic metabolic pathways and the transfer of virulence genes between <i>V. mimicus</i> and <i>V. cholerae</i> . <i>PLoS ONE</i> , 2011 , 6, e21299	3.7	20
14	A large scale comparative genomic analysis reveals insertion sites for newly acquired genomic islands in bacterial genomes. <i>BMC Microbiology</i> , 2011 , 11, 135	4.5	8
13	Toxin A-negative, toxin B-positive <i>Clostridium difficile</i> infection diagnosed by polymerase chain reaction. <i>Infection Control and Hospital Epidemiology</i> , 2011 , 32, 520-2	2	5
12	Whole-genome sequences of four <i>Mycobacterium bovis</i> BCG vaccine strains. <i>Journal of Bacteriology</i> , 2011 , 193, 3152-3	3.5	21
11	Complete genome sequences of <i>Mycobacterium tuberculosis</i> strains CCDC5079 and CCDC5080, which belong to the Beijing family. <i>Journal of Bacteriology</i> , 2011 , 193, 5591-2	3.5	28
10	Complete genome sequences of <i>Yersinia pestis</i> from natural foci in China. <i>Journal of Bacteriology</i> , 2010 , 192, 3551-2	3.5	15
9	A transcriptomic analysis of superhybrid rice LYP9 and its parents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 7695-701	11.5	162
8	Genomic research for important pathogenic bacteria in China. <i>Science in China Series C: Life Sciences</i> , 2009 , 52, 50-63		5
7	A glimpse of streptococcal toxic shock syndrome from comparative genomics of <i>S. suis</i> 2 Chinese isolates. <i>PLoS ONE</i> , 2007 , 2, e315	3.7	204
6	Differential gene expression in an elite hybrid rice cultivar (<i>Oryza sativa</i> , L) and its parental lines based on SAGE data. <i>BMC Plant Biology</i> , 2007 , 7, 49	5.3	33
5	Global genome expression analysis of rice in response to drought and high-salinity stresses in shoot, flag leaf, and panicle. <i>Plant Molecular Biology</i> , 2007 , 63, 591-608	4.6	227
4	Detection of HPV-2 and identification of novel mutations by whole genome sequencing from biopsies of two patients with multiple cutaneous horns. <i>Journal of Clinical Virology</i> , 2007 , 39, 34-42	14.5	10
3	The Genomes of <i>Oryza sativa</i> : a history of duplications. <i>PLoS Biology</i> , 2005 , 3, e38	9.7	695
2	Serial analysis of gene expression study of a hybrid rice strain (LYP9) and its parental cultivars. <i>Plant Physiology</i> , 2005 , 138, 1216-31	6.6	81
1	A microarray analysis of the rice transcriptome and its comparison to <i>Arabidopsis</i> . <i>Genome Research</i> , 2005 , 15, 1274-83	9.7	103