

# Chen Chen

## List of Publications by Year in descending order

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89  
papers

4,089  
citations

172457

29  
h-index

123424

61  
g-index

94  
all docs

94  
docs citations

94  
times ranked

7229  
citing authors

#	ARTICLE	IF	CITATIONS
1	Two-step fitness selection for intra-host variations in SARS-CoV-2. <i>Cell Reports</i> , 2022, 38, 110205.	6.4	38
2	Alteration of microbiota and immune response of mice gavaged with <i>Klebsiella oxytoca</i> . <i>Microbes and Infection</i> , 2022, , 104977.	1.9	0
3	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.	5.8	6
4	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.	4.9	1
5	COVID-19 reinfection in the presence of neutralizing antibodies. <i>National Science Review</i> , 2021, 8, nwab006.	9.5	24
6	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.	3.3	5
7	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.	3.3	3
8	High alcohol-producing <i>Klebsiella pneumoniae</i> causes fatty liver disease through 2,3-butanediol fermentation pathway <i>in vivo</i> . <i>Gut Microbes</i> , 2021, 13, 1979883.	9.8	20
9	Shedding light on autophagy coordinating with cell wall integrity signaling to govern pathogenicity of <i>Magnaporthe oryzae</i> . <i>Autophagy</i> , 2020, 16, 900-916.	9.1	72
10	SARS-CoV-2â€œPositive Sputum and Feces After Conversion of Pharyngeal Samples in Patients With COVID-19. <i>Annals of Internal Medicine</i> , 2020, 172, 832-834.	3.9	190
11	Genomic surveillance of COVID-19 cases in Beijing. <i>Nature Communications</i> , 2020, 11, 5503.	12.8	26
12	MINERVA: A Facile Strategy for SARS-CoV-2 Whole-Genome Deep Sequencing of Clinical Samples. <i>Molecular Cell</i> , 2020, 80, 1123-1134.e4.	9.7	13
13	Crosstalk of MicroRNAs and Oxidative Stress in the Pathogenesis of Cancer. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-13.	4.0	45
14	Metachronous primary lung adenocarcinomas harboring distinct KRAS mutations. <i>Thoracic Cancer</i> , 2020, 11, 2018-2022.	1.9	0
15	Safe management of bodies of deceased persons with suspected or confirmed COVID-19: a rapid systematic review. <i>BMJ Global Health</i> , 2020, 5, e002650.	4.7	42
16	A Comprehensive Review on Schisandrin B and Its Biological Properties. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-13.	4.0	64
17	ELISA and Chemiluminescent Enzyme Immunoassay for Sensitive and Specific Determination of Lead (II) in Water, Food and Feed Samples. <i>Foods</i> , 2020, 9, 305.	4.3	20
18	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.	4.1	37

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19	Novel Framework: Face Feature Selection Algorithm for Neonatal Facial and Related Attributes Recognition. <i>IEEE Access</i> , 2020, 8, 59100-59113.	4.2	12
20	Single-cell RNA-seq unveils critical regulators of human FOXP3+ regulatory T cell stability. <i>Science Bulletin</i> , 2020, 65, 1114-1124.	9.0	10
21	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.	2.1	27
22	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.	6.3	44
23	Mapping and validation of sex-linked SNP markers in the swimming crab <i>Portunus trituberculatus</i> . <i>Aquaculture</i> , 2020, 524, 735228.	3.5	10
24	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.	2.1	9
25	Bioinformatics Methods for Mass Spectrometry-Based Proteomics Data Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2873.	4.1	134
26	Lenticulostriate arteries appearance before thrombectomy predicts good outcome in acute middle cerebral artery occlusion. <i>BMC Neurology</i> , 2020, 20, 139.	1.8	3
27	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.	1.4	4
28	Fatty Liver Disease Caused by High-Alcohol-Producing <i>Klebsiella pneumoniae</i> . <i>Cell Metabolism</i> , 2019, 30, 675-688.e7.	16.2	294
29	GPA: A Microbial Genetic Polymorphisms Assignments Tool in Metagenomic Analysis by Bayesian Estimation. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 106-117.	6.9	6
30	Emergence of carbapenem-resistant hypervirulent <i>Klebsiella pneumoniae</i> . <i>Lancet Infectious Diseases</i> , 2018, 18, 23-24.	9.1	41
31	Phylogenomic analysis unravels evolution of yellow fever virus within hosts. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006738.	3.0	24
32	A survey on cellular RNA editing activity in response to <i>Candida albicans</i> infections. <i>BMC Genomics</i> , 2018, 19, 43.	2.8	4
33	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.	2.0	7
34	Genomic Characteristics of Chinese <i>Borrelia burgdorferi</i> Isolates. <i>PLoS ONE</i> , 2016, 11, e0153149.	2.5	3
35	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.	3.3	56
36	Intra-host dynamics of Ebola virus during 2014. <i>Nature Microbiology</i> , 2016, 1, 16151.	13.3	70

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37	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.	2.8	34
38	Identification of cardiac-related circulating microRNA profile in human chronic heart failure. <i>Oncotarget</i> , 2016, 7, 33-45.	1.8	76
39	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.	0.2	13
40	microRNA-299-3p inhibits laryngeal cancer cell growth by targeting human telomerase reverse transcriptase mRNA. <i>Molecular Medicine Reports</i> , 2015, 11, 4645-4649.	2.4	20
41	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.	2.8	12
42	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, 372-377.	2.3	10
43	Overexpression of Protein Kinase M1 $\eta$ in the Prelimbic Cortex Enhances the Formation of Long-Term Fear Memory. <i>Neuropsychopharmacology</i> , 2015, 40, 2146-2156.	5.4	29
44	Rapid and Sensitive <i>Salmonella</i> Typhi Detection in Blood and Fecal Samples Using Reverse Transcription Loop-Mediated Isothermal Amplification. <i>Foodborne Pathogens and Disease</i> , 2015, 12, 778-786.	1.8	20
45	Genome sequence of <i>Bacillus anthracis</i> attenuated vaccine strain A16R used for human in China. <i>Journal of Biotechnology</i> , 2015, 210, 15-16.	3.8	9
46	TCRklass: A New K-String-Based Algorithm for Human and Mouse TCR Repertoire Characterization. <i>Journal of Immunology</i> , 2015, 194, 446-454.	0.8	43
47	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.	1.8	3
48	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, 61-68.	5.3	16
49	Whole-genome sequence comparison as a method for improving bacterial species definition. <i>Journal of General and Applied Microbiology</i> , 2014, 60, 75-78.	0.7	45
50	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.	1.8	9
51	Sequence Variation in <i>Clostridium difficile</i> : ST37 with Truncated <i>cdA</i> as a Potential Epidemic Strain in China. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3264-3270.	3.9	55
52	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, 105-115.	1.8	14
53	Conserved alanine rich protein Rv3878 in <i>Mycobacterium tuberculosis</i> contains sequence polymorphisms. <i>Tuberculosis</i> , 2014, 94, 245-251.	1.9	1
54	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, 241-249.	2.3	1

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55	Rapid Identification of Bacterial Species Associated with Bronchiectasis via Metagenomic Approach. <i>Biomedical and Environmental Sciences</i> , 2014, 27, 898-901.	0.2	11
56	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.	3.3	59
57	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.	1.8	7
58	Comparative Analysis of Gene Expression Profiles Between Cortex and Thalamus in Chinese Fatal Familial Insomnia Patients. <i>Molecular Neurobiology</i> , 2013, 48, 36-48.	4.0	26
59	The genome of VP3, a T7-like phage used for the typing of <i>Vibrio cholerae</i> . <i>Archives of Virology</i> , 2013, 158, 1865-1876.	2.1	7
60	Reducing exposure to avian influenza H7N9. <i>Lancet</i> , The, 2013, 381, 1815-1816.	13.7	33
61	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
62	Polymorphism of Antigen MPT64 in <i>Mycobacterium tuberculosis</i> Strains. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1558-1562.	3.9	22
63	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, 1-7.	6.5	7
64	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, 676-688.	4.0	14
65	Comparative Genomic Analysis of <i>Brucella melitensis</i> Vaccine Strain M5 Provides Insights into Virulence Attenuation. <i>PLoS ONE</i> , 2013, 8, e70852.	2.5	15
66	pstS1 polymorphisms of <i>Mycobacterium tuberculosis</i> strains may reflect ongoing immune evasion. <i>Tuberculosis</i> , 2013, 93, 475-481.	1.9	12
67	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.	2.5	11
68	T4SP: a novel tool and database for type IV secretion systems in bacterial genomes. <i>Biomedical and Environmental Sciences</i> , 2013, 26, 614-7.	0.2	2
69	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, 4146-4147.	2.2	15
70	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.	2.0	1
71	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.	2.5	42
72	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, 520-522.	1.8	5

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73	All-optical virtual private network and ONUs communication in optical OFDM-based PON system. <i>Optics Express</i> , 2011, 19, 24816.	3.4	30
74	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.	2.5	25
75	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.	2.5	25
76	A large scale comparative genomic analysis reveals insertion sites for newly acquired genomic islands in bacterial genomes. <i>BMC Microbiology</i> , 2011, 11, 135.	3.3	10
77	Whole-Genome Sequences of Four <i>Mycobacterium bovis</i> BCG Vaccine Strains. <i>Journal of Bacteriology</i> , 2011, 193, 3152-3153.	2.2	28
78	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, 5591-5592.	2.2	34
79	Complete Genome Sequences of <i>Yersinia pestis</i> from Natural Foci in China. <i>Journal of Bacteriology</i> , 2010, 192, 3551-3552.	2.2	17
80	A transcriptomic analysis of superhybrid rice <i>LYP9</i> and its parents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7695-7701.	7.1	184
81	Genomic research for important pathogenic bacteria in China. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 50-63.	1.3	6
82	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.	3.1	16
83	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.	2.5	244
84	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.	3.6	41
85	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.	3.9	275
86	Analysis of oligo hybridization properties by high-resolution tiling microarrays in rice. , 2007, , .		0
87	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	5.6	808
88	Serial Analysis of Gene Expression Study of a Hybrid Rice Strain (LYP9) and Its Parental Cultivars. <i>Plant Physiology</i> , 2005, 138, 1216-1231.	4.8	86
89	A microarray analysis of the rice transcriptome and its comparison to <i>Arabidopsis</i> . <i>Genome Research</i> , 2005, 15, 1274-1283.	5.5	112