

Jian Yang

List of Publications by Year in descending order

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Version: 2024-02-01

97
papers

10,315
citations

117571

34
h-index

37183

96
g-index

101
all docs

101
docs citations

101
times ranked

14203
citing authors

#	ARTICLE	IF	CITATIONS
1	VFDB: a reference database for bacterial virulence factors. <i>Nucleic Acids Research</i> , 2004, 33, D325-D328.	6.5	1,287
2	VFDB 2019: a comparative pathogenomic platform with an interactive web interface. <i>Nucleic Acids Research</i> , 2019, 47, D687-D692.	6.5	1,286
3	VFDB 2016: hierarchical and refined dataset for big data analysis—10 years on. <i>Nucleic Acids Research</i> , 2016, 44, D694-D697.	6.5	1,188
4	Identification of a novel coronavirus causing severe pneumonia in human: a descriptive study. <i>Chinese Medical Journal</i> , 2020, 133, 1015-1024.	0.9	928
5	VFDB 2012 update: toward the genetic diversity and molecular evolution of bacterial virulence factors. <i>Nucleic Acids Research</i> , 2012, 40, D641-D645.	6.5	457
6	Genome sequence of <i>Shigella flexneri</i> 2a: insights into pathogenicity through comparison with genomes of <i>Escherichia coli</i> K12 and O157. <i>Nucleic Acids Research</i> , 2002, 30, 4432-4441.	6.5	431
7	VFDB 2022: a general classification scheme for bacterial virulence factors. <i>Nucleic Acids Research</i> , 2022, 50, D912-D917.	6.5	372
8	Genome dynamics and diversity of <i>Shigella</i> species, the etiologic agents of bacillary dysentery. <i>Nucleic Acids Research</i> , 2005, 33, 6445-6458.	6.5	361
9	Nitrogen fixation island and rhizosphere competence traits in the genome of root-associated <i>Pseudomonas stutzeri</i> A1501. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7564-7569.	3.3	325
10	Deciphering the bat virome catalog to better understand the ecological diversity of bat viruses and the bat origin of emerging infectious diseases. <i>ISME Journal</i> , 2016, 10, 609-620.	4.4	249
11	Virome Analysis for Identification of Novel Mammalian Viruses in Bat Species from Chinese Provinces. <i>Journal of Virology</i> , 2012, 86, 10999-11012.	1.5	244
12	A <i>Pseudomonas aeruginosa</i> Type VI Secretion Phospholipase D Effector Targets Both Prokaryotic and Eukaryotic Cells. <i>Cell Host and Microbe</i> , 2014, 15, 600-610.	5.1	230
13	Cold-chain food contamination as the possible origin of COVID-19 resurgence in Beijing. <i>National Science Review</i> , 2020, 7, 1861-1864.	4.6	175
14	Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. <i>Microbiome</i> , 2018, 6, 178.	4.9	150
15	Unbiased Parallel Detection of Viral Pathogens in Clinical Samples by Use of a Metagenomic Approach. <i>Journal of Clinical Microbiology</i> , 2011, 49, 3463-3469.	1.8	147
16	VFDB 2008 release: an enhanced web-based resource for comparative pathogenomics. <i>Nucleic Acids Research</i> , 2007, 36, D539-D542.	6.5	138
17	Clinically prevalent mutations in <i>Mycobacterium tuberculosis</i> alter propionate metabolism and mediate multidrug tolerance. <i>Nature Microbiology</i> , 2018, 3, 1032-1042.	5.9	132
18	DBatVir: the database of bat-associated viruses. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau021.	1.4	123

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19	Revisiting the Molecular Evolutionary History of <i>Shigella</i> spp.. <i>Journal of Molecular Evolution</i> , 2007, 64, 71-79.	0.8	107
20	Gut microbiota associated with pulmonary tuberculosis and dysbiosis caused by anti-tuberculosis drugs. <i>Journal of Infection</i> , 2019, 78, 317-322.	1.7	82
21	Transcriptional Profiles of the Response to Ketoconazole and Amphotericin B in <i>Trichophyton rubrum</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 144-153.	1.4	74
22	Complete genome sequence of <i>Shigella flexneri</i> 5b and comparison with <i>Shigella flexneri</i> 2a. <i>BMC Genomics</i> , 2006, 7, 173.	1.2	69
23	The use of global transcriptional analysis to reveal the biological and cellular events involved in distinct development phases of <i>Trichophyton rubrum</i> conidial germination. <i>BMC Genomics</i> , 2007, 8, 100.	1.2	67
24	Complete Genome Sequence of <i>Haemophilus parasuis</i> SH0165. <i>Journal of Bacteriology</i> , 2009, 191, 1359-1360.	1.0	67
25	Characterization of ST-4821 complex, a unique <i>Neisseria meningitidis</i> clone. <i>Genomics</i> , 2008, 91, 78-87.	1.3	66
26	Global transcriptional analysis of nitrogen fixation and ammonium repression in root-associated <i>Pseudomonas stutzeri</i> A1501. <i>BMC Genomics</i> , 2010, 11, 11.	1.2	65
27	The molecular evolutionary history of <i>Shigella</i> spp. and enteroinvasive <i>Escherichia coli</i> . <i>Infection, Genetics and Evolution</i> , 2009, 9, 147-152.	1.0	60
28	Complete Genome Sequence of the Nitrogen-Fixing and Rhizosphere-Associated Bacterium <i>Pseudomonas stutzeri</i> Strain DSM4166. <i>Journal of Bacteriology</i> , 2011, 193, 3422-3423.	1.0	58
29	Recent dermatophyte divergence revealed by comparative and phylogenetic analysis of mitochondrial genomes. <i>BMC Genomics</i> , 2009, 10, 238.	1.2	46
30	Causative Species and Serotypes of Shigellosis in Mainland China: Systematic Review and Meta-Analysis. <i>PLoS ONE</i> , 2012, 7, e52515.	1.1	45
31	A Whole-genome Sequencing Analysis of <i>Neisseria gonorrhoeae</i> Isolates in China: An Observational Study. <i>EClinicalMedicine</i> , 2019, 7, 47-54.	3.2	45
32	Genome-wide Identification and Characterization of a Superfamily of Bacterial Extracellular Contractile Injection Systems. <i>Cell Reports</i> , 2019, 29, 511-521.e2.	2.9	44
33	Analysis of the dermatophyte <i>Trichophyton rubrum</i> expressed sequence tags. <i>BMC Genomics</i> , 2006, 7, 255.	1.2	43
34	Decoding the RNA viromes in rodent lungs provides new insight into the origin and evolutionary patterns of rodent-borne pathogens in Mainland Southeast Asia. <i>Microbiome</i> , 2021, 9, 18.	4.9	43
35	GenomeComp: a visualization tool for microbial genome comparison. <i>Journal of Microbiological Methods</i> , 2003, 54, 423-426.	0.7	42
36	Bacterial Genome-Wide Association Identifies Novel Factors That Contribute to Ethionamide and Prothionamide Susceptibility in <i>Mycobacterium tuberculosis</i> . <i>MBio</i> , 2019, 10, .	1.8	39

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37	Proteomic profile of dormant <i>Trichophyton Rubrum</i> conidia. <i>BMC Genomics</i> , 2008, 9, 303.	1.2	36
38	The first succinylome profile of <i>Trichophyton rubrum</i> reveals lysine succinylation on proteins involved in various key cellular processes. <i>BMC Genomics</i> , 2017, 18, 577.	1.2	36
39	The First Whole-Cell Proteome- and Lysine-Acetylome-Based Comparison between <i>Trichophyton rubrum</i> Conidial and Mycelial Stages. <i>Journal of Proteome Research</i> , 2018, 17, 1436-1451.	1.8	36
40	Complete Genome Sequence of the Extremophilic <i>Bacillus cereus</i> Strain Q1 with Industrial Applications. <i>Journal of Bacteriology</i> , 2009, 191, 1120-1121.	1.0	35
41	Complete Genome Sequence of the Neonatal-Meningitis-Associated <i>Escherichia coli</i> Strain CE10. <i>Journal of Bacteriology</i> , 2011, 193, 7005-7005.	1.0	34
42	Integrated microRNA and mRNA analysis in the pathogenic filamentous fungus <i>Trichophyton rubrum</i> . <i>BMC Genomics</i> , 2018, 19, 933.	1.2	32
43	The use of comparative genomic hybridization to characterize genome dynamics and diversity among the serotypes of <i>Shigella</i> . <i>BMC Genomics</i> , 2006, 7, 218.	1.2	31
44	Analysis of the Secretome and Identification of Novel Constituents from Culture Filtrate of <i>Bacillus Calmette-Guérin</i> Using High-resolution Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2081-2095.	2.5	31
45	Full Genome of Influenza A (H7N9) Virus Derived by Direct Sequencing without Culture. <i>Emerging Infectious Diseases</i> , 2013, 19, 1881-4.	2.0	30
46	The impact of combined gene mutations in <i>inhA</i> and <i>ahpC</i> genes on high levels of isoniazid resistance amongst <i>katG</i> non-315 in multidrug-resistant tuberculosis isolates from China. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-10.	3.0	30
47	Transcriptional profiles of response to terbinafine in <i>Trichophyton rubrum</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 82, 1123-1130.	1.7	28
48	Comprehensive Proteomic Analysis of <i>Shigella flexneri</i> 2a Membrane Proteins. <i>Journal of Proteome Research</i> , 2006, 5, 1860-1865.	1.8	27
49	TrED: the <i>Trichophyton rubrum</i> Expression Database. <i>BMC Genomics</i> , 2007, 8, 250.	1.2	27
50	ShiBASE: an integrated database for comparative genomics of <i>Shigella</i> . <i>Nucleic Acids Research</i> , 2006, 34, D398-D401.	6.5	25
51	ZOVER: the database of zoonotic and vector-borne viruses. <i>Nucleic Acids Research</i> , 2022, 50, D943-D949.	6.5	25
52	Evaluating de Bruijn Graph Assemblers on 454 Transcriptomic Data. <i>PLoS ONE</i> , 2012, 7, e51188.	1.1	24
53	Structural insights into VirB-DNA complexes reveal mechanism of transcriptional activation of virulence genes. <i>Nucleic Acids Research</i> , 2013, 41, 10529-10541.	6.5	24
54	Prevalence of 10 Human Polyomaviruses in Fecal Samples from Children with Acute Gastroenteritis: a Case-Control Study. <i>Journal of Clinical Microbiology</i> , 2013, 51, 3107-3109.	1.8	24

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55	DRodVir: A resource for exploring the virome diversity in rodents. <i>Journal of Genetics and Genomics</i> , 2017, 44, 259-264.	1.7	23
56	Bacterial Genotoxin Accelerates Transient Infection-Driven Murine Colon Tumorigenesis. <i>Cancer Discovery</i> , 2022, 12, 236-249.	7.7	23
57	Genome-wide dissection reveals diverse pathogenic roles of bacterial Tc toxins. <i>PLoS Pathogens</i> , 2021, 17, e1009102.	2.1	21
58	cDNA microarray analysis of the expression profiles of <i>Trichophyton rubrum</i> in response to novel synthetic fatty acid synthase inhibitor PHS11A. <i>Fungal Genetics and Biology</i> , 2007, 44, 1252-1261.	0.9	20
59	Subclinical Infection with the Novel Influenza A (H1N1) Virus. <i>Clinical Infectious Diseases</i> , 2009, 49, 1622-1623.	2.9	20
60	Metagenomic analysis of the lung microbiome in pulmonary tuberculosis - a pilot study. <i>Emerging Microbes and Infections</i> , 2020, 9, 1444-1452.	3.0	19
61	Effective siRNAs inhibit the replication of novel influenza A (H1N1) virus. <i>Antiviral Research</i> , 2010, 85, 559-561.	1.9	18
62	A comprehensive proteomic analysis of <i>Mycobacterium bovis</i> bacillus Calmette-Guérin using high resolution Fourier transform mass spectrometry. <i>Journal of Proteomics</i> , 2012, 77, 357-371.	1.2	18
63	Characterization of serogroup C meningococci isolated from 14 provinces of China during 1966-2005 using comparative genomic hybridization. <i>Science in China Series C: Life Sciences</i> , 2007, 50, 1-6.	1.3	17
64	Proteome-Wide Identification of Lysine Propionylation in the Conidial and Mycelial Stages of <i>Trichophyton rubrum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2613.	1.5	17
65	Identification and characterization of simple sequence repeats in the genomes of <i>Shigella</i> species. <i>Gene</i> , 2003, 322, 85-92.	1.0	16
66	Draft Genome of a Brazilian Avian-Pathogenic <i>Escherichia coli</i> Strain and <i>In Silico</i> Characterization of Virulence-Related Genes. <i>Journal of Bacteriology</i> , 2012, 194, 3023-3023.	1.0	16
67	The prevalence of STL polyomavirus in stool samples from Chinese children. <i>Journal of Clinical Virology</i> , 2015, 66, 19-23.	1.6	16
68	Cultured Bacteria Provide Insight into the Functional Potential of the Coral-Associated Microbiome. <i>MSystems</i> , 2022, 7, .	1.7	14
69	Gene expression profiling of the pH response in <i>Shigella flexneri</i> 2a. <i>FEMS Microbiology Letters</i> , 2007, 270, 12-20.	0.7	13
70	An elaborate landscape of the human antibody repertoire against enterovirus 71 infection is revealed by phage display screening and deep sequencing. <i>MAbs</i> , 2017, 9, 342-349.	2.6	13
71	Identification and characterization of a novel rodent bocavirus from different rodent species in China. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-11.	3.0	13
72	Proteogenomic Analysis and Discovery of Immune Antigens in <i>Mycobacterium vaccae</i> . <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1578-1590.	2.5	12

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73	Complete genome sequence of <i>Shewanella benthica</i> DB21MT-2, an obligate piezophilic bacterium isolated from the deepest Mariana Trench sediment. <i>Marine Genomics</i> , 2019, 44, 52-56.	0.4	12
74	Learning transferable deep convolutional neural networks for the classification of bacterial virulence factors. <i>Bioinformatics</i> , 2020, 36, 3693-3702.	1.8	11
75	An Integrated Approach for Finding Overlooked Genes in <i>Shigella</i> . <i>PLoS ONE</i> , 2011, 6, e18509.	1.1	10
76	Complete Genome Sequence of <i>Neisseria meningitidis</i> Serogroup A Strain NMA510612, Isolated from a Patient with Bacterial Meningitis in China. <i>Genome Announcements</i> , 2014, 2, .	0.8	10
77	The outer membrane phospholipase A is essential for membrane integrity and type III secretion in <i>Shigella flexneri</i> . <i>Open Biology</i> , 2016, 6, 160073.	1.5	10
78	N-Glycans and sulfated glycosaminoglycans contribute to the action of diverse Tc toxins on mammalian cells. <i>PLoS Pathogens</i> , 2021, 17, e1009244.	2.1	10
79	Subproteomic tools to increase genome annotation complexity. <i>Proteomics</i> , 2008, 8, 4209-4213.	1.3	9
80	Genome Sequences of Avian Pathogenic <i>Escherichia coli</i> Strains Isolated from Brazilian Commercial Poultry. <i>Genome Announcements</i> , 2013, 1, e0011013.	0.8	9
81	Analysis of part of the <i>Trichophyton rubrum</i> ESTs. <i>Science in China Series C: Life Sciences</i> , 2004, 47, 389.	1.3	9
82	CloudLCA: finding the lowest common ancestor in metagenome analysis using cloud computing. <i>Protein and Cell</i> , 2012, 3, 148-152.	4.8	8
83	Mutations of Novel Influenza A(H10N8) Virus in Chicken Eggs and MDCK Cells. <i>Emerging Infectious Diseases</i> , 2014, 20, 1541-1543.	2.0	8
84	Biodiversity of rodent anelloviruses in China. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-3.	3.0	8
85	Transcriptional profile of the <i>Shigella flexneri</i> response to an alkaloid: berberine. <i>FEMS Microbiology Letters</i> , 2010, 303, 169-175.	0.7	7
86	Proteogenomic Analysis of <i>Trichophyton rubrum</i> Aided by RNA Sequencing. <i>Journal of Proteome Research</i> , 2015, 14, 2207-2218.	1.8	7
87	Genomic research for important pathogenic bacteria in China. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 50-63.	1.3	6
88	Research progress in <i>Shigella</i> in the postgenomic era. <i>Science China Life Sciences</i> , 2010, 53, 1284-1290.	2.3	6
89	Identification and characterisation of non-coding small RNAs in the pathogenic filamentous fungus <i>Trichophyton rubrum</i> . <i>BMC Genomics</i> , 2013, 14, 931.	1.2	6
90	Comparison between gene expression of conidia and germinating phase in <i>Trichophyton rubrum</i> . <i>Science in China Series C: Life Sciences</i> , 2007, 50, 377-384.	1.3	5

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91	Evaluating the Value of Defensins for Diagnosing Secondary Bacterial Infections in Influenza-Infected Patients. <i>Frontiers in Microbiology</i> , 2018, 9, 2762.	1.5	5
92	Global transcriptional profiles of <i>Trichophyton rubrum</i> in response to Flucytosine. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 1173-1185.	1.3	4
93	Comparative genomic analysis of obligately piezophilic <i>Moritella yayanosii</i> DB21MT-5 reveals bacterial adaptation to the Challenger Deep, Mariana Trench. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
94	<i>Shigella</i> Genomes: a Tale of Convergent Evolution and Specialization through IS Expansion and Genome Reduction. , 0, , 23-39.		4
95	Comparative analysis of whole genome structure of <i>Streptococcus suis</i> using whole genome PCR scanning. <i>Science in China Series C: Life Sciences</i> , 2008, 51, 21-26.	1.3	2
96	Identification of novel drug targets in bovine respiratory disease: an essential step in applying biotechnologic techniques to develop more effective therapeutic treatments. <i>Drug Design, Development and Therapy</i> , 2018, Volume 12, 1135-1146.	2.0	2
97	Metagenomics: A New Approach for Microbial Identification. <i>Air & Water Borne Diseases</i> , 2012, 01, .	0.3	0