

# Jian Yang

## List of Publications by Year in descending order

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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	ZOVER: the database of zoonotic and vector-borne viruses. <i>Nucleic Acids Research</i> , 2022, 50, D943-D949.	6.5	25
2	Bacterial Genotoxin Accelerates Transient Infection-Driven Murine Colon Tumorigenesis. <i>Cancer Discovery</i> , 2022, 12, 236-249.	7.7	23
3	VFDB 2022: a general classification scheme for bacterial virulence factors. <i>Nucleic Acids Research</i> , 2022, 50, D912-D917.	6.5	372
4	Cultured Bacteria Provide Insight into the Functional Potential of the Coral-Associated Microbiome. <i>MSystems</i> , 2022, 7, .	1.7	14
5	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
6	Genome-wide dissection reveals diverse pathogenic roles of bacterial Tc toxins. <i>PLoS Pathogens</i> , 2021, 17, e1009102.	2.1	21
7	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
8	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
9	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
10	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
11	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
12	Learning transferable deep convolutional neural networks for the classification of bacterial virulence factors. <i>Bioinformatics</i> , 2020, 36, 3693-3702.	1.8	11
13	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
14	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
15	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
16	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
17	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
18	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

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19	VFDB 2019: a comparative pathogenomic platform with an interactive web interface. <i>Nucleic Acids Research</i> , 2019, 47, D687-D692.	6.5	1,286
20	Biodiversity of rodent anelloviruses in China. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-3.	3.0	8
21	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
22	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
23	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
24	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
25	Integrated microRNA and mRNA analysis in the pathogenic filamentous fungus <i>Trichophyton rubrum</i> . <i>BMC Genomics</i> , 2018, 19, 933.	1.2	32
26	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
27	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
28	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
29	DRodVir: A resource for exploring the virome diversity in rodents. <i>Journal of Genetics and Genomics</i> , 2017, 44, 259-264.	1.7	23
30	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
31	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
32	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
33	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
34	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
35	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
36	The prevalence of STL polyomavirus in stool samples from Chinese children. <i>Journal of Clinical Virology</i> , 2015, 66, 19-23.	1.6	16

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37	Proteogenomic Analysis of <i>Trichophyton rubrum</i> Aided by RNA Sequencing. <i>Journal of Proteome Research</i> , 2015, 14, 2207-2218.	1.8	7
38	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
39	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
40	DBatVir: the database of bat-associated viruses. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau021.	1.4	123
41	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
42	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
43	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
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	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
47	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
48	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
49	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
50	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
51	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
52	Evaluating de Bruijn Graph Assemblers on 454 Transcriptomic Data. <i>PLoS ONE</i> , 2012, 7, e51188.	1.1	24
53	Causative Species and Serotypes of Shigellosis in Mainland China: Systematic Review and Meta-Analysis. <i>PLoS ONE</i> , 2012, 7, e52515.	1.1	45
54	Metagenomics: A New Approach for Microbial Identification. <i>Air &amp; Water Borne Diseases</i> , 2012, 01, .	0.3	0

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55	CloudLCA: finding the lowest common ancestor in metagenome analysis using cloud computing. <i>Protein and Cell</i> , 2012, 3, 148-152.	4.8	8
56	An Integrated Approach for Finding Overlooked Genes in <i>Shigella</i> . <i>PLoS ONE</i> , 2011, 6, e18509.	1.1	10
57	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
58	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
59	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
60	Research progress in <i>Shigella</i> in the postgenomic era. <i>Science China Life Sciences</i> , 2010, 53, 1284-1290.	2.3	6
61	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
62	Effective siRNAs inhibit the replication of novel influenza A (H1N1) virus. <i>Antiviral Research</i> , 2010, 85, 559-561.	1.9	18
63	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
64	Subclinical Infection with the Novel Influenza A (H1N1) Virus. <i>Clinical Infectious Diseases</i> , 2009, 49, 1622-1623.	2.9	20
65	Complete Genome Sequence of <i>Haemophilus parasuis</i> SH0165. <i>Journal of Bacteriology</i> , 2009, 191, 1359-1360.	1.0	67
66	Recent dermatophyte divergence revealed by comparative and phylogenetic analysis of mitochondrial genomes. <i>BMC Genomics</i> , 2009, 10, 238.	1.2	46
67	Genomic research for important pathogenic bacteria in China. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 50-63.	1.3	6
68	Transcriptional profiles of response to terbinafine in <i>Trichophyton rubrum</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 82, 1123-1130.	1.7	28
69	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
70	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
71	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
72	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

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73	Subproteomic tools to increase genome annotation complexity. <i>Proteomics</i> , 2008, 8, 4209-4213.	1.3	9
74	Proteomic profile of dormant <i>Trichophyton Rubrum</i> conidia. <i>BMC Genomics</i> , 2008, 9, 303.	1.2	36
75	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
76	Characterization of ST-4821 complex, a unique <i>Neisseria meningitidis</i> clone. <i>Genomics</i> , 2008, 91, 78-87.	1.3	66
77	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
78	VFDB 2008 release: an enhanced web-based resource for comparative pathogenomics. <i>Nucleic Acids Research</i> , 2007, 36, D539-D542.	6.5	138
79	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
80	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
81	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
82	TrED: the <i>Trichophyton rubrum</i> Expression Database. <i>BMC Genomics</i> , 2007, 8, 250.	1.2	27
83	Revisiting the Molecular Evolutionary History of <i>Shigella</i> spp.. <i>Journal of Molecular Evolution</i> , 2007, 64, 71-79.	0.8	107
84	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
85	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
86	Comprehensive Proteomic Analysis of <i>Shigella flexneri</i> 2a Membrane Proteins. <i>Journal of Proteome Research</i> , 2006, 5, 1860-1865.	1.8	27
87	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
88	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
89	Analysis of the dermatophyte <i>Trichophyton rubrum</i> expressed sequence tags. <i>BMC Genomics</i> , 2006, 7, 255.	1.2	43
90	ShiBASE: an integrated database for comparative genomics of <i>Shigella</i> . <i>Nucleic Acids Research</i> , 2006, 34, D398-D401.	6.5	25

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91	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
92	VFDB: a reference database for bacterial virulence factors. <i>Nucleic Acids Research</i> , 2004, 33, D325-D328.	6.5	1,287
93	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
94	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
95	GenomeComp: a visualization tool for microbial genome comparison. <i>Journal of Microbiological Methods</i> , 2003, 54, 423-426.	0.7	42
96	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
97	<i>Shigella</i> Genomes: a Tale of Convergent Evolution and Specialization through IS Expansion and Genome Reduction. , 0, , 23-39.		4