Junping Peng

List of Publications by Year in descending order

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		394286	276775
56	1,758	19	41
papers	citations	h-index	g-index

56	56	56	2220
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome dynamics and diversity of Shigella species, the etiologic agents of bacillary dysentery. Nucleic Acids Research, 2005, 33, 6445-6458.	6.5	361
2	Nitrogen fixation island and rhizosphere competence traits in the genome of root-associated Pseudomonas stutzeri A1501. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7564-7569.	3.3	325
3	Transcriptional Profiles of the Response to Ketoconazole and Amphotericin B in Trichophyton rubrum. Antimicrobial Agents and Chemotherapy, 2007, 51, 144-153.	1.4	74
4	Complete genome sequence of Shigella flexneri 5b and comparison with Shigella flexneri 2a. BMC Genomics, 2006, 7, 173.	1.2	69
5	The use of global transcriptional analysis to reveal the biological and cellular events involved in distinct development phases of Trichophyton rubrum conidial germination. BMC Genomics, 2007, 8, 100.	1.2	67
6	Characterization of ST-4821 complex, a unique Neisseria meningitidis clone. Genomics, 2008, 91, 78-87.	1.3	66
7	Global transcriptional analysis of nitrogen fixation and ammonium repression in root-associated Pseudomonas stutzeri A1501. BMC Genomics, 2010, 11, 11.	1.2	65
8	The molecular evolutionary history of Shigella spp. and enteroinvasive Escherichia coli. Infection, Genetics and Evolution, 2009, 9, 147-152.	1.0	60
9	Establishment and Application of a Universal Coronavirus Screening Method Using MALDI-TOF Mass Spectrometry. Frontiers in Microbiology, 2017, 8, 1510.	1.5	50
10	Multiplex PCR/mass spectrometry screening of biological carcinogenic agents in human mammary tumors. Journal of Clinical Virology, 2014, 61, 255-259.	1.6	39
11	Sensitive and rapid detection of viruses associated with hand foot and mouth disease using multiplexed MALDI-TOF analysis. Journal of Clinical Virology, 2013, 56, 170-174.	1.6	36
12	Identification of multidrug-resistant Neisseria gonorrhoeae isolates with combined resistance to both ceftriaxone and azithromycin, China, 2017â€“2018. Emerging Microbes and Infections, 2019, 8, 1546-1549.	3.0	36
13	Type-Specific Detection of 30 Oncogenic Human Papillomaviruses by Genotyping both E6 and L1 Genes. Journal of Clinical Microbiology, 2013, 51, 402-408.	1.8	34
14	The use of comparative genomic hybridization to characterize genome dynamics and diversity among the serotypes of Shigella. BMC Genomics, 2006, 7, 218.	1.2	31
15	Transcriptional profiles of response to terbinafine in Trichophyton rubrum. Applied Microbiology and Biotechnology, 2009, 82, 1123-1130.	1.7	28
16	Transcriptional profiles ofTrichophyton rubrumin response to itraconazole. Medical Mycology, 2009, 47, 237-247.	0.3	26
17	Application of Multiplex PCR Coupled with Matrix-Assisted Laser Desorption Ionizationâ€“Time of Flight Analysis for Simultaneous Detection of 21 Common Respiratory Viruses. Journal of Clinical Microbiology, 2015, 53, 2549-2554.	1.8	26
18	Prevalence of 10 Human Polyomaviruses in Fecal Samples from Children with Acute Gastroenteritis: a Case-Control Study. Journal of Clinical Microbiology, 2013, 51, 3107-3109.	1.8	24

#	Article	IF	Citations
19	cDNA microarray analysis of the expression profiles of Trichophyton rubrum in response to novel synthetic fatty acid synthase inhibitor PHS11A. Fungal Genetics and Biology, 2007, 44, 1252-1261.	0.9	20
20	Simultaneous Detection of Key Bacterial Pathogens Related to Pneumonia and Meningitis Using Multiplex PCR Coupled With Mass Spectrometry. Frontiers in Cellular and Infection Microbiology, 2018, 8, 107.	1.8	18
21	Emergence of ceftriaxone-resistant Neisseria gonorrhoeae strains harbouring a novel mosaic penA gene in China. Journal of Antimicrobial Chemotherapy, 2020, 75, 907-910.	1.3	18
22	Multiplex High-Resolution Melting Assay for Simultaneous Identification of Molecular Markers Associated with Extended-Spectrum Cephalosporins and Azithromycin Resistance in Neisseria gonorrhoeae. Journal of Molecular Diagnostics, 2020, 22, 1344-1355.	1.2	18
23	Characterization of serogroup C meningococci isolated from 14 provinces of China during 1966â€“2005 using comparative genomic hybridization. Science in China Series C: Life Sciences, 2007, 50, 1-6.	1.3	17
24	Co-occurrence of amikacin-resistant and -susceptible Mycobacterium tuberculosis isolates in clinical samples from Beijing, China. Journal of Antimicrobial Chemotherapy, 2013, 68, 1537-1542.	1.3	17
25	Genotypic characterization of Neisseria meningitidis serogroup B strains circulating in China. Journal of Infection, 2008, 56, 211-218.	1.7	16
26	The prevalence of STL polyomavirus in stool samples from Chinese children. Journal of Clinical Virology, 2015, 66, 19-23.	1.6	16
27	Simultaneous detection of eleven sexually transmitted agents using multiplexed PCR coupled with MALDI-TOF analysis . Infection and Drug Resistance, 2019, Volume 12, 2671-2682.	1.1	15
28	High-resolution melting analysis for rapid detection of the internationally spreading ceftriaxone-resistant Neisseria gonorrhoeae FC428 clone. Journal of Antimicrobial Chemotherapy, 2020, 75, 106-109.	1.3	14
29	Gene expression profiling of the pH response inShigella flexneri2a. FEMS Microbiology Letters, 2007, 270, 12-20.	0.7	13
30	Identification and characterization of a novel rodent bocavirus from different rodent species in China. Emerging Microbes and Infections, 2018, 7, 1-11.	3.0	13
31	Determining antimicrobial resistance profiles and identifying novel mutations of Neisseria gonorrhoeae genomes obtained by multiplexed MinION sequencing. Science China Life Sciences, 2020, 63, 1063-1070.	2.3	13
32	A multiplex assay for characterization of antimicrobial resistance in Neisseria gonorrhoeae using multi-PCR coupled with mass spectrometry. Journal of Antimicrobial Chemotherapy, 2020, 75, 2817-2825.	1.3	11
33	Multiplex PCR and Nanopore Sequencing of Genes Associated with Antimicrobial Resistance in Neisseria gonorrhoeae Directly from Clinical Samples. Clinical Chemistry, 2021, 67, 610-620.	1.5	11
34	Transcriptional profile induced by furazolidone treatment of Shigella flexneri. Applied Microbiology and Biotechnology, 2007, 77, 657-667.	1.7	10
35	An Integrated Approach for Finding Overlooked Genes in Shigella. PLoS ONE, 2011, 6, e18509.	1.1	10
36	Subproteomic tools to increase genome annotation complexity. Proteomics, 2008, 8, 4209-4213.	1.3	9

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37	Emergence and Characterization of a Ceftriaxone-Resistant Neisseria gonorrhoeae FC428 Clone Evolving Moderate-Level Resistance to Azithromycin in Shenzhen, China. Infection and Drug Resistance, 2021, Volume 14, 4271-4276.	1.1	9
38	Characterization of a new Neisseria meningitidis serogroup C clone from China. Scandinavian Journal of Infectious Diseases, 2008, 40, 63-66.	1.5	8
39	A molecular screening assay to identify Chlamydia trachomatis and distinguish new variants of C. trachomatis from wildâ€type. Microbial Biotechnology, 2021, 14, 668-676.	2.0	8
40	Distribution of surface-protein variants of hyperinvasive meningococci in China. Journal of Infection, 2009, 58, 358-367.	1.7	7
41	Typing of Neisseria gonorrhoeae Isolates in Shenzhen, China, from 2014 to 2018 Reveals the Shift of Genotypes Significantly Associated with Antimicrobial Resistance. Antimicrobial Agents and Chemotherapy, 2021, 65, .	1.4	7
42	Research progress in Shigella in the postgenomic era. Science China Life Sciences, 2010, 53, 1284-1290.	2.3	6
43	Comparison between gene expression of conidia and germinating phase in Trichophyton rubrum. Science in China Series C: Life Sciences, 2007, 50, 377-384.	1.3	5
44	Human papillomavirus and polyomavirus coinfections among Chinese men who have sex with men. Journal of Infection, 2016, 72, 118-120.	1.7	5
45	Use of Ultra-Deep Sequencing in a Patient with Tuberculous Coxitis Shows Its Limitations in Extrapulmonary Tuberculosis Diagnostics: A Case Report . Infection and Drug Resistance, 2019, Volume 12, 3739-3743.	1.1	5
46	Global transcriptional profiles of Trichophyton rubrum in response to Flucytosine. Science in China Series C: Life Sciences, 2009, 52, 1173-1185.	1.3	4
47	A multiplex molecular assay for detection of six penA codons to predict decreased susceptibility to cephalosporins in Neisseria gonorrhoeae. Antimicrobial Agents and Chemotherapy, 2022, , AAC0170921.	1.4	4
48	Detection and classification of SARSâ€CoVâ€2 using highâ€resolution melting analysis. Microbial Biotechnology, 2022, , .	2.0	4
49	Genomic compositions and phylogenetic analysis of Shigella boydii subgroup. Science in China Series C: Life Sciences, 2006, 49, 46-52.	1.3	3
50	Construction, detection and microarray analysis on Shigella dysenteriae A1 IroN, ShuA single, double mutants. Science in China Series C: Life Sciences, 2006, 49, 251-258.	1.3	2
51	Comparative analysis of whole genome structure of Streptococcus suis using whole genome PCR scanning. Science in China Series C: Life Sciences, 2008, 51, 21-26.	1.3	2
52	Comprehensive Description of Pathogens and Antibiotic Treatment Guidance in Children With Community-Acquired Pneumonia Using Combined Mass Spectrometry Methods. Frontiers in Cellular and Infection Microbiology, 2021, 11, 695134.	1.8	2
53	Comparative genomics and phylogenetic analysis of S. dysenteriae subgroup. Science in China Series C: Life Sciences, 2005, 48, 406.	1.3	1
54	Common Changes in Global Gene Expression Induced by RNA Polymerase Inhibitors in shigella flexneri. PLoS ONE, 2012, 7, e33240.	1.1	0

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55	Advances in research on the resistance mechanism of <italic>Neisseria gonorrhoeae</italic>. Scientia Sinica Vitae, 2021, 51, 412-420.	0.1	0
56	Editorial: Progress in Pathogen Identification Based on Mass Spectrometry. Frontiers in Cellular and Infection Microbiology, 2021, 11, 813133.	1.8	0