

Dake Zhang

List of Publications by Year in descending order

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31
papers

652
citations

623188

14
h-index

642321

23
g-index

33
all docs

33
docs citations

33
times ranked

1051
citing authors

#	ARTICLE	IF	CITATIONS
1	A Novel Gene, Encoding 6-Hydroxy-3-Succinoylpyridine Hydroxylase, Involved in Nicotine Degradation by <i>Pseudomonas putida</i> Strain S16. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1567-1574.	1.4	63
2	Metagenomic Profile of the Viral Communities in <i>Rhipicephalus</i> spp. Ticks from Yunnan, China. <i>PLoS ONE</i> , 2015, 10, e0121609.	1.1	59
3	A Novel NADH-dependent and FAD-containing Hydroxylase Is Crucial for Nicotine Degradation by <i>Pseudomonas putida</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 39179-39187.	1.6	56
4	Scleral HIF-1 α is a prominent regulatory candidate for genetic and environmental interactions in human myopia pathogenesis. <i>EBioMedicine</i> , 2020, 57, 102878.	2.7	56
5	Conjunctival Microbiome Changes Associated With Soft Contact Lens and Orthokeratology Lens Wearing. , 2017, 58, 128.		55
6	Whole genome HBV deletion profiles and the accumulation of preS deletion mutant during antiviral treatment. <i>BMC Microbiology</i> , 2012, 12, 307.	1.3	34
7	Genome-wide DNA methylation profiles of low- and high-grade adenoma reveals potential biomarkers for early detection of colorectal carcinoma. <i>Clinical Epigenetics</i> , 2020, 12, 56.	1.8	33
8	Prevalent HBV point mutations and mutation combinations at BCP/preC region and their association with liver disease progression. <i>BMC Infectious Diseases</i> , 2010, 10, 271.	1.3	32
9	Four-Generation Pedigree of Monozygotic Female Twins Reveals Genetic Factors in Twinning Process by Whole-Genome Sequencing. <i>Twin Research and Human Genetics</i> , 2018, 21, 361-368.	0.3	32
10	Evolutionary selection associated with the multi-function of overlapping genes in the hepatitis B virus. <i>Infection, Genetics and Evolution</i> , 2010, 10, 84-88.	1.0	31
11	Metagenomic Profiling of Ocular Surface Microbiome Changes in Meibomian Gland Dysfunction. , 2020, 61, 22.		27
12	IFN- α -mediated Base Excision Repair Pathway Correlates with Antiviral Response Against Hepatitis B Virus Infection. <i>Scientific Reports</i> , 2017, 7, 12715.	1.6	25
13	Hypomethylation in HBV integration regions aids non-invasive surveillance to hepatocellular carcinoma by low-pass genome-wide bisulfite sequencing. <i>BMC Medicine</i> , 2020, 18, 200.	2.3	25
14	Noninvasive chimeric DNA profiling identifies tumor-originated HBV integrants contributing to viral antigen expression in liver cancer. <i>Hepatology International</i> , 2020, 14, 326-337.	1.9	20
15	Whole genome characterization of hepatitis B virus quasispecies with massively parallel pyrosequencing. <i>Clinical Microbiology and Infection</i> , 2015, 21, 280-287.	2.8	19
16	Mechanisms of DNA Methylation in Virus-Host Interaction in Hepatitis B Infection: Pathogenesis and Oncogenetic Properties. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9858.	1.8	15
17	Applications and potentials of nanopore sequencing in the (epi)genome and (epi)transcriptome era. <i>Innovation(China)</i> , 2021, 2, 100153.	5.2	15
18	Constructing an initial map of transmission distortion based on high density HapMap SNPs across the human autosomes. <i>Journal of Genetics and Genomics</i> , 2009, 36, 703-709.	1.7	7

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19	Positive selection signals of hepatitis B virus and their association with disease stages and viral genotypes. <i>Infection, Genetics and Evolution</i> , 2013, 19, 176-187.	1.0	7
20	High Copy-Number Variation Burdens in Cranial Meningiomas From Patients With Diverse Clinical Phenotypes Characterized by Hot Genomic Structure Changes. <i>Frontiers in Oncology</i> , 2020, 10, 1382.	1.3	7
21	HBV Integration Induces Complex Interactions between Host and Viral Genomic Functions at the Insertion Site. <i>Journal of Clinical and Translational Hepatology</i> , 2021, 000, 000-000.	0.7	6
22	Genetic Flux Between H1 and H2 Haplotypes of the 17q21.31 Inversion in European Population. <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 113-118.	3.0	4
23	Gene2DGE: A Perl Package for Gene Model Renewal with Digital Gene Expression Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 51-54.	3.0	4
24	In vitro Transcriptome Analysis of Two Chinese Isolates of <i>Streptococcus suis</i> Serotype 2. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 266-275.	3.0	4
25	A cross-talk between Hepatitis B virus and host mRNAs confers viral adaptation to liver. <i>Scientific Reports</i> , 2015, 5, 10572.	1.6	4
26	<i>TGFβ3</i> downregulation causing chondromagenesis and its tumor suppression role maintained by Smad7. <i>Carcinogenesis</i> , 2021, 42, 913-923.	1.3	4
27	Birt-Hogg-Dubé Syndrome with Clear Cell Renal Cell Carcinoma in a Chinese Family. <i>Internal Medicine</i> , 2014, 53, 2825-2828.	0.3	3
28	Scanning for Genomic Regions Subject to Selective Sweeps Using SNP-MaP Strategy. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 256-261.	3.0	1
29	Viral integration profiles in the plasma cell-free DNA from patients with HBV infection well represent tumor clone compositions during HCC development. <i>Journal of Hepatology</i> , 2018, 68, S121-S122.	1.8	1
30	Common Postzygotic Mutational Signatures in Healthy Adult Tissues Related to Embryonic Hypoxia. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 177-191.	3.0	1
31	Remediation of ABCG5-Linked Macrothrombocytopenia With Ezetimibe Therapy. <i>Frontiers in Genetics</i> , 2021, 12, 769699.	1.1	1