

Dake Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

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	Common Postzygotic Mutational Signatures in Healthy Adult Tissues Related to Embryonic Hypoxia. Genomics, Proteomics and Bioinformatics, 2022, 20, 177-191.	3.0	1
2	<i>TGFβ3</i> downregulation causing chordomagenesis and its tumor suppression role maintained by Smad7. Carcinogenesis, 2021, 42, 913-923.	1.3	4
3	HBV Integration Induces Complex Interactions between Host and Viral Genomic Functions at the Insertion Site. Journal of Clinical and Translational Hepatology, 2021, 000, 000-000.	0.7	6
4	Mechanisms of DNA Methylation in Virus-Host Interaction in Hepatitis B Infection: Pathogenesis and Oncogenetic Properties. International Journal of Molecular Sciences, 2021, 22, 9858.	1.8	15
5	Applications and potentials of nanopore sequencing in the (epi)genome and (epi)transcriptome era. Innovation(China), 2021, 2, 100153.	5.2	15
6	Remediation of ABCG5-Linked Macrothrombocytopenia With Ezetimibe Therapy. Frontiers in Genetics, 2021, 12, 769699.	1.1	1
7	Scleral HIF-1 α is a prominent regulatory candidate for genetic and environmental interactions in human myopia pathogenesis. EBioMedicine, 2020, 57, 102878.	2.7	56
8	Metagenomic Profiling of Ocular Surface Microbiome Changes in Meibomian Gland Dysfunction. , 2020, 61, 22.		27
9	Hypomethylation in HBV integration regions aids non-invasive surveillance to hepatocellular carcinoma by low-pass genome-wide bisulfite sequencing. BMC Medicine, 2020, 18, 200.	2.3	25
10	High Copy-Number Variation Burdens in Cranial Meningiomas From Patients With Diverse Clinical Phenotypes Characterized by Hot Genomic Structure Changes. Frontiers in Oncology, 2020, 10, 1382.	1.3	7
11	Noninvasive chimeric DNA profiling identifies tumor-originated HBV integrants contributing to viral antigen expression in liver cancer. Hepatology International, 2020, 14, 326-337.	1.9	20
12	Genome-wide DNA methylation profiles of low- and high-grade adenoma reveals potential biomarkers for early detection of colorectal carcinoma. Clinical Epigenetics, 2020, 12, 56.	1.8	33
13	Viral integration profiles in the plasma cell-free DNA from patients with HBV infection well represent tumor clone compositions during HCC development. Journal of Hepatology, 2018, 68, S121-S122.	1.8	1
14	Four-Generation Pedigree of Monozygotic Female Twins Reveals Genetic Factors in Twinning Process by Whole-Genome Sequencing. Twin Research and Human Genetics, 2018, 21, 361-368.	0.3	32
15	IFN- α -mediated Base Excision Repair Pathway Correlates with Antiviral Response Against Hepatitis B Virus Infection. Scientific Reports, 2017, 7, 12715.	1.6	25
16	Conjunctival Microbiome Changes Associated With Soft Contact Lens and Orthokeratology Lens Wearing. , 2017, 58, 128.		55
17	A cross-talk between Hepatitis B virus and host mRNAs confers viral adaptation to liver. Scientific Reports, 2015, 5, 10572.	1.6	4
18	Whole genome characterization of hepatitis B virus quasispecies with massively parallel pyrosequencing. Clinical Microbiology and Infection, 2015, 21, 280-287.	2.8	19

#	ARTICLE	IF	CITATIONS
19	Metagenomic Profile of the Viral Communities in Rhipicephalus spp. Ticks from Yunnan, China. PLoS ONE, 2015, 10, e0121609.	1.1	59
20	In vitro Transcriptome Analysis of Two Chinese Isolates of Streptococcus suis Serotype 2. Genomics, Proteomics and Bioinformatics, 2014, 12, 266-275.	3.0	4
21	Birt-Hogg-DubÃ© Syndrome with Clear Cell Renal Cell Carcinoma in a Chinese Family. Internal Medicine, 2014, 53, 2825-2828.	0.3	3
22	Positive selection signals of hepatitis B virus and their association with disease stages and viral genotypes. Infection, Genetics and Evolution, 2013, 19, 176-187.	1.0	7
23	Gene2DGE: A Perl Package for Gene Model Renewal with Digital Gene Expression Data. Genomics, Proteomics and Bioinformatics, 2012, 10, 51-54.	3.0	4
24	Whole genome HBV deletion profiles and the accumulation of preS deletion mutant during antiviral treatment. BMC Microbiology, 2012, 12, 307.	1.3	34
25	Genetic Flux Between H1 and H2 Haplotypes of the 17q21.31 Inversion in European Population. Genomics, Proteomics and Bioinformatics, 2011, 9, 113-118.	3.0	4
26	A Novel NADH-dependent and FAD-containing Hydroxylase Is Crucial for Nicotine Degradation by Pseudomonas putida. Journal of Biological Chemistry, 2011, 286, 39179-39187.	1.6	56
27	Evolutionary selection associated with the multi-function of overlapping genes in the hepatitis B virus. Infection, Genetics and Evolution, 2010, 10, 84-88.	1.0	31
28	Prevalent HBV point mutations and mutation combinations at BCP/preC region and their association with liver disease progression. BMC Infectious Diseases, 2010, 10, 271.	1.3	32
29	Scanning for Genomic Regions Subject to Selective Sweeps Using SNP-MaP Strategy. Genomics, Proteomics and Bioinformatics, 2010, 8, 256-261.	3.0	1
30	Constructing an initial map of transmission distortion based on high density HapMap SNPs across the human autosomes. Journal of Genetics and Genomics, 2009, 36, 703-709.	1.7	7
31	A Novel Gene, Encoding 6-Hydroxy-3-Succinoylpyridine Hydroxylase, Involved in Nicotine Degradation by <i>Pseudomonas putida</i> Strain S16. Applied and Environmental Microbiology, 2008, 74, 1567-1574.	1.4	63