

Mingkun Li

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

3,237
citations

331538

21
h-index

395590

33
g-index

35
all docs

35
docs citations

35
times ranked

7736
citing authors

#	ARTICLE	IF	CITATIONS
1	CircleBase: an integrated resource and analysis platform for human eccDNAs. <i>Nucleic Acids Research</i> , 2022, 50, D72-D82.	6.5	20
2	Genomic Perspectives on the Emerging SARS-CoV-2 Omicron Variant. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 60-69.	3.0	46
3	Possible recombination between two variants of concern in a COVID-19 patient. <i>Emerging Microbes and Infections</i> , 2022, 11, 552-555.	3.0	29
4	The transmission of human mitochondrial DNA in four-generation pedigrees. <i>Human Mutation</i> , 2022, 43, 1259-1267.	1.1	2
5	Chinese gut microbiota and its associations with staple food type, ethnicity, and urbanization. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 71.	2.9	37
6	N6-methyladenosine regulates RNA abundance of SARS-CoV-2. <i>Cell Discovery</i> , 2021, 7, 7.	3.1	7
7	Genomic Epidemiology of SARS-CoV-2 in Pakistan. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 727-740.	3.0	8
8	Population Genetics of SARS-CoV-2: Disentangling Effects of Sampling Bias and Infection Clusters. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 640-647.	3.0	44
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	Dynamics of severe acute respiratory syndrome coronavirus 2 genome variants in the feces during convalescence. <i>Journal of Genetics and Genomics</i> , 2020, 47, 610-617.	1.7	30
11	Heightened Innate Immune Responses in the Respiratory Tract of COVID-19 Patients. <i>Cell Host and Microbe</i> , 2020, 27, 883-890.e2.	5.1	811
12	Genomic Diversity of Severe Acute Respiratory Syndrome Coronavirus 2 in Patients With Coronavirus Disease 2019. <i>Clinical Infectious Diseases</i> , 2020, 71, 713-720.	2.9	455
13	Sharing of heteroplasmies between human liver lobes varies across the mtDNA genome. <i>Scientific Reports</i> , 2019, 9, 11219.	1.6	9
14	Evidence of Neutral Evolution of Mitochondrial DNA in Human Hepatocellular Carcinoma. <i>Genome Biology and Evolution</i> , 2019, 11, 2909-2916.	1.1	3
15	OncoBase: a platform for decoding regulatory somatic mutations in human cancers. <i>Nucleic Acids Research</i> , 2019, 47, D1044-D1055.	6.5	33
16	Application of next generation sequencing technology on contamination monitoring in microbiology laboratory. <i>Biosafety and Health</i> , 2019, 1, 25-31.	1.2	5
17	Patterned progression of gut microbiota associated with necrotizing enterocolitis and late onset sepsis in preterm infants: a prospective study in a Chinese neonatal intensive care unit. <i>PeerJ</i> , 2019, 7, e7310.	0.9	18
18	Transcriptionally Active Lung Microbiome and Its Association with Bacterial Biomass and Host Inflammatory Status. <i>MSystems</i> , 2018, 3, .	1.7	58

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19	Genotyping of human rhinovirus in adult patients with acute respiratory infections identified predominant infections of genotype A21. <i>Scientific Reports</i> , 2017, 7, 41601.	1.6	14
20	Metagenomic Analysis Identified Human Rhinovirus B91 Infection in an Adult Suffering from Severe Pneumonia. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 1535-1536.	2.5	9
21	Transmission of human mtDNA heteroplasmy in the Genome of the Netherlands families: support for a variable-size bottleneck. <i>Genome Research</i> , 2016, 26, 417-426.	2.4	84
22	Extensive tissue-related and allele-related mtDNA heteroplasmy suggests positive selection for somatic mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2491-2496.	3.3	174
23	Comparative analysis of the human saliva microbiome from different climate zones: Alaska, Germany, and Africa. <i>BMC Microbiology</i> , 2014, 14, 316.	1.3	134
24	Human paternal and maternal demographic histories: insights from high-resolution Y chromosome and mtDNA sequences. <i>Investigative Genetics</i> , 2014, 5, 13.	3.3	145
25	Improved Calibration of the Human Mitochondrial Clock Using Ancient Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 2780-2792.	3.5	99
26	Early Austronesians: Into and Out Of Taiwan. <i>American Journal of Human Genetics</i> , 2014, 94, 426-436.	2.6	170
27	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	1.8	73
28	Complete mtDNA genomes of Filipino ethnolinguistic groups: a melting pot of recent and ancient lineages in the Asia-Pacific region. <i>European Journal of Human Genetics</i> , 2014, 22, 228-237.	1.4	49
29	Transmission from centenarians to their offspring of mtDNA heteroplasmy revealed by ultra-deep sequencing. <i>Aging</i> , 2014, 6, 454-467.	1.4	28
30	Fidelity of capture-enrichment for mtDNA genome sequencing: influence of NUMTs. <i>Nucleic Acids Research</i> , 2012, 40, e137-e137.	6.5	103
31	A new approach for detecting low-level mutations in next-generation sequence data. <i>Genome Biology</i> , 2012, 13, R34.	13.9	86
32	Detecting Heteroplasmy from High-Throughput Sequencing of Complete Human Mitochondrial DNA Genomes. <i>American Journal of Human Genetics</i> , 2010, 87, 237-249.	2.6	274