

Jeremy R Wang

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

2,250
citations

567281

15
h-index

477307

29
g-index

40
all docs

40
docs citations

40
times ranked

3215
citing authors

#	ARTICLE	IF	CITATIONS
1	Subspecific origin and haplotype diversity in the laboratory mouse. <i>Nature Genetics</i> , 2011, 43, 648-655.	21.4	439
2	Genetic analysis of complex traits in the emerging Collaborative Cross. <i>Genome Research</i> , 2011, 21, 1213-1222.	5.5	327
3	Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. <i>Nature Genetics</i> , 2015, 47, 353-360.	21.4	204
4	Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. <i>PLoS Pathogens</i> , 2013, 9, e1003196.	4.7	183
5	Evidence for extensive horizontal gene transfer from the draft genome of a tardigrade. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15976-15981.	7.1	145
6	Status and access to the Collaborative Cross population. <i>Mammalian Genome</i> , 2012, 23, 706-712.	2.2	134
7	Widespread introgression across a phylogeny of 155 <i>Drosophila</i> genomes. <i>Current Biology</i> , 2022, 32, 111-123.e5.	3.9	132
8	Highly contiguous assemblies of 101 drosophilid genomes. <i>ELife</i> , 2021, 10, .	6.0	108
9	FMLRC: Hybrid long read error correction using an FM-index. <i>BMC Bioinformatics</i> , 2018, 19, 50.	2.6	94
10	Tumor-intrinsic and -extrinsic determinants of response to blinatumomab in adults with B-ALL. <i>Blood</i> , 2021, 137, 471-484.	1.4	70
11	Comparative analysis and visualization of multiple collinear genomes. <i>BMC Bioinformatics</i> , 2012, 13, S13.	2.6	54
12	Imputation of Single-Nucleotide Polymorphisms in Inbred Mice Using Local Phylogeny. <i>Genetics</i> , 2012, 190, 449-458.	2.9	42
13	Genetic Architecture of Skewed X Inactivation in the Laboratory Mouse. <i>PLoS Genetics</i> , 2013, 9, e1003853.	3.5	41
14	A vertebrate adaptive radiation is assembled from an ancient and disjunct spatiotemporal landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	35
15	Long transposon-rich centromeres in an oomycete reveal divergence of centromere features in Stramenopila-Alveolata-Rhizaria lineages. <i>PLoS Genetics</i> , 2020, 16, e1008646.	3.5	29
16	Nonlinear sequence similarity between the <i>Xist</i> and <i>Rsx</i> long noncoding RNAs suggests shared functions of tandem repeat domains. <i>Rna</i> , 2019, 25, 1004-1019.	3.5	21
17	Genetic Diversity and Thermal Performance in Invasive and Native Populations of African Fig Flies. <i>Molecular Biology and Evolution</i> , 2020, 37, 1893-1906.	8.9	19
18	Transcriptome Atlases of Mouse Brain Reveals Differential Expression Across Brain Regions and Genetic Backgrounds. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 203-211.	1.8	18

#	ARTICLE	IF	CITATIONS
19	Correcting nucleotide-specific biases in high-throughput sequencing data. BMC Bioinformatics, 2017, 18, 357.	2.6	18
20	Genome-wide compatible SNP intervals and their properties. , 2010, 2010, 43-52.		15
21	The Emulsifier Carboxymethylcellulose Induces More Aggressive Colitis in Humanized Mice with Inflammatory Bowel Disease Microbiota Than Polysorbate-80. Nutrients, 2021, 13, 3565.	4.1	15
22	Paternally Inherited P-Element Copy Number Affects the Magnitude of Hybrid Dysgenesis in <i>Drosophila simulans</i> and <i>D. melanogaster</i> . Genome Biology and Evolution, 2020, 12, 808-826.	2.5	13
23	Genomic epidemiology of <i>Escherichia coli</i> isolates from a tertiary referral center in Lilongwe, Malawi. Microbial Genomics, 2021, 7, .	2.0	12
24	Crohn's Disease Differentially Affects Region-Specific Composition and Aerotolerance Profiles of Mucosally Adherent Bacteria. Inflammatory Bowel Diseases, 2020, 26, 1843-1855.	1.9	9
25	Long-read sequencing to interrogate strain-level variation among adherent-invasive <i>Escherichia coli</i> isolated from human intestinal tissue. PLoS ONE, 2021, 16, e0259141.	2.5	7
26	<i>P</i> elements strengthen reproductive isolation within the <i>Drosophila simulans</i> species complex. Evolution; International Journal of Organic Evolution, 2021, 75, 2425-2440.	2.3	6
27	Collaboration between Clinical and Academic Laboratories for Sequencing SARS-CoV-2 Genomes. Journal of Clinical Microbiology, 2022, 60, JCM0128821.	3.9	4
28	Fast alignment filtering of nanopore sequencing reads using locality-sensitive hashing. , 2015, , .		3
29	A <i>nadA</i> Mutation Confers Nicotinic Acid Auxotrophy in Pro-carcinogenic Intestinal <i>Escherichia coli</i> NC101. Frontiers in Microbiology, 2021, 12, 670005.	3.5	3
30	Dynamic visualization and comparative analysis of multiple collinear genomic data. , 2011, 2011, 335-339.		2
31	Acute Leukemia Classification Using Transcriptional Profiles From Low-Cost Nanopore mRNA Sequencing. JCO Precision Oncology, 2022, 6, e2100326.	3.0	2