Jeremy R Wang

List of Publications by Year in descending order

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Version: 2024-02-01

567281 477307 2,250 31 15 29 citations g-index h-index papers 40 40 40 3215 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Widespread introgression across a phylogeny of 155 Drosophila genomes. Current Biology, 2022, 32, 111-123.e5.	3.9	132
2	Collaboration between Clinical and Academic Laboratories for Sequencing SARS-CoV-2 Genomes. Journal of Clinical Microbiology, 2022, 60, JCM0128821.	3.9	4
3	Acute Leukemia Classification Using Transcriptional Profiles From Low-Cost Nanopore mRNA Sequencing. JCO Precision Oncology, 2022, 6, e2100326.	3.0	2
4	Tumor-intrinsic and -extrinsic determinants of response to blinatumomab in adults with B-ALL. Blood, 2021, 137, 471-484.	1.4	70
5	A vertebrate adaptive radiation is assembled from an ancient and disjunct spatiotemporal landscape. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	35
6	A nadA Mutation Confers Nicotinic Acid Auxotrophy in Pro-carcinogenic Intestinal Escherichia coli NC101. Frontiers in Microbiology, 2021, 12, 670005.	3.5	3
7	Highly contiguous assemblies of 101 drosophilid genomes. ELife, 2021, 10, .	6.0	108
8	<i>P</i> â€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
9	Genomic epidemiology of Escherichia coli isolates from a tertiary referral center in Lilongwe, Malawi. Microbial Genomics, 2021, 7, .	2.0	12
10	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
11	Long-read sequencing to interrogate strain-level variation among adherent-invasive Escherichia coli isolated from human intestinal tissue. PLoS ONE, 2021, 16, e0259141.	2.5	7
12	Paternally Inherited P-Element Copy Number Affects the Magnitude of Hybrid Dysgenesis in Drosophila simulans and D.Âmelanogaster. Genome Biology and Evolution, 2020, 12, 808-826.	2.5	13
13	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
14	Long transposon-rich centromeres in an oomycete reveal divergence of centromere features in Stramenopila-Alveolata-Rhizaria lineages. PLoS Genetics, 2020, 16, e1008646.	3.5	29
15	Genetic Diversity and Thermal Performance in Invasive and Native Populations of African Fig Flies. Molecular Biology and Evolution, 2020, 37, 1893-1906.	8.9	19
16	Nonlinear sequence similarity between the <i>Xist</i> and <i>Rsx</i> long noncoding RNAs suggests shared functions of tandem repeat domains. Rna, 2019, 25, 1004-1019.	3.5	21
17	FMLRC: Hybrid long read error correction using an FM-index. BMC Bioinformatics, 2018, 19, 50.	2.6	94
18	Correcting nucleotide-specific biases in high-throughput sequencing data. BMC Bioinformatics, 2017, 18, 357.	2.6	18

#	Article	IF	CITATIONS
19	Fast alignment filtering of nanopore sequencing reads using locality-sensitive hashing. , 2015, , .		3
20	Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. Nature Genetics, 2015, 47, 353-360.	21.4	204
21	Evidence for extensive horizontal gene transfer from the draft genome of a tardigrade. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15976-15981.	7.1	145
22	Genetic Architecture of Skewed X Inactivation in the Laboratory Mouse. PLoS Genetics, 2013, 9, e1003853.	3.5	41
23	Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. PLoS Pathogens, 2013, 9, e1003196.	4.7	183
24	Transcriptome Atlases of Mouse Brain Reveals Differential Expression Across Brain Regions and Genetic Backgrounds. G3: Genes, Genomes, Genetics, 2012, 2, 203-211.	1.8	18
25	Imputation of Single-Nucleotide Polymorphisms in Inbred Mice Using Local Phylogeny. Genetics, 2012, 190, 449-458.	2.9	42
26	Status and access to the Collaborative Cross population. Mammalian Genome, 2012, 23, 706-712.	2.2	134
27	Comparative analysis and visualization of multiple collinear genomes. BMC Bioinformatics, 2012, 13, S13.	2.6	54
28	Subspecific origin and haplotype diversity in the laboratory mouse. Nature Genetics, 2011, 43, 648-655.	21.4	439
29	Dynamic visualization and comparative analysis of multiple collinear genomic data., 2011, 2011, 335-339.		2
30	Genetic analysis of complex traits in the emerging Collaborative Cross. Genome Research, 2011, 21, 1213-1222.	5.5	327
31	Genome-wide compatible SNP intervals and their properties. , 2010, 2010, 43-52.		15