

Sarah B Kingan

List of Publications by Year in descending order

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Version: 2024-02-01

13
papers

2,805
citations

840776

11
h-index

1125743

13
g-index

23
all docs

23
docs citations

23
times ranked

3776
citing authors

#	ARTICLE	IF	CITATIONS
1	A draft phased assembly of the diploid Cascade hop (<i>Humulus lupulus</i>) genome. <i>Plant Genome</i> , 2021, 14, e20072.	2.8	25
2	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. <i>Nature Communications</i> , 2021, 12, 1935.	12.8	64
3	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
4	Genomic Resources to Guide Improvement of the Shea Tree. <i>Frontiers in Plant Science</i> , 2021, 12, 720670.	3.6	11
5	Genomic analysis of powdery mildew resistance in a hop (<i>Humulus lupulus</i> L.) bi-parental population segregating for <i>âœR6-locus</i> . <i>Euphytica</i> , 2020, 216, 1.	1.2	10
6	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. <i>Nature Communications</i> , 2020, 11, 2071.	12.8	84
7	A high-quality genome assembly from a single, field-collected spotted lanternfly (<i>Lycorma delicatula</i>) using the PacBio Sequel II system. <i>GigaScience</i> , 2019, 8, .	6.4	35
8	A High-Quality De novo Genome Assembly from a Single Mosquito Using PacBio Sequencing. <i>Genes</i> , 2019, 10, 62.	2.4	121
9	Chromosome-level assembly of the water buffalo genome surpasses human and goat genomes in sequence contiguity. <i>Nature Communications</i> , 2019, 10, 260.	12.8	161
10	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , 2018, 563, 501-507.	27.8	426
11	De novo assembly of haplotype-resolved genomes with trio binning. <i>Nature Biotechnology</i> , 2018, 36, 1174-1182.	17.5	352
12	A High-Quality, Long-Read De Novo Genome Assembly to Aid Conservation of Hawaiiâ€™s Last Remaining Crow Species. <i>Genes</i> , 2018, 9, 393.	2.4	22
13	De novo PacBio long-read and phased avian genome assemblies correct and add to reference genes generated with intermediate and short reads. <i>GigaScience</i> , 2017, 6, 1-16.	6.4	165