

Masahiro Kasahara

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

2,276
citations

840119

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996533

15
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24
docs citations

24
times ranked

3341
citing authors

#	ARTICLE	IF	CITATIONS
1	The medaka draft genome and insights into vertebrate genome evolution. <i>Nature</i> , 2007, 447, 714-719.	13.7	1,037
2	The Genome Sequence of Silkworm, <i>Bombyx mori</i> . <i>DNA Research</i> , 2004, 11, 27-35.	1.5	594
3	Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. <i>Science</i> , 2009, 323, 401-404.	6.0	122
4	Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. <i>Nature Ecology and Evolution</i> , 2017, 1, 59.	3.4	99
5	Performance comparison of second- and third-generation sequencers using a bacterial genome with two chromosomes. <i>BMC Genomics</i> , 2014, 15, 699.	1.2	93
6	Large Scale Full-Length cDNA Sequencing Reveals a Unique Genomic Landscape in a Lepidopteran Model Insect, <i>Bombyx mori</i> . <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1481-1492.	0.8	87
7	Introducing difference recurrence relations for faster semi-global alignment of long sequences. <i>BMC Bioinformatics</i> , 2018, 19, 45.	1.2	75
8	UTGB/medaka: genomic resource database for medaka biology. <i>Nucleic Acids Research</i> , 2007, 36, D747-D752.	6.5	32
9	Long-read sequencing for non-small-cell lung cancer genomes. <i>Genome Research</i> , 2020, 30, 1243-1257.	2.4	28
10	MoMI-G: modular multi-scale integrated genome graph browser. <i>BMC Bioinformatics</i> , 2019, 20, 548.	1.2	22
11	Segmental duplications in the silkworm genome. <i>BMC Genomics</i> , 2013, 14, 521.	1.2	18
12	Cost-Effective Sequencing of Full-Length cDNA Clones Powered by a De Novo-Reference Hybrid Assembly. <i>PLoS ONE</i> , 2010, 5, e10517.	1.1	11
13	Development of diagnostic PCR and LAMP markers for MALE STERILITY 1 (MS1) in <i>Cryptomeria japonica</i> D. Don. <i>BMC Research Notes</i> , 2020, 13, 457.	0.6	10
14	Visualization tools for human structural variations identified by whole-genome sequencing. <i>Journal of Human Genetics</i> , 2020, 65, 49-60.	1.1	9
15	Large-Scale Genome Sequence Processing. , 2006, , .		7
16	Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. , 2011, , 39-47.		1
17	LPMX: a pure rootless composable container system. <i>BMC Bioinformatics</i> , 2022, 23, 112.	1.2	1
18	A Graph Genome Browser: Visualization of Structural Variations between Genomes using a Graph Structure. <i>Journal of the Visualization Society of Japan</i> , 2020, 40, 14-18.	0.0	0