

Satoshi Natsume

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

3,645
citations

623734

14
h-index

839539

18
g-index

22
all docs

22
docs citations

22
times ranked

3870
citing authors

#	ARTICLE	IF	CITATIONS
1	High-performance pipeline for MutMap and QTL-seq. PeerJ, 2022, 10, e13170.	2.0	22
2	Population Genomics of Yams: Evolution and Domestication of Dioscorea Species. Population Genomics, 2021, , .	0.5	13
3	Genome analyses reveal the hybrid origin of the staple crop white Guinea yam (<i>Dioscorea</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2020, 117, 31987-31992.	7.1	40
4	Identification of candidate flowering and sex genes in white Guinea yam (<i>D. rotundata</i> Poir.) by SuperSAGE transcriptome profiling. PLoS ONE, 2019, 14, e0216912.	2.5	16
5	Next-Generation Breeding of Rice by Whole-Genome Approaches. , 2018, , 511-522.		4
6	Screening of rice mutants with improved saccharification efficiency results in the identification of CONSTITUTIVE PHOTOMORPHOGENIC 1 and GOLD HULL AND INTERNODE 1. Planta, 2017, 246, 61-74.	3.2	5
7	Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination. BMC Biology, 2017, 15, 86.	3.8	114
8	A chloroplastâ€localized protein <i>LESION AND LAMINA BENDING</i> affects defence and growth responses in rice. New Phytologist, 2016, 210, 1282-1297.	7.3	33
9	Host specialization of the blast fungus <i>Magnaporthe oryzae</i> is associated with dynamic gain and loss of genes linked to transposable elements. BMC Genomics, 2016, 17, 370.	2.8	157
10	MutMap accelerates breeding of a salt-tolerant rice cultivar. Nature Biotechnology, 2015, 33, 445-449.	17.5	265
11	A cytochrome P450, OsDSS1, is involved in growth and drought stress responses in rice (<i>Oryza sativa</i>) Tj ETQq1 1 0.784314 rgBT /Overl 3.9	3.9	111
12	The rice (<i>Oryza sativa</i> L.) <i>LESION MIMIC RESEMBLING</i> , which encodes an AAA-type ATPase, is implicated in defense response. Molecular Genetics and Genomics, 2015, 290, 611-622.	2.1	66
13	The Draft Genome of Hop (<i>Humulus lupulus</i>), an Essence for Brewing. Plant and Cell Physiology, 2015, 56, 428-441.	3.1	111
14	<i>MutMap</i> : whole-genome resequencing of mutant <i>F2</i> progeny bulk combined with <i>de novo</i> assembly of gap regions identifies the rice blast resistance gene <i>Pii</i> . New Phytologist, 2013, 200, 276-283.	7.3	196
15	<i>QTL-seq</i> : rapid mapping of quantitative trait loci in rice by whole genome resequencing of <i>DNA</i> from two bulked populations. Plant Journal, 2013, 74, 174-183.	5.7	1,065
16	MutMap+: Genetic Mapping and Mutant Identification without Crossing in Rice. PLoS ONE, 2013, 8, e68529.	2.5	267
17	Coval: Improving Alignment Quality and Variant Calling Accuracy for Next-Generation Sequencing Data. PLoS ONE, 2013, 8, e75402.	2.5	58
18	Whole genome sequencing and future breeding of rice. Journal of Plant Biochemistry and Biotechnology, 2012, 21, 10-14.	1.7	2

#	ARTICLE	IF	CITATIONS
19	Genome sequencing reveals agronomically important loci in rice using MutMap. Nature Biotechnology, 2012, 30, 174-178.	17.5	1,087