

Karen Aitken

List of Publications by Year in descending order

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56
papers

2,404
citations

218381

26
h-index

214527

47
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57
all docs

57
docs citations

57
times ranked

1761
citing authors

#	ARTICLE	IF	CITATIONS
1	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. <i>Nature Communications</i> , 2018, 9, 2638.	5.8	299
2	Sugarcane biotechnology: The challenges and opportunities. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2005, 41, 345-363.	0.9	181
3	A combination of AFLP and SSR markers provides extensive map coverage and identification of homo(eo)logous linkage groups in a sugarcane cultivar. <i>Theoretical and Applied Genetics</i> , 2005, 110, 789-801.	1.8	174
4	Targeted single nucleotide polymorphism (SNP) discovery in a highly polyploid plant species using 454 sequencing. <i>Plant Biotechnology Journal</i> , 2009, 7, 347-354.	4.1	134
5	Associations between DNA markers and resistance to diseases in sugarcane and effects of population substructure. <i>Theoretical and Applied Genetics</i> , 2006, 114, 155-164.	1.8	97
6	Complete Genome Sequence of <i>Sporisorium scitamineum</i> and Biotrophic Interaction Transcriptome with Sugarcane. <i>PLoS ONE</i> , 2015, 10, e0129318.	1.1	93
7	Quantitative trait loci identified for sugar related traits in a sugarcane (<i>Saccharum</i> spp.) cultivar— <i>Saccharum officinarum</i> population. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1306-1317.	1.8	85
8	Genetic control of yield related stalk traits in sugarcane. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1191-1203.	1.8	82
9	Evaluation of Sugarcane × <i>Saccharum spontaneum</i> Progeny for Biomass Composition and Yield Components. <i>Crop Science</i> , 2008, 48, 951-961.	0.8	68
10	Verification of the introgression of <i>Erianthus arundinaceus</i> germplasm into sugarcane using molecular markers. <i>Plant Breeding</i> , 2005, 124, 322-328.	1.0	66
11	A comprehensive genetic map of sugarcane that provides enhanced map coverage and integrates high-throughput Diversity Array Technology (DArT) markers. <i>BMC Genomics</i> , 2014, 15, 152.	1.2	61
12	Accelerating Genetic Gain in Sugarcane Breeding Using Genomic Selection. <i>Agronomy</i> , 2020, 10, 585.	1.3	60
13	Diversity Arrays Technology effectively reveals DNA polymorphism in a large and complex genome of sugarcane. <i>Molecular Breeding</i> , 2011, 28, 37-55.	1.0	56
14	RNAseq Transcriptional Profiling following Whip Development in Sugarcane Smut Disease. <i>PLoS ONE</i> , 2016, 11, e0162237.	1.1	56
15	A preliminary assessment of the genetic relationship between <i>Erianthus rockii</i> and the <i>Saccharum</i> complex—using microsatellite (SSR) and AFLP markers. <i>Plant Science</i> , 2005, 169, 976-984.	1.7	54
16	Construction of a genetic linkage map for <i>Saccharum officinarum</i> incorporating both simplex and duplex markers to increase genome coverage. <i>Genome</i> , 2007, 50, 742-756.	0.9	52
17	Characterisation of genome regions incorporated from an important wild relative into Australian sugarcane. <i>Molecular Breeding</i> , 2005, 15, 367-381.	1.0	47
18	AFLP analysis of genetic diversity within <i>Saccharum officinarum</i> and comparison with sugarcane cultivars. <i>Australian Journal of Agricultural Research</i> , 2006, 57, 1167.	1.5	45

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19	Comparative mapping in the Poaceae family reveals translocations in the complex polyploid genome of sugarcane. <i>BMC Plant Biology</i> , 2014, 14, 190.	1.6	43
20	The identification and characterisation of alleles of sucrose phosphate synthase gene family III in sugarcane. <i>Molecular Breeding</i> , 2006, 18, 39-50.	1.0	39
21	Analysis of the resistance mechanisms in sugarcane during <i>Sporisorium scitamineum</i> infection using RNA-seq and microscopy. <i>PLoS ONE</i> , 2018, 13, e0197840.	1.1	37
22	Characterization of intergeneric hybrids of <i>Erianthus rockii</i> and <i>Saccharum</i> using molecular markers. <i>Genetic Resources and Crop Evolution</i> , 2007, 54, 1395-1405.	0.8	35
23	A high-resolution genetic map of the cereal crown rot pathogen <i>Fusarium pseudograminearum</i> provides a near-complete genome assembly. <i>Molecular Plant Pathology</i> , 2018, 19, 217-226.	2.0	35
24	Genomic prediction of sugar content and cane yield in sugar cane clones in different stages of selection in a breeding program, with and without pedigree information. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	35
25	Comparative genetics in sugarcane enables structured map enhancement and validation of marker-trait associations. <i>Molecular Breeding</i> , 2008, 21, 233-247.	1.0	32
26	Identification of QTL for reaction to three races of <i>Colletotrichum trifolii</i> and further analysis of inheritance of resistance in autotetraploid lucerne. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1417-1426.	1.8	28
27	Identifying the Risks of Transgene Escape from Sugarcane Crops to Related Species, with Particular Reference to <i>Saccharum spontaneum</i> in Australia. <i>Tropical Plant Biology</i> , 2008, 1, 58-71.	1.0	28
28	Improved genomic prediction of clonal performance in sugarcane by exploiting non-additive genetic effects. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2235-2252.	1.8	27
29	Sugarcane Smut, Caused by <i>Sporisorium scitamineum</i> , a Major Disease of Sugarcane: A Contemporary Review. <i>Phytopathology</i> , 2021, 111, 1905-1917.	1.1	27
30	Accuracy of genomic prediction of complex traits in sugarcane. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1455-1462.	1.8	26
31	Identification of QTL for resistance and susceptibility to <i>Stagonospora meliloti</i> in autotetraploid lucerne. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1427-1435.	1.8	25
32	Genetic control of monoterpene composition in the essential oil of <i>Melaleuca alternifolia</i> (Cheel). <i>Theoretical and Applied Genetics</i> , 2002, 105, 377-383.	1.8	20
33	A genetic linkage map in autotetraploid lucerne adapted to northern Australia, and use of the map to identify DNA markers linked to resistance to <i>Phytophthora medicaginis</i> . <i>Australian Journal of Agricultural Research</i> , 2005, 56, 333.	1.5	19
34	Bayesian estimation of marker dosage in sugarcane and other autopolyploids. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1653-1672.	1.8	18
35	Assessment of the genetic diversity in a collection of <i>Erianthus arundinaceus</i> . <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 1483-1491.	0.8	16
36	Strategies and considerations for implementing genomic selection to improve traits with additive and non-additive genetic architectures in sugarcane breeding. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1493-1511.	1.8	16

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37	History and Development of Molecular Markers for Sugarcane Breeding. Sugar Tech, 2022, 24, 341-353.	0.9	15
38	A Survey Sequence Comparison of Saccharum Genotypes Reveals Allelic Diversity Differences. Tropical Plant Biology, 2014, 7, 71-83.	1.0	14
39	Worldwide Genetic Diversity of the Wild Species <i>Saccharum spontaneum</i> and Level of Diversity Captured within Sugarcane Breeding Programs. Crop Science, 2018, 58, 218-229.	0.8	14
40	Genomic Selection in Sugarcane: Current Status and Future Prospects. Frontiers in Plant Science, 2021, 12, 708233.	1.7	14
41	DNA markers linked to yield, yield components, and morphological traits in autotetraploid lucerne (<i>Medicago sativa</i> L.). Australian Journal of Agricultural Research, 2006, 57, 801.	1.5	14
42	Genetic improvement of lucerne for anthracnose (<i>Colletotrichum trifolii</i>) resistance. Australasian Plant Pathology, 2006, 35, 573.	0.5	13
43	A quantitative genetics approach to nitrogen use efficiency in sugarcane. Functional Plant Biology, 2010, 37, 448.	1.1	12
44	Characterisation of alleles of the sucrose phosphate synthase gene family in sugarcane and their association with sugar-related traits. Molecular Breeding, 2015, 35, 1.	1.0	12
45	Evidence for second division restitution as the basis for 2n+2n maternal chromosome transmission in a sugarcane cross. Euphytica, 2012, 187, 359-368.	0.6	11
46	Construction of Molecular Genetic Linkage Map of Sugarcane Based on SSR and AFLP Markers. Acta Agronomica Sinica(China), 2010, 36, 177-183.	0.1	11
47	Conversion of AFLP markers to high-throughput markers in a complex polyploid, sugarcane. Molecular Breeding, 2011, 27, 395-407.	1.0	10
48	Using quantitative PCR with retrotransposon-based insertion polymorphisms as markers in sugarcane. Journal of Experimental Botany, 2015, 66, 4239-4250.	2.4	10
49	Flow cytometric characterisation of the complex polyploid genome of <i>Saccharum officinarum</i> and modern sugarcane cultivars. Scientific Reports, 2019, 9, 19362.	1.6	8
50	DNA Marker Transmission and Linkage Analysis in Populations Derived from a Sugarcane (<i>Saccharum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tt	1.1	7
51	A linkage disequilibrium-based approach to position unmapped SNPs in crop species. BMC Genomics, 2021, 22, 773.	1.2	7
52	A New Approach for Copy Number Estimation in Polyploids. Journal of Heredity, 2010, 101, 521-524.	1.0	6
53	A perfect storm: ploidy and preadaptation facilitate <i>Saccharum spontaneum</i> escape and invasion in the Republic of Panama. Biological Invasions, 2021, 23, 1101-1115.	1.2	6
54	DETECTION OF GENETIC DIVERSITY USING RAPD MARKERS IN THE GENUS MELALEUCA. Acta Horticulturae, 1998, , 209-218.	0.1	2

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55	Resistance mechanisms and expression of disease resistance-related genes in sugarcane (<i>Saccharum</i>) Tj ETQq1 1 0.784314 rgBT /Over	1.1	2
56	Isolation and sequencing of a single copy of an introgressed chromosome from a complex genome for gene and SNP identification. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1279-1292.	1.8	0