

Amanda J Burridge

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

2,182
citations

430874

18
h-index

315739

38
g-index

48
all docs

48
docs citations

48
times ranked

2200
citing authors

#	ARTICLE	IF	CITATIONS
1	High-density SNP genotyping array for hexaploid wheat and its secondary and tertiary gene pool. <i>Plant Biotechnology Journal</i> , 2016, 14, 1195-1206.	8.3	462
2	Characterization of a Wheat Breeders' Array suitable for high-throughput SNP genotyping of global accessions of hexaploid bread wheat (<i>Triticum aestivum</i>). <i>Plant Biotechnology Journal</i> , 2017, 15, 390-401.	8.3	334
3	CerealsDB 2.0: an integrated resource for plant breeders and scientists. <i>BMC Bioinformatics</i> , 2012, 13, 219.	2.6	194
4	Discovery and development of exome-based, co-dominant single nucleotide polymorphism markers in hexaploid wheat (<i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2013, 11, 279-295.	8.3	161
5	Targeted resequencing of the allohexaploid wheat exome. <i>Plant Biotechnology Journal</i> , 2012, 10, 733-742.	8.3	133
6	A step change in the transfer of interspecific variation into wheat from <i>Amblyopyrum muticum</i> . <i>Plant Biotechnology Journal</i> , 2017, 15, 217-226.	8.3	124
7	Wheat Landrace Genome Diversity. <i>Genetics</i> , 2017, 205, 1657-1676.	2.9	76
8	Characterisation of <i>Thinopyrum bessarabicum</i> chromosomes through genome-wide introgressions into wheat. <i>Theoretical and Applied Genetics</i> , 2018, 131, 389-406.	3.6	74
9	High-density genotyping of the A.E. Watkins Collection of hexaploid landraces identifies a large molecular diversity compared to elite bread wheat. <i>Plant Biotechnology Journal</i> , 2018, 16, 165-175.	8.3	67
10	Introgression of <i>Aegilops speltoides</i> segments in <i>Triticum aestivum</i> and the effect of the gametocidal genes. <i>Annals of Botany</i> , 2018, 121, 229-240.	2.9	57
11	Detecting SARS-CoV-2 variants with SNP genotyping. <i>PLoS ONE</i> , 2021, 16, e0243185.	2.5	53
12	CerealsDB 3.0: expansion of resources and data integration. <i>BMC Bioinformatics</i> , 2016, 17, 256.	2.6	42
13	Development and validation of an exome-based SNP marker set for identification of the St, Jr and Jvs genomes of <i>Thinopyrum intermedium</i> in a wheat background. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1555-1570.	3.6	37
14	The role of gene flow and chromosomal instability in shaping the bread wheat genome. <i>Nature Plants</i> , 2021, 7, 172-183.	9.3	36
15	Conversion of array-based single nucleotide polymorphic markers for use in targeted genotyping by sequencing in hexaploid wheat (<i>Triticum aestivum</i>). <i>Plant Biotechnology Journal</i> , 2018, 16, 867-876.	8.3	27
16	Detection of <i>T. urartu</i> Introgressions in Wheat and Development of a Panel of Interspecific Introgression Lines. <i>Frontiers in Plant Science</i> , 2018, 9, 1565.	3.6	27
17	Development and characterisation of interspecific hybrid lines with genome-wide introgressions from <i>Triticum timopheevii</i> in a hexaploid wheat background. <i>BMC Plant Biology</i> , 2019, 19, 183.	3.6	25
18	Exploiting the genome of <i>Thinopyrum elongatum</i> to expand the gene pool of hexaploid wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2213-2226.	3.6	25

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19	Variation in key leaf photosynthetic traits across wheat wild relatives is accession dependent not species dependent. <i>New Phytologist</i> , 2020, 228, 1767-1780.	7.3	23
20	FANCM promotes class I interfering crossovers and suppresses class II non-interfering crossovers in wheat meiosis. <i>Nature Communications</i> , 2022, 13, .	12.8	21
21	Developing a High-Throughput SNP-Based Marker System to Facilitate the Introgression of Traits From <i>Aegilops</i> Species Into Bread Wheat (<i>Triticum aestivum</i>). <i>Frontiers in Plant Science</i> , 2018, 9, 1993.	3.6	20
22	Identification of a major QTL and associated molecular marker for high arabinoxylan fibre in white wheat flour. <i>PLoS ONE</i> , 2020, 15, e0227826.	2.5	20
23	Examining the Effects of Temperature on Recombination in Wheat. <i>Frontiers in Plant Science</i> , 2020, 11, 230.	3.6	18
24	CerealsDBâ€™ new tools for the analysis of the wheat genome: update 2020. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	16
25	Historical changes in the contents and compositions of fibre components and polar metabolites in white wheat flour. <i>Scientific Reports</i> , 2020, 10, 5920.	3.3	13
26	Genetic variation in wheat grain quality is associated with differences in the galactolipid content of flour and the gas bubble properties of dough liquor. <i>Food Chemistry: X</i> , 2020, 6, 100093.	4.3	12
27	Development of a minimal KASP marker panel for distinguishing genotypes in apple collections. <i>PLoS ONE</i> , 2020, 15, e0242940.	2.5	12
28	High-Density SNP Genotyping Array for Hexaploid Wheat and Its Relatives. <i>Methods in Molecular Biology</i> , 2017, 1679, 293-306.	0.9	11
29	Population structure and genome-wide association studies in bread wheat for phosphorus efficiency traits using 35ÅK Wheat Breederâ€™s Affymetrix array. <i>Scientific Reports</i> , 2021, 11, 7601.	3.3	11
30	Segregation distortion: Utilizing simulated genotyping data to evaluate statistical methods. <i>PLoS ONE</i> , 2020, 15, e0228951.	2.5	10
31	Molecular Diversity within a Mediterranean and European Panel of Tetraploid Wheat (<i>T. turgidum</i>) Tj ETQq1 1 0.784314 rgBT /Overlo 414.	3.0	7
32	Generation of Doubled Haploid Wheat-Triticum urartu Introgression Lines and Their Characterisation Using Chromosome-Specific KASP Markers. <i>Frontiers in Plant Science</i> , 2021, 12, 643636.	3.6	7
33	Identification of a novel stripe rust resistance gene from the European winter wheat cultivar â€ˆAciendaâ€™: A step towards rust proofing wheat cultivation. <i>PLoS ONE</i> , 2022, 17, e0264027.	2.5	7
34	Quantifying rooting at depth in a wheat doubled haploid population with introgression from wild emmer. <i>Annals of Botany</i> , 2017, 120, 457-470.	2.9	6
35	Genomic and proteomic analyses of plant response to radiation in the environment â€ˆ“ an abiotic stress context. <i>Radioprotection</i> , 2009, 44, 887-890.	1.0	5
36	The Long Ashton Legacy: Characterising United Kingdom West Country cider apples using a genotyping by targeted sequencing approach. <i>Plants People Planet</i> , 2020, 2, 167-175.	3.3	4

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37	CerealsDB: A Whistle-Stop Tour of an Open Access SNP Resource. <i>Methods in Molecular Biology</i> , 2022, 2443, 133-146.	0.9	1
38	The Use and Limitations of Exome Capture to Detect Novel Variation in the Hexaploid Wheat Genome. <i>Frontiers in Plant Science</i> , 2022, 13, 841855.	3.6	1
39	Development of a minimal KASP marker panel for distinguishing genotypes in apple collections. , 2020, 15, e0242940.		0
40	Development of a minimal KASP marker panel for distinguishing genotypes in apple collections. , 2020, 15, e0242940.		0
41	Development of a minimal KASP marker panel for distinguishing genotypes in apple collections. , 2020, 15, e0242940.		0
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44	Development of a minimal KASP marker panel for distinguishing genotypes in apple collections. , 2020, 15, e0242940.		0