

Timothy Sutton

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

2,726
citations

257357

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289141

40
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all docs

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docs citations

41
times ranked

3101
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic prediction of preliminary yield trials in chickpea: Effect of functional annotation of SNPs and environment. <i>Plant Genome</i> , 2022, 15, e20166.	1.6	7
2	Fine Mapping of a Vigor QTL in Chickpea (<i>Cicer arietinum</i> L.) Reveals a Potential Role for Ca4_TIFY4B in Regulating Leaf and Seed Size. <i>Frontiers in Plant Science</i> , 2022, 13, 829566.	1.7	6
3	Cause of Death: Phytophthora or Flood? Effects of Waterlogging on Phytophthora medicaginis and Resistance of Chickpea (<i>Cicer arietinum</i>). <i>Agronomy</i> , 2022, 12, 89.	1.3	7
4	Genetic analysis of boron tolerance in burr medic (<i>Medicago polymorpha</i> L.). <i>Crop and Pasture Science</i> , 2021, 72, 634.	0.7	3
5	Ph2 encodes the mismatch repair protein MSH7-3D that inhibits wheat homoeologous recombination. <i>Nature Communications</i> , 2021, 12, 803.	5.8	49
6	Novel Salinity Tolerance Loci in Chickpea Identified in Glasshouse and Field Environments. <i>Frontiers in Plant Science</i> , 2021, 12, 667910.	1.7	20
7	The genetics of vigour-related traits in chickpea (<i>Cicer arietinum</i> L.): insights from genomic data. <i>Theoretical and Applied Genetics</i> , 2021, 135, 107.	1.8	4
8	Evidence for the Application of Emerging Technologies to Accelerate Crop Improvement – A Collaborative Pipeline to Introgress Herbicide Tolerance Into Chickpea. <i>Frontiers in Plant Science</i> , 2021, 12, 779122.	1.7	4
9	A QTL on the Ca7 chromosome of chickpea affects resistance to the root-lesion nematode <i>Pratylenchus thornei</i> . <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	32
10	A hydroponics based high throughput screening system for Phytophthora root rot resistance in chickpea (<i>Cicer arietinum</i> L.). <i>Plant Methods</i> , 2019, 15, 82.	1.9	11
11	Bread Wheat With High Salinity and Sodicity Tolerance. <i>Frontiers in Plant Science</i> , 2019, 10, 1280.	1.7	74
12	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. <i>Nature Genetics</i> , 2019, 51, 857-864.	9.4	219
13	Phenotypic and molecular characterisation of novel <i>Vicia faba</i> germplasm with tolerance to acetohydroxyacid synthase-inhibiting herbicides (AHAS) developed through mutagenesis techniques. <i>Pest Management Science</i> , 2019, 75, 2698-2705.	1.7	3
14	Mapping resistance to Phytophthora root rot identifies independent loci from cultivated (<i>Cicer</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22 2019, 132, 1017-1033.	1.8	24
15	Investigating Drought Tolerance in Chickpea Using Genome-Wide Association Mapping and Genomic Selection Based on Whole-Genome Resequencing Data. <i>Frontiers in Plant Science</i> , 2018, 9, 190.	1.7	111
16	Exploring genetic variation for salinity tolerance in chickpea using image-based phenotyping. <i>Scientific Reports</i> , 2017, 7, 1300.	1.6	94
17	Genome Analysis Identified Novel Candidate Genes for Ascochyta Blight Resistance in Chickpea Using Whole Genome Re-sequencing Data. <i>Frontiers in Plant Science</i> , 2017, 8, 359.	1.7	53
18	Quantifying the Onset and Progression of Plant Senescence by Color Image Analysis for High Throughput Applications. <i>PLoS ONE</i> , 2016, 11, e0157102.	1.1	26

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19	Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. <i>Frontiers in Plant Science</i> , 2016, 7, 1666.	1.7	127
20	QTL-seq for rapid identification of candidate genes for 100-seed weight and root/total plant dry weight ratio under rainfed conditions in chickpea. <i>Plant Biotechnology Journal</i> , 2016, 14, 2110-2119.	4.1	177
21	Phenotypic plasticity and its genetic regulation for yield, nitrogen fixation and ^{13}C in chickpea crops under varying water regimes. <i>Journal of Experimental Botany</i> , 2016, 67, 4339-4351.	2.4	50
22	A Barley Efflux Transporter Operates in a Na^+ -Dependent Manner, as Revealed by a Multidisciplinary Platform. <i>Plant Cell</i> , 2016, 28, 202-218.	3.1	29
23	Prioritization of candidate genes in a QTL-hotspot region for drought tolerance in chickpea (<i>Cicer</i>) Tj ETQq1 1,0,784314,rgBT /Ove	1.6	131
24	Diversity in boron toxicity tolerance of Australian barley (<i>Hordeum vulgare</i> L.) genotypes. <i>BMC Plant Biology</i> , 2015, 15, 231.	1.6	15
25	Genotyping-by-sequencing based intra-specific genetic map refines a QTL-hotspot region for drought tolerance in chickpea. <i>Molecular Genetics and Genomics</i> , 2015, 290, 559-571.	1.0	180
26	Quantitative profiling of polar primary metabolites of two chickpea cultivars with contrasting responses to salinity. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2015, 1000, 1-13.	1.2	96
27	High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in <i>Cicer arietinum</i> and <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2015, 128, 1039-1047.	1.8	76
28	Molecular basis of adaptation to high soil boron in wheat landraces and elite cultivars. <i>Nature</i> , 2014, 514, 88-91.	13.7	106
29	Germanium as a tool to dissect boron toxicity effects in barley and wheat. <i>Functional Plant Biology</i> , 2013, 40, 618.	1.1	26
30	Boron toxicity and deficiency in Triticeae: Update on tolerance mechanisms and transporters. <i>New Biotechnology</i> , 2012, 29, S137.	2.4	0
31	Genes mapping to boron tolerance QTL in barley identified by suppression subtractive hybridization. <i>Plant, Cell and Environment</i> , 2010, 33, 188-198.	2.8	11
32	Boron Toxicity Tolerance in Barley through Reduced Expression of the Multifunctional Aquaporin HvNIP2;1 Å. <i>Plant Physiology</i> , 2010, 153, 1706-1715.	2.3	159
33	Boron toxicity tolerance in wheat and barley: Australian perspectives. <i>Breeding Science</i> , 2010, 60, 297-304.	0.9	60
34	Comparative transcriptomics in the Triticeae. <i>BMC Genomics</i> , 2009, 10, 285.	1.2	62
35	The Bo1-specific PCR marker AWW5L7 is predictive of boron tolerance status in a range of exotic durum and bread wheats. <i>Genome</i> , 2008, 51, 963-971.	0.9	26
36	Boron-Toxicity Tolerance in Barley Arising from Efflux Transporter Amplification. <i>Science</i> , 2007, 318, 1446-1449.	6.0	422

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37	Fine mapping and targeted SNP survey using rice-wheat gene colinearity in the region of the Bo1 boron toxicity tolerance locus of bread wheat. <i>Theoretical and Applied Genetics</i> , 2007, 115, 451-461.	1.8	53
38	Identification of transposons, retroelements, and a gene family predominantly expressed in floral tissues in chromosome 3DS of the hexaploid wheat progenitor <i>Aegilops tauschii</i> . <i>Functional and Integrative Genomics</i> , 2006, 7, 37-52.	1.4	9
39	Microarray expression analysis of meiosis and microsporogenesis in hexaploid bread wheat. <i>BMC Genomics</i> , 2006, 7, 267.	1.2	82
40	WM5: Isolation and characterisation of a gene expressed during early meiosis and shoot meristem development in wheat. <i>Functional Plant Biology</i> , 2005, 32, 249.	1.1	9
41	ThePh2pairing homoeologous locus of wheat (<i>Triticum aestivum</i>): identification of candidate meiotic genes using a comparative genetics approach. <i>Plant Journal</i> , 2003, 36, 443-456.	2.8	73