

John McCallum

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

2,138
citations

201674

27
h-index

233421

45
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51
all docs

51
docs citations

51
times ranked

1703
citing authors

#	ARTICLE	IF	CITATIONS
1	First Chromosome-Scale Assembly and Deep Floral-Bud Transcriptome of a Male Kiwifruit. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	9
2	Construction of a high-density genetic map for hexaploid kiwifruit (<i>Actinidia chinensis</i> var.) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.8	5
3	QTL Mapping for Resistance to Cankers Induced by <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> (Psa) in a Tetraploid <i>Actinidia chinensis</i> Kiwifruit Population. <i>Pathogens</i> , 2020, 9, 967.	2.8	14
4	Molecular Characterisation of a Supergene Conditioning Super-High Vitamin C in Kiwifruit Hybrids. <i>Plants</i> , 2019, 8, 237.	3.5	7
5	Multiple quantitative trait loci contribute to resistance to bacterial canker incited by <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> in kiwifruit (<i>Actinidia chinensis</i>). <i>Horticulture Research</i> , 2019, 6, 101.	6.3	24
6	A manually annotated <i>Actinidia chinensis</i> var. <i>chinensis</i> (kiwifruit) genome highlights the challenges associated with draft genomes and gene prediction in plants. <i>BMC Genomics</i> , 2018, 19, 257.	2.8	167
7	A Guide for the Cultivation of Onion under Controlled Environment Conditions. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2018, 53, 1746-1749.	1.0	5
8	Molecular Mapping of Genes and QTL: Progress to Date and Development of New Population Resources for NGS Genetics. <i>Compendium of Plant Genomes</i> , 2018, , 181-196.	0.5	0
9	Gene Family Evolution in <i>Allium</i> Species. <i>Compendium of Plant Genomes</i> , 2018, , 145-159.	0.5	1
10	The Onion (<i>Allium cepa</i> L.) R2R3-MYB Gene MYB1 Regulates Anthocyanin Biosynthesis. <i>Frontiers in Plant Science</i> , 2016, 7, 1865.	3.6	91
11	Enhancing onion breeding using molecular tools. <i>Plant Breeding</i> , 2016, 135, 9-20.	1.9	50
12	Building strong relationships between conservation genetics and primary industry leads to mutually beneficial genomic advances. <i>Molecular Ecology</i> , 2016, 25, 5267-5281.	3.9	16
13	Doubled Haploid <i>~CUDH2107~™</i> as a Reference for Bulb Onion (<i>Allium cepa</i> L.) Research: Development of a Transcriptome Catalogue and Identification of Transcripts Associated with Male Fertility. <i>PLoS ONE</i> , 2016, 11, e0166568.	2.5	14
14	A DNA-based diagnostic for differentiating among New Zealand endemic <i>Podocarpus</i> . <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	7
15	Genetic analyses of bolting in bulb onion (<i>Allium cepa</i> L.). <i>Theoretical and Applied Genetics</i> , 2014, 127, 535-547.	3.6	31
16	FLOWERING LOCUS T genes control onion bulb formation and flowering. <i>Nature Communications</i> , 2013, 4, 2884.	12.8	197
17	Measurement of the distribution of non-structural carbohydrate composition in onion populations by a high-throughput microplate enzymatic assay. <i>Journal of the Science of Food and Agriculture</i> , 2013, 93, 2470-2477.	3.5	11
18	Chromosomal Organization and Sequence Diversity of Genes Encoding Lachrymatory Factor Synthase in <i>Allium cepa</i> L.. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 643-651.	1.8	16

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19	Development of robust genomic simple sequence repeat markers for estimation of genetic diversity within and among bulb onion (<i>Allium cepa</i> L.) populations. <i>Molecular Breeding</i> , 2012, 30, 1401-1411.	2.1	77
20	Genotypic variation in sulfur assimilation and metabolism of onion (<i>Allium cepa</i> L.) III. Characterization of sulfite reductase. <i>Phytochemistry</i> , 2012, 83, 34-42.	2.9	10
21	AlliumMap-A comparative genomics resource for cultivated <i>Allium</i> vegetables. <i>BMC Genomics</i> , 2012, 13, 168.	2.8	41
22	The Diversity and Abundance of Small Arthropods in Onion, <i>Allium cepa</i> , Seed Crops, and their Potential Role in Pollination. <i>Journal of Insect Science</i> , 2011, 11, 1-12.	1.5	5
23	Genotypic variation in sulphur assimilation and metabolism of onion (<i>Allium cepa</i> L.). II: Characterisation of ATP sulphurylase activity. <i>Phytochemistry</i> , 2011, 72, 888-896.	2.9	8
24	Genotypic variation in the sulfur assimilation and metabolism of onion (<i>Allium cepa</i> L.) I. Plant composition and transcript accumulation. <i>Phytochemistry</i> , 2011, 72, 882-887.	2.9	13
25	Designing a Framework for End User Applications. <i>Lecture Notes in Computer Science</i> , 2011, , 67-75.	1.3	2
26	Pilot sequencing of onion genomic DNA reveals fragments of transposable elements, low gene densities, and significant gene enrichment after methyl filtration. <i>Molecular Genetics and Genomics</i> , 2008, 280, 287-92.	2.1	48
27	Conversion of chromosome-specific RAPDs into SCAR-based anchor markers for onion linkage maps and its application to genetic analyses in other <i>Allium</i> species. <i>Scientia Horticulturae</i> , 2008, 115, 323-328.	3.6	5
28	Biochemical and Genetic Analysis of Carbohydrate Accumulation in <i>Allium cepa</i> L. <i>Plant and Cell Physiology</i> , 2008, 49, 730-739.	3.1	31
29	Genetic Diversity Analysis and Single-nucleotide Polymorphism Marker Development in Cultivated Bulb Onion Based on Expressed Sequence Tag "Simple Sequence Repeat Markers. <i>Journal of the American Society for Horticultural Science</i> , 2008, 133, 810-818.	1.0	60
30	Complex formation between recombinant ATP sulfurylase and APS reductase of <i>Allium cepa</i> (L.). <i>FEBS Letters</i> , 2007, 581, 4139-4147.	2.8	20
31	Onion. , 2007, , 331-347.		7
32	Genetic mapping of sulfur assimilation genes reveals a QTL for onion bulb pungency. <i>Theoretical and Applied Genetics</i> , 2007, 114, 815-822.	3.6	57
33	Genetic mapping of a major gene affecting onion bulb fructan content. <i>Theoretical and Applied Genetics</i> , 2006, 112, 958-967.	3.6	93
34	Purification and cloning of a β -glutamyl transpeptidase from onion (<i>Allium cepa</i>). <i>Phytochemistry</i> , 2005, 66, 515-522.	2.9	63
35	Molecular and biochemical characterisation of a serine acetyltransferase of onion, <i>Allium cepa</i> (L.). <i>Phytochemistry</i> , 2005, 66, 1407-1416.	2.9	15
36	Genetic mapping of expressed sequences in onion and in silico comparisons with rice show scant colinearity. <i>Molecular Genetics and Genomics</i> , 2005, 274, 197-204.	2.1	110

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37	Sulfur and nitrogen fertility affects flavour of field-grown onions. <i>Plant and Soil</i> , 2005, 269, 151-158.	3.7	43
38	Linkage Mapping of QTL for Seed Yield, Yield Components, and Developmental Traits in Pea. <i>Crop Science</i> , 2005, 45, 1336-1344.	1.8	54
39	Single Nucleotide Polymorphisms, Indels, and Simple Sequence Repeats for Onion Cultivar Identification. <i>Journal of the American Society for Horticultural Science</i> , 2005, 130, 912-917.	1.0	50
40	A Unique Set of 11,008 Onion Expressed Sequence Tags Reveals Expressed Sequence and Genomic Differences between the Monocot Orders Asparagales and Poales[W]. <i>Plant Cell</i> , 2004, 16, 114-125.	6.6	144
41	Molecular Tagging of the Ms Locus in Onion. <i>Journal of the American Society for Horticultural Science</i> , 2002, 127, 576-582.	1.0	37
42	Expressed sequence markers for genetic analysis of bulb onion (<i>Allium cepa</i> L.). <i>Theoretical and Applied Genetics</i> , 2001, 103, 979-991.	3.6	61
43	A low-density genetic map of onion reveals a role for tandem duplication in the evolution of an extremely large diploid genome. <i>Theoretical and Applied Genetics</i> , 1998, 96, 52-62.	3.6	133
44	A linkage map of the pea (<i>Pisum sativum</i> L.) genome containing cloned sequences of known function and expressed sequence tags (ESTs). <i>Theoretical and Applied Genetics</i> , 1997, 95, 1289-1299.	3.6	82
45	Biosynthesis of flavan-3-ols by leaf extracts of <i>Onobrychis viciifolia</i> . <i>Phytochemistry</i> , 1997, 44, 425-432.	2.9	30
46	Biochemical and Genetic Linkage Analysis of Green Seed Color in Field Pea. <i>Journal of the American Society for Horticultural Science</i> , 1997, 122, 218-225.	1.0	32
47	Developmental changes in the composition of proanthocyanidins from leaves of sainfoin (<i>Onobrychis</i>) Tj ETQq1 1 0.784314 rgBT /Ovst 1066-1070.	5.2	57
48	Identification of the constituent flavanoid units in sainfoin proanthocyanidins by reversed-phase high-performance liquid chromatography. <i>Journal of Chromatography A</i> , 1992, 594, 117-123.	3.7	49
49	Spectrophotometric assay and electrophoretic detection of trans-feruloyl esterase activity. <i>Analytical Biochemistry</i> , 1991, 196, 360-366.	2.4	35