

Noel O I Cogan

List of Publications by Year in descending order

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Version: 2024-02-01

97
papers

4,194
citations

109321

35
h-index

133252

59
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99
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99
docs citations

99
times ranked

4526
citing authors

#	ARTICLE	IF	CITATIONS
1	St<scp>AMPP</scp>: an R package for calculation of genetic differentiation and structure of mixed ploidy level populations. <i>Molecular Ecology Resources</i> , 2013, 13, 946-952.	4.8	541
2	Transcriptome sequencing of lentil based on second-generation technology permits large-scale unigene assembly and SSR marker discovery. <i>BMC Genomics</i> , 2011, 12, 265.	2.8	180
3	Transcriptome sequencing of field pea and faba bean for discovery and validation of SSR genetic markers. <i>BMC Genomics</i> , 2012, 13, 104.	2.8	149
4	Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance. <i>GigaScience</i> , 2019, 8, .	6.4	132
5	Prospects for genomic selection in forage plant species. <i>Plant Breeding</i> , 2013, 132, 133-143.	1.9	125
6	SNP marker discovery, linkage map construction and identification of QTLs for enhanced salinity tolerance in field pea (<i>Pisum sativum</i> L.). <i>BMC Plant Biology</i> , 2013, 13, 161.	3.6	120
7	Improving Genetic Gain with Genomic Selection in Autotetraploid Potato. <i>Plant Genome</i> , 2016, 9, plantgenome2016.02.0021.	2.8	115
8	EST-SNP discovery and dense genetic mapping in lentil (<i>Lens culinaris</i> Medik.) enable candidate gene selection for boron tolerance. <i>Theoretical and Applied Genetics</i> , 2014, 127, 703-713.	3.6	91
9	SNP discovery and high-density genetic mapping in faba bean (<i>Vicia faba</i> L.) permits identification of QTLs for ascochyta blight resistance. <i>Plant Science</i> , 2014, 217-218, 47-55.	3.6	86
10	Genetic map construction and QTL mapping of resistance to blackleg (<i>Leptosphaeria maculans</i>) disease in Australian canola (<i>Brassica napus</i> L.) cultivars. <i>Theoretical and Applied Genetics</i> , 2009, 120, 71-83.	3.6	85
11	Genetic Gain and Inbreeding from Genomic Selection in a Simulated Commercial Breeding Program for Perennial Ryegrass. <i>Plant Genome</i> , 2016, 9, plantgenome2015.06.0046.	2.8	83
12	Gene-associated single nucleotide polymorphism discovery in perennial ryegrass (<i>Lolium perenne</i> L.). <i>Molecular Genetics and Genomics</i> , 2006, 276, 101-112.	2.1	78
13	Assessment of genetic variation within a global collection of lentil (<i>Lens culinaris</i> Medik.) cultivars and landraces using SNP markers. <i>BMC Genetics</i> , 2014, 15, 150.	2.7	76
14	Improving breeding efficiency in potato using molecular and quantitative genetics. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2279-2292.	3.6	74
15	Evolutionary history of tall fescue morphotypes inferred from molecular phylogenetics of the <i>Lolium-Festuca</i> species complex. <i>BMC Evolutionary Biology</i> , 2010, 10, 303.	3.2	70
16	Improving the analysis of low heritability complex traits for enhanced genetic gain in potato. <i>Theoretical and Applied Genetics</i> , 2014, 127, 809-820.	3.6	66
17	A neurotropic herpesvirus infecting the gastropod, abalone, shares ancestry with oyster herpesvirus and a herpesvirus associated with the amphioxus genome. <i>Virology Journal</i> , 2010, 7, 308.	3.4	63
18	SNP-Based Linkage Mapping for Validation of QTLs for Resistance to Ascochyta Blight in Lentil. <i>Frontiers in Plant Science</i> , 2016, 7, 1604.	3.6	62

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19	Metagenomic arbovirus detection using MinION nanopore sequencing. <i>Journal of Virological Methods</i> , 2017, 249, 79-84.	2.1	60
20	Genetic marker discovery, intraspecific linkage map construction and quantitative trait locus analysis of ascochyta blight resistance in chickpea (<i>Cicer arietinum</i> L.). <i>Molecular Breeding</i> , 2014, 33, 297-313.	2.1	58
21	SNP discovery, validation, haplotype structure and linkage disequilibrium in full-length herbage nutritive quality genes of perennial ryegrass (<i>Lolium perenne</i> L.). <i>Molecular Genetics and Genomics</i> , 2007, 278, 585-597.	2.1	57
22	Fine-scale comparative genetic and physical mapping supports map-based cloning strategies for the self-incompatibility loci of perennial ryegrass (<i>Lolium perenne</i> L.). <i>Plant Molecular Biology</i> , 2010, 72, 343-355.	3.9	52
23	Consensus Genetic Map Construction for Field Pea (<i>Pisum sativum</i> L.), Trait Dissection of Biotic and Abiotic Stress Tolerance and Development of a Diagnostic Marker for the <i>er1</i> Powdery Mildew Resistance Gene. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1391-1403.	1.8	51
24	Effective mosquito and arbovirus surveillance using metabarcoding. <i>Molecular Ecology Resources</i> , 2018, 18, 32-40.	4.8	51
25	Evaluation and implementation of a potential diagnostic molecular marker for <i>H1</i> conferred potato cyst nematode resistance in potato (<i>Solanum tuberosum</i> L.). <i>Plant Breeding</i> , 2012, 131, 315-321.	1.9	50
26	Cost analysis of the application of marker-assisted selection in potato breeding. <i>Molecular Breeding</i> , 2013, 32, 299-310.	2.1	49
27	De novo assembly and characterisation of the field pea transcriptome using RNA-Seq. <i>BMC Genomics</i> , 2015, 16, 611.	2.8	49
28	Generation and Characterisation of a Reference Transcriptome for Lentil (<i>Lens culinaris</i> Medik.). <i>International Journal of Molecular Sciences</i> , 2016, 17, 1887.	4.1	49
29	Exploitation of data from breeding programs supports rapid implementation of genomic selection for key agronomic traits in perennial ryegrass. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1891-1902.	3.6	49
30	Assessment of genetic diversity in cultivars of white clover (<i>Trifolium repens</i> L.) detected by SSR polymorphisms. <i>Genome</i> , 2006, 49, 919-930.	2.0	45
31	Quantitative Trait Locus (QTL) meta-analysis and comparative genomics for candidate gene prediction in perennial ryegrass (<i>Lolium perenne</i> L.). <i>BMC Genetics</i> , 2012, 13, 101.	2.7	45
32	Genotyping-by-sequencing through transcriptomics: implementation in a range of crop species with varying reproductive habits and ploidy levels. <i>Plant Biotechnology Journal</i> , 2018, 16, 877-889.	8.3	45
33	Generation of a Comprehensive Transcriptome Atlas and Transcriptome Dynamics in Medicinal Cannabis. <i>Scientific Reports</i> , 2019, 9, 16583.	3.3	45
34	Development of a Brassica napus (Canola) Crop Containing Fish Oil-Like Levels of DHA in the Seed Oil. <i>Frontiers in Plant Science</i> , 2020, 11, 727.	3.6	45
35	Development and validation of a TaqMan [®] PCR assay for the Australian abalone herpes-like virus. <i>Diseases of Aquatic Organisms</i> , 2010, 92, 1-10.	1.0	44
36	Genomic Prediction Using Prior Quantitative Trait Loci Information Reveals a Large Reservoir of Underutilised Blackleg Resistance in Diverse Canola (<i>Brassica napus</i> L.) Lines. <i>Plant Genome</i> , 2018, 11, 170100.	2.8	40

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37	Using Next-Generation Sequencing for DNA Barcoding: Capturing Allelic Variation in <i>ITS2</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 19-29.	1.8	38
38	Identification of genetic factors influencing salt stress tolerance in white clover (<i>Trifolium repens</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	36
39	Plastome Sequence Determination and Comparative Analysis for Members of the <i>Lolium</i> - <i>Festuca</i> Grass Species Complex. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 607-616.	1.8	36
40	Validation of Genotyping by Sequencing Using Transcriptomics for Diversity and Application of Genomic Selection in Tetraploid Potato. <i>Frontiers in Plant Science</i> , 2019, 10, 670.	3.6	36
41	Identification of homologous, homoeologous and paralogous sequence variants in an outbreeding allopolyploid species based on comparison with progenitor taxa. <i>Molecular Genetics and Genomics</i> , 2008, 280, 293-304.	2.1	35
42	Molecular characterisation and interpretation of genetic diversity within globally distributed germplasm collections of tall fescue (<i>Festuca arundinacea</i> Schreb.) and meadow fescue (<i>F. pratensis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	35
43	Safety Assessment of Genetically Modified Feed: Is There Any Difference From Food?. <i>Frontiers in Plant Science</i> , 2019, 10, 1592.	3.6	35
44	Boosting Genetic Gain in Allogamous Crops via Speed Breeding and Genomic Selection. <i>Frontiers in Plant Science</i> , 2019, 10, 1364.	3.6	35
45	Molecular characterisation and genetic mapping of candidate genes for qualitative disease resistance in perennial ryegrass (<i>Lolium perenne</i> L.). <i>BMC Plant Biology</i> , 2009, 9, 62.	3.6	34
46	Assessment of genetic diversity in Australian canola (<i>Brassica napus</i> L.) cultivars using SSR markers. <i>Crop and Pasture Science</i> , 2009, 60, 1193.	1.5	34
47	Assessment of Genetic Diversity in Faba Bean Based on Single Nucleotide Polymorphism. <i>Diversity</i> , 2014, 6, 88-101.	1.7	34
48	Validation of molecular markers associated with boron tolerance, powdery mildew resistance and salinity tolerance in field peas. <i>Frontiers in Plant Science</i> , 2015, 6, 917.	3.6	34
49	Assignment of Individual Genotypes to Specific Forage Cultivars of Perennial Ryegrass Based on SSR Markers. <i>Crop Science</i> , 2009, 49, 49-58.	1.8	32
50	Targeted genotyping-by-sequencing permits cost-effective identification and discrimination of pasture grass species and cultivars. <i>Theoretical and Applied Genetics</i> , 2016, 129, 991-1005.	3.6	31
51	Diversity and Genome Analysis of Australian and Global Oilseed Brassica napus L. Germplasm Using Transcriptomics and Whole Genome Re-sequencing. <i>Frontiers in Plant Science</i> , 2018, 9, 508.	3.6	29
52	Using Sensors and Unmanned Aircraft Systems for High-Throughput Phenotyping of Biomass in Perennial Ryegrass Breeding Trials. <i>Frontiers in Plant Science</i> , 2019, 10, 1381.	3.6	29
53	Identification of QTLs for morphological traits influencing waterlogging tolerance in perennial ryegrass (<i>Lolium perenne</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 122, 609-622.	3.6	27
54	Optimizing Resource Allocation in a Genomic Breeding Program for Perennial Ryegrass to Balance Genetic Gain, Cost, and Inbreeding. <i>Crop Science</i> , 2017, 57, 243-252.	1.8	27

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55	Characterization of Genetic and Allelic Diversity Amongst Cultivated and Wild Lentil Accessions for Germplasm Enhancement. <i>Frontiers in Genetics</i> , 2020, 11, 546.	2.3	26
56	Biology and Genetics of Crown Rust Disease in Ryegrasses. <i>Crop Science</i> , 2010, 50, 1605-1624.	1.8	25
57	Horizontal transfer of a 1,6-glucanase gene from an ancestral species of fungal endophyte to a cool-season grass host. <i>Scientific Reports</i> , 2017, 7, 9024.	3.3	25
58	Evaluation and Recommendations for Routine Genotyping Using Skim Whole Genome Re-sequencing in Canola. <i>Frontiers in Plant Science</i> , 2018, 9, 1809.	3.6	24
59	Development and Application of Image-Based High-Throughput Phenotyping Methodology for Salt Tolerance in Lentils. <i>Agronomy</i> , 2020, 10, 1992.	3.0	23
60	A simple method for semi-random DNA amplicon fragmentation using the methylation-dependent restriction enzyme MspI. <i>BMC Biotechnology</i> , 2015, 15, 25.	3.3	22
61	A multiplex PCR for rapid identification of Brassica species in the triangle of U. <i>Plant Methods</i> , 2017, 13, 49.	4.3	20
62	Development and implementation of a multiplexed single nucleotide polymorphism genotyping tool for differentiation of ryegrass species and cultivars. <i>Molecular Breeding</i> , 2014, 33, 435-451.	2.1	19
63	Design of an F1 hybrid breeding strategy for ryegrasses based on selection of self-incompatibility locus-specific alleles. <i>Frontiers in Plant Science</i> , 2015, 6, 764.	3.6	18
64	Evidence for Heterosis in Italian Ryegrass (<i>Lolium multiflorum</i> Lam.) Based on Inbreeding Depression in F2 Generation Offspring from Biparental Crosses. <i>Agronomy</i> , 2016, 6, 49.	3.0	18
65	Comparison of genome structure between white clover and <i>Medicago truncatula</i> supports homoeologous group nomenclature based on conserved synteny. <i>Genome</i> , 2008, 51, 905-911.	2.0	17
66	The characterization of key physiological traits of medicinal cannabis (<i>Cannabis sativa</i> L.) as a tool for precision breeding. <i>BMC Plant Biology</i> , 2021, 21, 294.	3.6	17
67	Screening for Resistance to PVY in Australian Potato Germplasm. <i>Genes</i> , 2020, 11, 429.	2.4	15
68	Genome-wide SNP identification in multiple morphotypes of allohexaploid tall fescue (<i>Festuca</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	2.8	14
69	Field Spectroscopy to Determine Nutritive Value Parameters of Individual Ryegrass Plants. <i>Agronomy</i> , 2019, 9, 293.	3.0	13
70	Machine Learning Algorithms to Predict Forage Nutritive Value of In Situ Perennial Ryegrass Plants Using Hyperspectral Canopy Reflectance Data. <i>Remote Sensing</i> , 2020, 12, 928.	4.0	13
71	Genomic Prediction and Genetic Correlation of Agronomic, Blackleg Disease, and Seed Quality Traits in Canola (<i>Brassica napus</i> L.). <i>Plants</i> , 2020, 9, 719.	3.5	13
72	Comparison of homoeolocus organisation in paired BAC clones from white clover (<i>Trifolium repens</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.6	12

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73	Prospects for applications of genomic tools in registration testing and seed certification of ryegrass varieties. <i>Plant Breeding</i> , 2016, 135, 405-412.	1.9	12
74	Development and Application of Droplet Digital PCR Tools for the Detection of Transgenes in Pastures and Pasture-Based Products. <i>Frontiers in Plant Science</i> , 2019, 9, 1923.	3.6	12
75	Application of Genomics to Understand Salt Tolerance in Lentil. <i>Genes</i> , 2021, 12, 332.	2.4	12
76	Application of Genomics Approaches for the Improvement in Ascochyta Blight Resistance in Chickpea. <i>Agronomy</i> , 2021, 11, 1937.	3.0	12
77	Gene Discovery and Molecular Marker Development, Based on High-Throughput Transcript Sequencing of <i>Paspalum dilatatum</i> Poir. <i>PLoS ONE</i> , 2014, 9, e85050.	2.5	12
78	Breeding Differentlyâ€™the Digital Revolution: High-Throughput Phenotyping and Genotyping. <i>Potato Research</i> , 2017, 60, 337-352.	2.7	11
79	Molecular genetic marker-based analysis of species-differentiated phenotypic characters in an interspecific ryegrass mapping population. <i>Crop and Pasture Science</i> , 2011, 62, 892.	1.5	10
80	Comparative Genomics in Perennial Ryegrass (<i>Lolium perenne</i>): Identification and Characterisation of an Orthologue for the Rice Plant Architecture-Controlling Gene <i>OsABCG5</i> . <i>International Journal of Plant Genomics</i> , 2011, 2011, 1-12.	2.2	9
81	Candidate gene-based association genetics analysis of herbage quality traits in perennial ryegrass (<i>Lolium perenne</i> L.). <i>Crop and Pasture Science</i> , 2013, 64, 244.	1.5	9
82	Construction of an integrated linkage map and trait dissection for bacterial blight resistance in field pea (<i>Pisum sativum</i> L.). <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	9
83	Generation and Characterisation of a Reference Transcriptome for Phalaris (<i>Phalaris aquatica</i> L.). <i>Agronomy</i> , 2017, 7, 14.	3.0	8
84	Rapid and Detailed Characterization of Transgene Insertion Sites in Genetically Modified Plants via Nanopore Sequencing. <i>Frontiers in Plant Science</i> , 2020, 11, 602313.	3.6	8
85	DNA Metabarcoding Enables High-Throughput Detection of Spotted Wing Drosophila (<i>Drosophila</i>) Tj ETQq1 1 0.784314 rgBT /Overlo 2.2 8	2.2	8
86	Reference transcriptome assembly and annotation for perennial ryegrass. <i>Genome</i> , 2017, 60, 1086-1088.	2.0	7
87	Genome Enhanced Marker Improvement for Potato Virus Y Disease Resistance in Potato. <i>Agronomy</i> , 2021, 11, 832.	3.0	7
88	A new and improved genome sequence of <i>Cannabis sativa</i> . <i>GigaByte</i> , 0, 2020, 1-13.	0.0	7
89	Manipulation of Cannabinoid Biosynthesis via Transient RNAi Expression. <i>Frontiers in Plant Science</i> , 2021, 12, 773474.	3.6	5
90	Genetic Diversity in Australasian Populations of the Crown Rust Pathogen of Ryegrasses (<i>Puccinia</i>) Tj ETQq0 0 0 rgBT /Overloçk 10 Tf 50		

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91	Interpretation of SNP Haplotype Complexity in White Clover (<i>Trifolium repens</i> L.), an Outbreeding Allotetraploid Species. , 2009, , 211-220.		4
92	Nucleotide diversity of vernalization and flowering time related genes in a germplasm collection of meadow fescue (<i>Festuca pratensis</i> Huds. syn. <i>Festuca ovina</i> L.) Tj ETQq0 0 0.0gBT /Overlock 10 T		
93	Evaluation of endophyte toxin production and its interaction with transgenic perennial ryegrass (<i>Lolium perenne</i> L.) with altered expression of fructosyltransferases. Transgenic Research, 2018, 27, 397-407.	2.4	2
94	Advances in lentil production through heterosis: Evaluating generations and breeding systems. PLoS ONE, 2022, 17, e0262857.	2.5	2
95	Utilizing Linkage Disequilibrium and Association Mapping to Implement Candidate Gene Based Markers in Perennial Ryegrass Breeding. , 2009, , 259-274.		1
96	Development of Protocols for Regeneration and Transformation of Apomitic and Sexual Forms of Dallisgrass (<i>Paspalum dilatatum</i> Poir.). Frontiers in Plant Science, 2021, 12, 787549.	3.6	1
97	Homology-based enzymatic DNA fragment assembly-based illumina sequencing library preparation. Biology Methods and Protocols, 2018, 3, bpy001.	2.2	0