

Noel O I Cogan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9893523/publications.pdf>

Version: 2024-02-01

97
papers

4,194
citations

109321

35
h-index

133252

59
g-index

99
all docs

99
docs citations

99
times ranked

4526
citing authors

#	ARTICLE	IF	CITATIONS
1	Advances in lentil production through heterosis: Evaluating generations and breeding systems. <i>PLoS ONE</i> , 2022, 17, e0262857.	2.5	2
2	DNA Metabarcoding Enables High-Throughput Detection of Spotted Wing Drosophila (<i>Drosophila</i>) Tj ETQq0 0 0 rgBT ₂ /Overlogk 10 Tf 50	2.2	10
3	Application of Genomics to Understand Salt Tolerance in Lentil. <i>Genes</i> , 2021, 12, 332.	2.4	12
4	Genome Enhanced Marker Improvement for Potato Virus Y Disease Resistance in Potato. <i>Agronomy</i> , 2021, 11, 832.	3.0	7
5	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
6	Application of Genomics Approaches for the Improvement in Ascochyta Blight Resistance in Chickpea. <i>Agronomy</i> , 2021, 11, 1937.	3.0	12
7	Development of Protocols for Regeneration and Transformation of Apomitic and Sexual Forms of Dallisgrass (<i>Paspalum dilatatum</i> Poir.). <i>Frontiers in Plant Science</i> , 2021, 12, 787549.	3.6	1
8	Manipulation of Cannabinoid Biosynthesis via Transient RNAi Expression. <i>Frontiers in Plant Science</i> , 2021, 12, 773474.	3.6	5
9	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
10	Development and Application of Image-Based High-Throughput Phenotyping Methodology for Salt Tolerance in Lentils. <i>Agronomy</i> , 2020, 10, 1992.	3.0	23
11	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
12	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
13	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
14	Screening for Resistance to PVY in Australian Potato Germplasm. <i>Genes</i> , 2020, 11, 429.	2.4	15
15	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
16	Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance. <i>GigaScience</i> , 2019, 8, .	6.4	132
17	Field Spectroscopy to Determine Nutritive Value Parameters of Individual Ryegrass Plants. <i>Agronomy</i> , 2019, 9, 293.	3.0	13
18	Generation of a Comprehensive Transcriptome Atlas and Transcriptome Dynamics in Medicinal Cannabis. <i>Scientific Reports</i> , 2019, 9, 16583.	3.3	45

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Safety Assessment of Genetically Modified Feed: Is There Any Difference From Food?. <i>Frontiers in Plant Science</i> , 2019, 10, 1592.	3.6	35
22	Boosting Genetic Gain in Allogamous Crops via Speed Breeding and Genomic Selection. <i>Frontiers in Plant Science</i> , 2019, 10, 1364.	3.6	35
23	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
24	Effective mosquito and arbovirus surveillance using metabarcoding. <i>Molecular Ecology Resources</i> , 2018, 18, 32-40.	4.8	51
25	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
26	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
27	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
28	Homology-based enzymatic DNA fragment assembly-based illumina sequencing library preparation. <i>Biology Methods and Protocols</i> , 2018, 3, bpy001.	2.2	0
29	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
30	Evaluation of endophyte toxin production and its interaction with transgenic perennial ryegrass (<i>Lolium perenne</i> L.) with altered expression of fructosyltransferases. <i>Transgenic Research</i> , 2018, 27, 397-407.	2.4	2
31	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
32	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
33	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
34	Reference transcriptome assembly and annotation for perennial ryegrass. <i>Genome</i> , 2017, 60, 1086-1088.	2.0	7
35	Metagenomic arbovirus detection using MinION nanopore sequencing. <i>Journal of Virological Methods</i> , 2017, 249, 79-84.	2.1	60
36	Horizontal transfer of a β -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

#	ARTICLE	IF	CITATIONS
37	A multiplex PCR for rapid identification of Brassica species in the triangle of U. Plant Methods, 2017, 13, 49.	4.3	20
38	Generation and Characterisation of a Reference Transcriptome for Phalaris (Phalaris aquatica L.). Agronomy, 2017, 7, 14.	3.0	8
39	Breeding Differentlyâ€™the Digital Revolution: High-Throughput Phenotyping and Genotyping. Potato Research, 2017, 60, 337-352.	2.7	11
40	Generation and Characterisation of a Reference Transcriptome for Lentil (Lens culinaris Medik.). International Journal of Molecular Sciences, 2016, 17, 1887.	4.1	49
41	Evidence for Heterosis in Italian Ryegrass (Lolium multiflorum Lam.) Based on Inbreeding Depression in F2 Generation Offspring from Biparental Crosses. Agronomy, 2016, 6, 49.	3.0	18
42	SNP-Based Linkage Mapping for Validation of QTLs for Resistance to Ascochyta Blight in Lentil. Frontiers in Plant Science, 2016, 7, 1604.	3.6	62
43	Improving Genetic Gain with Genomic Selection in Autotetraploid Potato. Plant Genome, 2016, 9, plantgenome2016.02.0021.	2.8	115
44	Prospects for applications of genomic tools in registration testing and seed certification of ryegrass varieties. Plant Breeding, 2016, 135, 405-412.	1.9	12
45	Genetic Gain and Inbreeding from Genomic Selection in a Simulated Commercial Breeding Program for Perennial Ryegrass. Plant Genome, 2016, 9, plantgenome2015.06.0046.	2.8	83
46	Targeted genotyping-by-sequencing permits cost-effective identification and discrimination of pasture grass species and cultivars. Theoretical and Applied Genetics, 2016, 129, 991-1005.	3.6	31
47	Design of an F1 hybrid breeding strategy for ryegrasses based on selection of self-incompatibility locus-specific alleles. Frontiers in Plant Science, 2015, 6, 764.	3.6	18
48	Validation of molecular markers associated with boron tolerance, powdery mildew resistance and salinity tolerance in field peas. Frontiers in Plant Science, 2015, 6, 917.	3.6	34
49	Construction of an integrated linkage map and trait dissection for bacterial blight resistance in field pea (Pisum sativum L.). Molecular Breeding, 2015, 35, 1.	2.1	9
50	Consensus Genetic Map Construction for Field Pea (Pisum sativum L.), Trait Dissection of Biotic and Abiotic Stress Tolerance and Development of a Diagnostic Marker for the er1 Powdery Mildew Resistance Gene. Plant Molecular Biology Reporter, 2015, 33, 1391-1403.	1.8	51
51	A simple method for semi-random DNA amplicon fragmentation using the methylation-dependent restriction enzyme MspI. BMC Biotechnology, 2015, 15, 25.	3.3	22
52	De novo assembly and characterisation of the field pea transcriptome using RNA-Seq. BMC Genomics, 2015, 16, 611.	2.8	49
53	Assessment of genetic variation within a global collection of lentil (Lens culinarisMedik.) cultivars and landraces using SNP markers. BMC Genetics, 2014, 15, 150.	2.7	76
54	Assessment of Genetic Diversity in Faba Bean Based on Single Nucleotide Polymorphism. Diversity, 2014, 6, 88-101.	1.7	34

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	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
58	Improving breeding efficiency in potato using molecular and quantitative genetics. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2279-2292.	3.6	74
59	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
60	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
61	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
62	Cost analysis of the application of marker-assisted selection in potato breeding. <i>Molecular Breeding</i> , 2013, 32, 299-310.	2.1	49
63	StAMPP: 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
64	Nucleotide diversity of vernalization and flowering time related genes in a germplasm collection of meadow fescue (<i>Festuca pratensis</i> Huds. syn. <i>Festuca Loliolum</i>) Tj ETQq0 0 0.8 BT / Overlock 10 T	2.8	14
65	Prospects for genomic selection in forage plant species. <i>Plant Breeding</i> , 2013, 132, 133-143.	1.9	125
66	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
67	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
68	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
69	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
70	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
71	Genome-wide SNP identification in multiple morphotypes of allohexaploid tall fescue (<i>Festuca</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10 T	2.8	14
72	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 0.8 BT / Overlock 10 T	2.8	14

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	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
76	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
77	Comparative Genomics in Perennial Ryegrass (<i>Lolium perenne</i> L.): 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
78	Biology and Genetics of Crown Rust Disease in Ryegrasses. <i>Crop Science</i> , 2010, 50, 1605-1624.	1.8	25
79	Identification of genetic factors influencing salt stress tolerance in white clover (<i>Trifolium repens</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	3.6	36
80	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
81	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
82	Comparison of homoeolocus organisation in paired BAC clones from white clover (<i>Trifolium repens</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	12
83	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
84	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
85	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
86	Genetic Diversity in Australasian Populations of the Crown Rust Pathogen of Ryegrasses (<i>Puccinia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	4
87	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
88	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
89	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
90	Interpretation of SNP Haplotype Complexity in White Clover (<i>Trifolium repens</i> L.), an Outbreeding Allotetraploid Species. , 2009, , 211-220.		4

#	ARTICLE	IF	CITATIONS
91	Utilizing Linkage Disequilibrium and Association Mapping to Implement Candidate Gene Based Markers in Perennial Ryegrass Breeding. , 2009, , 259-274.		1
92	Identification of homologous, homoeologous and paralogous sequence variants in an outbreeding allopolyploid species based on comparison with progenitor taxa. Molecular Genetics and Genomics, 2008, 280, 293-304.	2.1	35
93	Comparison of genome structure between white clover and <i>Medicago truncatula</i> supports homoeologous group nomenclature based on conserved synteny. Genome, 2008, 51, 905-911.	2.0	17
94	SNP discovery, validation, haplotype structure and linkage disequilibrium in full-length herbage nutritive quality genes of perennial ryegrass (<i>Lolium perenne</i> L.). Molecular Genetics and Genomics, 2007, 278, 585-597.	2.1	57
95	Gene-associated single nucleotide polymorphism discovery in perennial ryegrass (<i>Lolium perenne</i> L.). Molecular Genetics and Genomics, 2006, 276, 101-112.	2.1	78
96	Assessment of genetic diversity in cultivars of white clover (<i>Trifolium repens</i> L.) detected by SSR polymorphisms. Genome, 2006, 49, 919-930.	2.0	45
97	A new and improved genome sequence of <i>Cannabis sativa</i> . GigaByte, 0, 2020, 1-13.	0.0	7