

Donal M O'sullivan

List of Publications by Year in descending order

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56
papers

3,588
citations

201674

27
h-index

155660

55
g-index

62
all docs

62
docs citations

62
times ranked

4471
citing authors

#	ARTICLE	IF	CITATIONS
1	Trends of genetic changes uncovered by Env- and Eigen-GWAS in wheat and barley. Theoretical and Applied Genetics, 2022, 135, 667-678.	3.6	8
2	Recent advances in faba bean genetic and genomic tools for crop improvement. , 2021, 3, e75.		38
3	VC1 catalyses a key step in the biosynthesis of vicine in faba bean. Nature Plants, 2021, 7, 923-931.	9.3	34
4	Reprogramming of the wheat transcriptome in response to infection with <i>Claviceps purpurea</i> , the causal agent of ergot. BMC Plant Biology, 2021, 21, 316.	3.6	6
5	Conventional and Molecular Breeding Tools for Accelerating Genetic Gain in Faba Bean (<i>Vicia faba</i> L.). Frontiers in Plant Science, 2021, 12, 744259.	3.6	22
6	Identification and Quantification of Major Faba Bean Seed Proteins. Journal of Agricultural and Food Chemistry, 2020, 68, 8535-8544.	5.2	42
7	High-Density SNP-Based Association Mapping of Seed Traits in Fenugreek Reveals Homology with Clover. Genes, 2020, 11, 893.	2.4	5
8	Genetic and transcriptional dissection of resistance to <i>Claviceps purpurea</i> in the durum wheat cultivar Greenshank. Theoretical and Applied Genetics, 2020, 133, 1873-1886.	3.6	16
9	Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. Heredity, 2020, 125, 396-416.	2.6	124
10	Use of genetic markers for the detection of off-types for DUS phenotypic traits in the inbreeding crop, barley. Molecular Breeding, 2020, 40, 1.	2.1	16
11	A framework for gene mapping in wheat demonstrated using the Yr7 yellow rust resistance gene. PLoS ONE, 2020, 15, e0231157.	2.5	14
12	Eliminating vicine and convicine, the main anti-nutritional factors restricting faba bean usage. Trends in Food Science and Technology, 2019, 91, 549-556.	15.1	84
13	Breeding and genomics status in faba bean (<i>Vicia faba</i>). Plant Breeding, 2019, 138, 465-473.	1.9	61
14	Seed Storage Proteins of Faba Bean (<i>Vicia faba</i> L): Current Status and Prospects for Genetic Improvement. Journal of Agricultural and Food Chemistry, 2018, 66, 12617-12626.	5.2	67
15	Evaluation of <i>Claviceps purpurea</i> isolates on wheat reveals complex virulence and host susceptibility relationships. Canadian Journal of Plant Pathology, 2017, 39, 307-317.	1.4	11
16	Advances in Faba Bean Genetics and Genomics. Frontiers in Genetics, 2016, 7, 150.	2.3	51
17	Elevated temperature drives a shift from selfing to outcrossing in the insect-pollinated legume, faba bean (<i>Vicia faba</i>). Journal of Experimental Botany, 2016, 68, erw430.	4.8	21
18	A SNP-based consensus genetic map for synteny-based trait targeting in faba bean (<i>Vicia</i>)	8.3	101

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19	Mapping by sequencing in complex polyploid genomes using genic sequence capture: a case study to map yellow rust resistance in hexaploid wheat. <i>Plant Journal</i> , 2016, 87, 403-419.	5.7	47
20	Molecular and phenotypic characterization of the alternative seasonal growth habit and flowering time in barley (<i>Hordeum vulgare</i> ssp. <i>vulgare</i> L.). <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	16
21	Flanking SNP markers for vicine convicine concentration in faba bean (<i>Vicia faba</i> L.). <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	36
22	The identification of QTL controlling ergot sclerotia size in hexaploid wheat implicates a role for the Rht dwarfing alleles. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2447-2460.	3.6	15
23	An Eight-Parent Multiparent Advanced Generation Inter-Cross Population for Winter-Sown Wheat: Creation, Properties, and Validation. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1603-1610.	1.8	215
24	Use of synteny to identify candidate genes underlying QTL controlling stomatal traits in faba bean (<i>Vicia faba</i> L.). <i>Theoretical and Applied Genetics</i> , 2014, 127, 2371-2385.	3.6	61
25	The pgip family in soybean and three other legume species: evidence for a birth-and-death model of evolution. <i>BMC Plant Biology</i> , 2014, 14, 189.	3.6	15
26	Genetic analysis reveals a novel locus in <i>Vicia faba</i> decoupling pigmentation in the flower from that in the extra-floral nectaries. <i>Molecular Breeding</i> , 2014, 34, 1507-1513.	2.1	13
27	<i>Claviceps purpurea</i> expressing polygalacturonases escaping PGIP inhibition fully infects P _v PGIP2 wheat transgenic plants but its infection is delayed in wheat transgenic plants with increased level of pectin methyl esterification. <i>Plant Physiology and Biochemistry</i> , 2013, 73, 294-301.	5.8	20
28	Evaluation of the use of high-density SNP genotyping to implement UPOV Model 2 for DUS testing in barley. <i>Theoretical and Applied Genetics</i> , 2013, 126, 901-911.	3.6	30
29	Plant pathogen interactions: disease resistance in modern agriculture. <i>Trends in Genetics</i> , 2013, 29, 233-240.	6.7	254
30	Analysis of DNA polymorphism in ancient barley herbarium material: Validation of the KASP SNP genotyping platform. <i>Taxon</i> , 2013, 62, 779-789.	0.7	21
31	Plant-Symbiotic Fungi as Chemical Engineers: Multi-Genome Analysis of the Clavicipitaceae Reveals Dynamics of Alkaloid Loci. <i>PLoS Genetics</i> , 2013, 9, e1003323.	3.5	344
32	A baseline study of vicine convicine levels in faba bean (<i>Vicia faba</i> L.) germplasm. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2013, 11, 250-257.	0.8	35
33	Evaluation of diagnostic molecular markers for DUS phenotypic assessment in the cereal crop, barley (<i>Hordeum vulgare</i> ssp. <i>vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2012, 125, 1735-1749.	3.6	42
34	Heterozygosity and diversity analysis using mapped single nucleotide polymorphisms in a faba bean inbreeding programme. <i>Molecular Breeding</i> , 2012, 30, 1799-1809.	2.1	22
35	Genome Dynamics Explain the Evolution of Flowering Time CCT Domain Gene Families in the Poaceae. <i>PLoS ONE</i> , 2012, 7, e45307.	2.5	93
36	Genetic structure and linkage disequilibrium in landrace populations of barley in Sardinia. <i>Theoretical and Applied Genetics</i> , 2012, 125, 171-184.	3.6	22

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37	Genetic variation at flowering time loci in wild and cultivated barley. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 264-267.	0.8	26
38	Genome-wide association mapping to candidate polymorphism resolution in the unsequenced barley genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21611-21616.	7.1	259
39	Segmental chromosomal duplications harbouring group IV CONSTANS-like genes in cereals. <i>Genome</i> , 2010, 53, 231-240.	2.0	17
40	Whole-genome association mapping in elite inbred crop varieties This article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farming". <i>Genome</i> , 2010, 53, 967-972.	2.0	22
41	PCR-Based Markers Diagnostic for Spring and Winter Seasonal Growth Habit in Barley. <i>Crop Science</i> , 2009, 49, 403-410.	1.8	45
42	Association mapping of partitioning loci in barley. <i>BMC Genetics</i> , 2008, 9, 16.	2.7	75
43	Control of flowering time in temperate cereals: genes, domestication, and sustainable productivity. <i>Journal of Experimental Botany</i> , 2007, 58, 1231-1244.	4.8	422
44	The Role of Double-Stranded Break Repair in the Creation of Phenotypic Diversity at Cereal <i>VRN1</i> Loci. <i>Genetics</i> , 2007, 177, 2535-2539.	2.9	37
45	Haplotype analysis of vernalization loci in European barley germplasm reveals novel VRN-H1 alleles and a predominant winter VRN-H1/VRN-H2 multi-locus haplotype. <i>Theoretical and Applied Genetics</i> , 2007, 115, 993-1001.	3.6	139
46	Molecular barley breeding. <i>Euphytica</i> , 2007, 158, 295-303.	1.2	29
47	Non-concordance between Genetic Profiles of Olive Oil and Fruit: a Cautionary Note to the Use of DNA Markers for Provenance Testing. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 9221-9226.	5.2	59
48	Integration of Retrotransposons-Based Markers in a Linkage Map of Barley. <i>Molecular Breeding</i> , 2006, 17, 173-184.	2.1	16
49	Distribution of α -amylase I haplotypes among European cultivated barleys. <i>Molecular Breeding</i> , 2006, 18, 341-354.	2.1	20
50	Construction of a <i>Festuca pratensis</i> BAC library for map-based cloning in <i>Festulolium</i> substitution lines. <i>Theoretical and Applied Genetics</i> , 2005, 110, 846-851.	3.6	21
51	Characterization of the Complex Locus of Bean Encoding Polygalacturonase-Inhibiting Proteins Reveals Subfunctionalization for Defense against Fungi and Insects. <i>Plant Physiology</i> , 2004, 135, 2424-2435.	4.8	122
52	maternally expressed gene 1 is a Novel Maize Endosperm Transfer Cell-Specific Gene with a Maternal Parent-of-Origin Pattern of Expression [W]. <i>Plant Cell</i> , 2004, 16, 1288-1301.	6.6	174
53	A maize bacterial artificial chromosome (BAC) library from the European flint inbred line F2. <i>Theoretical and Applied Genetics</i> , 2001, 103, 425-432.	3.6	27
54	Novel Traits For Cereal Biotechnology - Positional Cloning Revisited. <i>Developments in Plant Genetics and Breeding</i> , 2000, 6, 91-100.	0.6	1

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55	Technique for Cloning and Sequencing the Ends of Bacterial Artificial Chromosome Inserts. BioTechniques, 2000, 29, 271-276.	1.8	9
56	Variation in genome organization of the plant pathogenic fungus <i>Colletotrichum lindemuthianum</i> . Current Genetics, 1998, 33, 291-298.	1.7	33