

# Donal M O'sullivan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9521726/publications.pdf>

Version: 2024-02-01

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	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
2	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
3	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
4	Plant-pathogen interactions: disease resistance in modern agriculture. <i>Trends in Genetics</i> , 2013, 29, 233-240.	6.7	254
5	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
6	maternally expressed gene1 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
7	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
8	Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. <i>Heredity</i> , 2020, 125, 396-416.	2.6	124
9	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
10	A SNP-based consensus genetic map for synteny-based trait targeting in faba bean ( <i>Vicia</i> ) Tj ET000000rgBT/Overlo	8.3	101
11	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
12	Eliminating vicine and convicine, the main anti-nutritional factors restricting faba bean usage. <i>Trends in Food Science and Technology</i> , 2019, 91, 549-556.	15.1	84
13	Association mapping of partitioning loci in barley. <i>BMC Genetics</i> , 2008, 9, 16.	2.7	75
14	Seed Storage Proteins of Faba Bean ( <i>Vicia faba</i> L): Current Status and Prospects for Genetic Improvement. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 12617-12626.	5.2	67
15	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
16	Breeding and genomics status in faba bean ( <i>Vicia faba</i> ). <i>Plant Breeding</i> , 2019, 138, 465-473.	1.9	61
17	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
18	Advances in Faba Bean Genetics and Genomics. <i>Frontiers in Genetics</i> , 2016, 7, 150.	2.3	51

#	ARTICLE	IF	CITATIONS
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	PCR-Based Markers Diagnostic for Spring and Winter Seasonal Growth Habit in Barley. <i>Crop Science</i> , 2009, 49, 403-410.	1.8	45
21	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
22	Identification and Quantification of Major Faba Bean Seed Proteins. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 8535-8544.	5.2	42
23	Recent advances in faba bean genetic and genomic tools for crop improvement. , 2021, 3, e75.		38
24	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
25	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
26	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
27	VC1 catalyses a key step in the biosynthesis of vicine in faba bean. <i>Nature Plants</i> , 2021, 7, 923-931.	9.3	34
28	Variation in genome organization of the plant pathogenic fungus <i>Colletotrichum lindemuthianum</i> . <i>Current Genetics</i> , 1998, 33, 291-298.	1.7	33
29	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
30	Molecular barley breeding. <i>Euphytica</i> , 2007, 158, 295-303.	1.2	29
31	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
32	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
33	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
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	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
36	Conventional and Molecular Breeding Tools for Accelerating Genetic Gain in Faba Bean ( <i>Vicia Faba</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 744259.	3.6	22

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	Elevated temperature drives a shift from selfing to outcrossing in the insect-pollinated legume, faba bean ( <i>Vicia faba</i> ). <i>Journal of Experimental Botany</i> , 2016, 68, erw430.	4.8	21
40	Distribution of $\beta$ -amylase I haplotypes among European cultivated barleys. <i>Molecular Breeding</i> , 2006, 18, 341-354.	2.1	20
41	<i>Claviceps purpurea</i> expressing polygalacturonases escaping PGIP inhibition fully infects PvPGIP2 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
42	Segmental chromosomal duplications harbouring group IV CONSTANS-like genes in cereals. <i>Genome</i> , 2010, 53, 231-240.	2.0	17
43	Integration of Retrotransposons-Based Markers in a Linkage Map of Barley. <i>Molecular Breeding</i> , 2006, 17, 173-184.	2.1	16
44	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
45	Genetic and transcriptional dissection of resistance to <i>Claviceps purpurea</i> in the durum wheat cultivar Greenshank. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1873-1886.	3.6	16
46	Use of genetic markers for the detection of off-types for DUS phenotypic traits in the inbreeding crop, barley. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	16
47	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
48	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
49	A framework for gene mapping in wheat demonstrated using the Yr7 yellow rust resistance gene. <i>PLoS ONE</i> , 2020, 15, e0231157.	2.5	14
50	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
51	Evaluation of <i>Claviceps purpurea</i> isolates on wheat reveals complex virulence and host susceptibility relationships. <i>Canadian Journal of Plant Pathology</i> , 2017, 39, 307-317.	1.4	11
52	Technique for Cloning and Sequencing the Ends of Bacterial Artificial Chromosome Inserts. <i>BioTechniques</i> , 2000, 29, 271-276.	1.8	9
53	Trends of genetic changes uncovered by Env- and Eigen-GWAS in wheat and barley. <i>Theoretical and Applied Genetics</i> , 2022, 135, 667-678.	3.6	8
54	Reprogramming of the wheat transcriptome in response to infection with <i>Claviceps purpurea</i> , the causal agent of ergot. <i>BMC Plant Biology</i> , 2021, 21, 316.	3.6	6

#	ARTICLE	IF	CITATIONS
55	High-Density SNP-Based Association Mapping of Seed Traits in Fenugreek Reveals Homology with Clover. <i>Genes</i> , 2020, 11, 893.	2.4	5
56	Novel Traits For Cereal Biotechnology - Positional Cloning Revisited. <i>Developments in Plant Genetics and Breeding</i> , 2000, 6, 91-100.	0.6	1