

# Daniel MacLean

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7675312/publications.pdf>

Version: 2024-02-01

74  
papers

8,510  
citations

87723

38  
h-index

76769

74  
g-index

89  
all docs

89  
docs citations

89  
times ranked

11565  
citing authors

#	ARTICLE	IF	CITATIONS
1	An Improved Assembly of the <i>Albugo candida</i> Ac2V Genome Reveals the Expansion of the CCG Class of Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 39-48.	1.4	6
2	Accurate plant pathogen effector protein classification ab initio with deepredef: an ensemble of convolutional neural networks. <i>BMC Bioinformatics</i> , 2021, 22, 372.	1.2	15
3	Chromatin accessibility landscapes activated by cell-surface and intracellular immune receptors. <i>Journal of Experimental Botany</i> , 2021, 72, 7927-7941.	2.4	14
4	Plant pathogens convergently evolved to counteract redundant nodes of an NLR immune receptor network. <i>PLoS Biology</i> , 2021, 19, e3001136.	2.6	69
5	High-resolution expression profiling of selected gene sets during plant immune activation. <i>Plant Biotechnology Journal</i> , 2020, 18, 1610-1619.	4.1	21
6	The calcium-permeable channel OSCA1.3 regulates plant stomatal immunity. <i>Nature</i> , 2020, 585, 569-573.	13.7	208
7	Using CRISPR/Cas9 genome editing in tomato to create a gibberellin-responsive dominant dwarf DELLA allele. <i>Plant Biotechnology Journal</i> , 2019, 17, 132-140.	4.1	64
8	The use of quantitative imaging to investigate regulators of membrane trafficking in Arabidopsis stomatal closure. <i>Traffic</i> , 2019, 20, 168-180.	1.3	21
9	Rapid fine mapping of causative mutations from sets of unordered, contig-sized fragments of genome sequence. <i>BMC Bioinformatics</i> , 2019, 20, 9.	1.2	6
10	Protein engineering expands the effector recognition profile of a rice NLR immune receptor. <i>ELife</i> , 2019, 8, .	2.8	118
11	The ash dieback invasion of Europe was founded by two genetically divergent individuals. <i>Nature Ecology and Evolution</i> , 2018, 2, 1000-1008.	3.4	82
12	<i>Arabidopsis</i> downy mildew effector HaRxL106 suppresses plant immunity by binding to RADICAL-INDUCED CELL DEATH1. <i>New Phytologist</i> , 2018, 220, 232-248.	3.5	51
13	A workflow for simplified analysis of ATAC-cap-seq data in R. <i>GigaScience</i> , 2018, 7, .	3.3	6
14	An automated quantitative image analysis tool for the identification of microtubule patterns in plants. <i>Traffic</i> , 2017, 18, 683-693.	1.3	18
15	Plant immune and growth receptors share common signalling components but localise to distinct plasma membrane nanodomains. <i>ELife</i> , 2017, 6, .	2.8	206
16	The Arabidopsis Protein Phosphatase PP2C38 Negatively Regulates the Central Immune Kinase BIK1. <i>PLoS Pathogens</i> , 2016, 12, e1005811.	2.1	113
17	A pigeonpea gene confers resistance to Asian soybean rust in soybean. <i>Nature Biotechnology</i> , 2016, 34, 661-665.	9.4	87
18	blastjs: a BLAST+ wrapper for Node.js. <i>BMC Research Notes</i> , 2016, 9, 130.	0.6	11

#	ARTICLE	IF	CITATIONS
19	The GOBLET training portal: a global repository of bioinformatics training materials, courses and trainers. <i>Bioinformatics</i> , 2015, 31, 140-142.	1.8	34
20	bio-samtools 2: a package for analysis and visualization of sequence and alignment data with SAMtools in Ruby. <i>Bioinformatics</i> , 2015, 31, 2565-2567.	1.8	61
21	Using 2 <i>k</i> -mer bubble searches to find single nucleotide polymorphisms in <i>k</i> -mer graphs. <i>Bioinformatics</i> , 2015, 31, 642-646.	1.8	6
22	Lessons from Fraxinus, a crowd-sourced citizen science game in genomics. <i>ELife</i> , 2015, 4, e07460.	2.8	21
23	Out of the woods. Ash dieback and the future of emergent pathogenomics. <i>Molecular Plant Pathology</i> , 2014, 15, 1-4.	2.0	6
24	Mapping mutations in plant genomes with the user-friendly web application CandiSNP. <i>Plant Methods</i> , 2014, 10, 41.	1.9	23
25	The Calcium-Dependent Protein Kinase CPK28 Buffers Plant Immunity and Regulates BIK1 Turnover. <i>Cell Host and Microbe</i> , 2014, 16, 605-615.	5.1	208
26	EXPRSS: an Illumina based high-throughput expression-profiling method to reveal transcriptional dynamics. <i>BMC Genomics</i> , 2014, 15, 341.	1.2	36
27	Reference-free SNP detection: dealing with the data deluge. <i>BMC Genomics</i> , 2014, 15, S10.	1.2	23
28	The Open Science Peer Review Oath. <i>F1000Research</i> , 2014, 3, 271.	0.8	15
29	An Open Science Peer Review Oath. <i>F1000Research</i> , 2014, 3, 271.	0.8	25
30	Crowdsourcing genomic analyses of ash and ash dieback “power to the people”. <i>GigaScience</i> , 2013, 2, 2.	3.3	29
31	Genome analyses of the wheat yellow (stripe) rust pathogen <i>Puccinia striiformis</i> f. sp. <i>tritici</i> reveal polymorphic and haustorial expressed secreted proteins as candidate effectors. <i>BMC Genomics</i> , 2013, 14, 270.	1.2	235
32	Resistance gene enrichment sequencing (R-Seq) enables reannotation of the LRR gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. <i>Plant Journal</i> , 2013, 76, 530-544.	2.8	367
33	SVGenes: a library for rendering genomic features in scalable vector graphic format. <i>Bioinformatics</i> , 2013, 29, 1890-1892.	1.8	2
34	Using False Discovery Rates to Benchmark SNP-callers in next-generation sequencing projects. <i>Scientific Reports</i> , 2013, 3, 1512.	1.6	37
35	Major Transcriptome Reprogramming Underlies Floral Mimicry Induced by the Rust Fungus <i>Puccinia monoica</i> in <i>Boechera stricta</i> . <i>PLoS ONE</i> , 2013, 8, e75293.	1.1	25
36	Identifying and Classifying Trait Linked Polymorphisms in Non-Reference Species by Walking Coloured de Bruijn Graphs. <i>PLoS ONE</i> , 2013, 8, e60058.	1.1	26

#	ARTICLE	IF	CITATIONS
37	Coval: Improving Alignment Quality and Variant Calling Accuracy for Next-Generation Sequencing Data. PLoS ONE, 2013, 8, e75402.	1.1	58
38	Changing the rules of the game. ELife, 2013, 2, e01294.	2.8	1
39	Biogem: an effective tool-based approach for scaling up open source software development in bioinformatics. Bioinformatics, 2012, 28, 1035-1037.	1.8	27
40	Genome Analyses of an Aggressive and Invasive Lineage of the Irish Potato Famine Pathogen. PLoS Pathogens, 2012, 8, e1002940.	2.1	321
41	Squeezing big data into a small organisation. , 2012, , 263-283.		0
42	Big data in small places. Nature Biotechnology, 2012, 30, 33-34.	9.4	17
43	Spatio-Temporal Cellular Dynamics of the <i>Arabidopsis</i> Flagellin Receptor Reveal Activation Status-Dependent Endosomal Sorting. Plant Cell, 2012, 24, 4205-4219.	3.1	226
44	Bio-samtools: Ruby bindings for SAMtools, a library for accessing BAM files containing high-throughput sequence alignments. Source Code for Biology and Medicine, 2012, 7, 6.	1.7	65
45	The microRNA miR393 re-directs secondary metabolite biosynthesis away from camalexin and towards glucosinolates. Plant Journal, 2011, 67, 218-231.	2.8	196
46	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	2.4	443
47	Gee Fu: a sequence version and web-services database tool for genomic assembly, genome feature and NGS data. Bioinformatics, 2011, 27, 2754-2755.	1.8	2
48	Gene Gain and Loss during Evolution of Obligate Parasitism in the White Rust Pathogen of <i>Arabidopsis thaliana</i> . PLoS Biology, 2011, 9, e1001094.	2.6	271
49	Disruption of Two Defensive Signaling Pathways by a Viral RNA Silencing Suppressor. Molecular Plant-Microbe Interactions, 2010, 23, 835-845.	1.4	169
50	Finding sRNA generative locales from high-throughput sequencing data with NiBLS. BMC Bioinformatics, 2010, 11, 93.	1.2	13
51	Genome-wide sequencing data reveals virulence factors implicated in banana Xanthomonas wilt. FEMS Microbiology Letters, 2010, 310, 182-192.	0.7	57
52	A Boolean Model of the <i>Pseudomonas syringae</i> hrp Regulon Predicts a Tightly Regulated System. PLoS ONE, 2010, 5, e9101.	1.1	19
53	High-Throughput Confocal Imaging of Intact Live Tissue Enables Quantification of Membrane Trafficking in <i>Arabidopsis</i> . Plant Physiology, 2010, 154, 1096-1104.	2.3	34
54	PhosPhAt: the <i>Arabidopsis thaliana</i> phosphorylation site database. An update. Nucleic Acids Research, 2010, 38, D828-D834.	6.5	346

#	ARTICLE	IF	CITATIONS
55	A Putative Phosphatase, LSF1, Is Required for Normal Starch Turnover in Arabidopsis Leaves. <i>Plant Physiology</i> , 2010, 152, 685-697.	2.3	102
56	Genome Evolution Following Host Jumps in the Irish Potato Famine Pathogen Lineage. <i>Science</i> , 2010, 330, 1540-1543.	6.0	440
57	Evidence for Large Complex Networks of Plant Short Silencing RNAs. <i>PLoS ONE</i> , 2010, 5, e9901.	1.1	44
58	Genome-Wide Analysis of Plastid Gene Expression in Potato Leaf Chloroplasts and Tuber Amyloplasts: Transcriptional and Posttranscriptional Control. <i>Plant Physiology</i> , 2009, 150, 2030-2044.	2.3	91
59	A draft genome sequence and functional screen reveals the repertoire of type III secreted proteins of <i>Pseudomonas syringae</i> pathovar <i>tabaci</i> 11528. <i>BMC Genomics</i> , 2009, 10, 395.	1.2	81
60	A draft genome sequence and functional screen reveals the repertoire of type III secreted proteins of <i>Pseudomonas syringae</i> pathovar <i>tabaci</i> 11528. <i>BMC Genomics</i> , 2009, 10, 569.	1.2	5
61	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	13.7	1,405
62	Application of 'next-generation' sequencing technologies to microbial genetics. <i>Nature Reviews Microbiology</i> , 2009, 7, 96-97.	13.6	269
63	In the News. <i>Nature Reviews Microbiology</i> , 2009, 7, 260-261.	13.6	158
64	Phosphoproteomic analysis of nuclei-enriched fractions from <i>Arabidopsis thaliana</i> . <i>Journal of Proteomics</i> , 2009, 72, 439-451.	1.2	84
65	A Draft Genome Sequence of <i>Pseudomonas syringae</i> pv. <i>tomato</i> T1 Reveals a Type III Effector Repertoire Significantly Divergent from That of <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 52-62.	1.4	134
66	Co-regulation of nuclear genes encoding plastid ribosomal proteins by light and plastid signals during seedling development in tobacco and <i>Arabidopsis</i> . <i>Plant Molecular Biology</i> , 2008, 66, 475-490.	2.0	20
67	PhosCalc: A tool for evaluating the sites of peptide phosphorylation from Mass Spectrometer data. <i>BMC Research Notes</i> , 2008, 1, 30.	0.6	50
68	A toolkit for analysing large-scale plant small RNA datasets. <i>Bioinformatics</i> , 2008, 24, 2252-2253.	1.8	299
69	GUN1 (GENOMES UNCOUPLED1) Encodes a Pentatricopeptide Repeat (PPR) Protein Involved in Plastid Protein Synthesis-Responsive Retrograde Signaling to the Nucleus. , 2008, , 1201-1205.		12
70	The F-Box Protein ACRE189/ACIF1 Regulates Cell Death and Defense Responses Activated during Pathogen Recognition in Tobacco and Tomato. <i>Plant Cell</i> , 2008, 20, 697-719.	3.1	154
71	Control of Plant Organ Size by KLUH/CYP78A5-Dependent Intercellular Signaling. <i>Developmental Cell</i> , 2007, 13, 843-856.	3.1	334
72	Disruption of essential plastid gene expression caused by T7 RNA polymerase-mediated transcription of plastid transgenes during early seedling development. <i>Transgenic Research</i> , 2007, 16, 415-428.	1.3	13

#	ARTICLE	IF	CITATIONS
73	Microarray analysis of chromatin-immunoprecipitated DNA identifies specific regions of tobacco genes associated with acetylated histones. <i>Plant Journal</i> , 2004, 37, 789-800.	2.8	31
74	Coordination of plastid and nuclear gene expression. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2003, 358, 135-145.	1.8	176