

# Daniel MacLean

## List of Publications by Year in descending order

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74  
papers

8,510  
citations

87888

38  
h-index

76900

74  
g-index

89  
all docs

89  
docs citations

89  
times ranked

11565  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	27.8	1,405
2	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	5.5	443
3	Genome Evolution Following Host Jumps in the Irish Potato Famine Pathogen Lineage. <i>Science</i> , 2010, 330, 1540-1543.	12.6	440
4	Resistance gene enrichment sequencing (<sc>R</sc>en<sc>S</sc>eq) enables reannotation of the <sc>NB</sc>-<sc>LRR</sc> gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. <i>Plant Journal</i> , 2013, 76, 530-544.	5.7	367
5	PhosPhAt: the <i>Arabidopsis thaliana</i> phosphorylation site database. An update. <i>Nucleic Acids Research</i> , 2010, 38, D828-D834.	14.5	346
6	Control of Plant Organ Size by KLUH/CYP78A5-Dependent Intercellular Signaling. <i>Developmental Cell</i> , 2007, 13, 843-856.	7.0	334
7	Genome Analyses of an Aggressive and Invasive Lineage of the Irish Potato Famine Pathogen. <i>PLoS Pathogens</i> , 2012, 8, e1002940.	4.7	321
8	A toolkit for analysing large-scale plant small RNA datasets. <i>Bioinformatics</i> , 2008, 24, 2252-2253.	4.1	299
9	Gene Gain and Loss during Evolution of Obligate Parasitism in the White Rust Pathogen of <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2011, 9, e1001094.	5.6	271
10	Application of 'next-generation' sequencing technologies to microbial genetics. <i>Nature Reviews Microbiology</i> , 2009, 7, 96-97.	28.6	269
11	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.	2.8	235
12	Spatio-Temporal Cellular Dynamics of the <i>Arabidopsis</i> Flagellin Receptor Reveal Activation Status-Dependent Endosomal Sorting. <i>Plant Cell</i> , 2012, 24, 4205-4219.	6.6	226
13	The Calcium-Dependent Protein Kinase CPK28 Buffers Plant Immunity and Regulates BIK1 Turnover. <i>Cell Host and Microbe</i> , 2014, 16, 605-615.	11.0	208
14	The calcium-permeable channel OSCA1.3 regulates plant stomatal immunity. <i>Nature</i> , 2020, 585, 569-573.	27.8	208
15	Plant immune and growth receptors share common signalling components but localise to distinct plasma membrane nanodomains. <i>ELife</i> , 2017, 6, .	6.0	206
16	The microRNA miR393 re-directs secondary metabolite biosynthesis away from camalexin and towards glucosinolates. <i>Plant Journal</i> , 2011, 67, 218-231.	5.7	196
17	Coordination of plastid and nuclear gene expression. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2003, 358, 135-145.	4.0	176
18	Disruption of Two Defensive Signaling Pathways by a Viral RNA Silencing Suppressor. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 835-845.	2.6	169

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19	In the News. <i>Nature Reviews Microbiology</i> , 2009, 7, 260-261.	28.6	158
20	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.	6.6	154
21	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.	2.6	134
22	Protein engineering expands the effector recognition profile of a rice NLR immune receptor. <i>ELife</i> , 2019, 8, .	6.0	118
23	The Arabidopsis Protein Phosphatase PP2C38 Negatively Regulates the Central Immune Kinase BIK1. <i>PLoS Pathogens</i> , 2016, 12, e1005811.	4.7	113
24	A Putative Phosphatase, LSF1, Is Required for Normal Starch Turnover in Arabidopsis Leaves. <i>Plant Physiology</i> , 2010, 152, 685-697.	4.8	102
25	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.	4.8	91
26	A pigeonpea gene confers resistance to Asian soybean rust in soybean. <i>Nature Biotechnology</i> , 2016, 34, 661-665.	17.5	87
27	Phosphoproteomic analysis of nuclei-enriched fractions from Arabidopsis thaliana. <i>Journal of Proteomics</i> , 2009, 72, 439-451.	2.4	84
28	The ash dieback invasion of Europe was founded by two genetically divergent individuals. <i>Nature Ecology and Evolution</i> , 2018, 2, 1000-1008.	7.8	82
29	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.	2.8	81
30	Plant pathogens convergently evolved to counteract redundant nodes of an NLR immune receptor network. <i>PLoS Biology</i> , 2021, 19, e3001136.	5.6	69
31	Bio-samtools: Ruby bindings for SAMtools, a library for accessing BAM files containing high-throughput sequence alignments. <i>Source Code for Biology and Medicine</i> , 2012, 7, 6.	1.7	65
32	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.	8.3	64
33	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.	4.1	61
34	Coval: Improving Alignment Quality and Variant Calling Accuracy for Next-Generation Sequencing Data. <i>PLoS ONE</i> , 2013, 8, e75402.	2.5	58
35	Genome-wide sequencing data reveals virulence factors implicated in banana <i>Xanthomonas</i> wilt. <i>FEMS Microbiology Letters</i> , 2010, 310, 182-192.	1.8	57
36	<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.	7.3	51

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37	PhosCalc: A tool for evaluating the sites of peptide phosphorylation from Mass Spectrometer data. BMC Research Notes, 2008, 1, 30.	1.4	50
38	Evidence for Large Complex Networks of Plant Short Silencing RNAs. PLoS ONE, 2010, 5, e9901.	2.5	44
39	Using False Discovery Rates to Benchmark SNP-callers in next-generation sequencing projects. Scientific Reports, 2013, 3, 1512.	3.3	37
40	EXPRSS: an Illumina based high-throughput expression-profiling method to reveal transcriptional dynamics. BMC Genomics, 2014, 15, 341.	2.8	36
41	High-Throughput Confocal Imaging of Intact Live Tissue Enables Quantification of Membrane Trafficking in Arabidopsis. Plant Physiology, 2010, 154, 1096-1104.	4.8	34
42	The GOBLET training portal: a global repository of bioinformatics training materials, courses and trainers. Bioinformatics, 2015, 31, 140-142.	4.1	34
43	Microarray analysis of chromatin-immunoprecipitated DNA identifies specific regions of tobacco genes associated with acetylated histones. Plant Journal, 2004, 37, 789-800.	5.7	31
44	Crowdsourcing genomic analyses of ash and ash dieback “ power to the people. GigaScience, 2013, 2, 2.	6.4	29
45	Biogem: an effective tool-based approach for scaling up open source software development in bioinformatics. Bioinformatics, 2012, 28, 1035-1037.	4.1	27
46	Identifying and Classifying Trait Linked Polymorphisms in Non-Reference Species by Walking Coloured de Bruijn Graphs. PLoS ONE, 2013, 8, e60058.	2.5	26
47	Major Transcriptome Reprogramming Underlies Floral Mimicry Induced by the Rust Fungus Puccinia monoica in Boechera stricta. PLoS ONE, 2013, 8, e75293.	2.5	25
48	An Open Science Peer Review Oath. F1000Research, 2014, 3, 271.	1.6	25
49	Mapping mutations in plant genomes with the user-friendly web application CandiSNP. Plant Methods, 2014, 10, 41.	4.3	23
50	Reference-free SNP detection: dealing with the data deluge. BMC Genomics, 2014, 15, S10.	2.8	23
51	The use of quantitative imaging to investigate regulators of membrane trafficking in Arabidopsis stomatal closure. Traffic, 2019, 20, 168-180.	2.7	21
52	High-resolution expression profiling of selected gene sets during plant immune activation. Plant Biotechnology Journal, 2020, 18, 1610-1619.	8.3	21
53	Lessons from Fraxinus, a crowd-sourced citizen science game in genomics. ELife, 2015, 4, e07460.	6.0	21
54	Co-regulation of nuclear genes encoding plastid ribosomal proteins by light and plastid signals during seedling development in tobacco and Arabidopsis. Plant Molecular Biology, 2008, 66, 475-490.	3.9	20

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55	A Boolean Model of the <i>Pseudomonas syringae</i> hrp Regulon Predicts a Tightly Regulated System. <i>PLoS ONE</i> , 2010, 5, e9101.	2.5	19
56	An automated quantitative image analysis tool for the identification of microtubule patterns in plants. <i>Traffic</i> , 2017, 18, 683-693.	2.7	18
57	Big data in small places. <i>Nature Biotechnology</i> , 2012, 30, 33-34.	17.5	17
58	Accurate plant pathogen effector protein classification ab initio with deepredef: an ensemble of convolutional neural networks. <i>BMC Bioinformatics</i> , 2021, 22, 372.	2.6	15
59	The Open Science Peer Review Oath. <i>F1000Research</i> , 2014, 3, 271.	1.6	15
60	Chromatin accessibility landscapes activated by cell-surface and intracellular immune receptors. <i>Journal of Experimental Botany</i> , 2021, 72, 7927-7941.	4.8	14
61	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.	2.4	13
62	Finding sRNA generative locales from high-throughput sequencing data with NiBLS. <i>BMC Bioinformatics</i> , 2010, 11, 93.	2.6	13
63	GUN1 (GENOMES UNCOUPLED1) Encodes a Pentatricopeptide Repeat (PPR) Protein Involved in Plastid Protein Synthesis-Responsive Retrograde Signaling to the Nucleus. , 2008, , 1201-1205.		12
64	blastjs: a BLAST+ wrapper for Node.js. <i>BMC Research Notes</i> , 2016, 9, 130.	1.4	11
65	Out of the woods. Ash dieback and the future of emergent pathogenomics. <i>Molecular Plant Pathology</i> , 2014, 15, 1-4.	4.2	6
66	Using 2 <i>k</i> - <i>h</i> bubble searches to find single nucleotide polymorphisms in <i>k</i> -mer graphs. <i>Bioinformatics</i> , 2015, 31, 642-646.	4.1	6
67	A workflow for simplified analysis of ATAC-cap-seq data in R. <i>GigaScience</i> , 2018, 7, .	6.4	6
68	Rapid fine mapping of causative mutations from sets of unordered, contig-sized fragments of genome sequence. <i>BMC Bioinformatics</i> , 2019, 20, 9.	2.6	6
69	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.	2.6	6
70	A draft genome sequence and functional screen reveals the repertoire of type III secreted proteins of <i>Pseudomonas syringae</i> pathovar tabaci 11528. <i>BMC Genomics</i> , 2009, 10, 569.	2.8	5
71	Gee Fu: a sequence version and web-services database tool for genomic assembly, genome feature and NGS data. <i>Bioinformatics</i> , 2011, 27, 2754-2755.	4.1	2
72	SVGenes: a library for rendering genomic features in scalable vector graphic format. <i>Bioinformatics</i> , 2013, 29, 1890-1892.	4.1	2

#	ARTICLE	IF	CITATIONS
73	Changing the rules of the game. ELife, 2013, 2, e01294.	6.0	1
74	Squeezing big data into a small organisation. , 2012, , 263-283.		0