

# Peter J Balint-Kurti

## List of Publications by Year in descending order

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87  
papers

5,601  
citations

94269

37  
h-index

88477

70  
g-index

94  
all docs

94  
docs citations

94  
times ranked

5710  
citing authors

#	ARTICLE	IF	CITATIONS
1	Close encounters in the corn field. <i>Molecular Plant</i> , 2022, , .	3.9	0
2	Genome-wide association study for morphological traits and resistance to <i>Peryonella pinodes</i> in the USDA pea single plant plus collection. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
3	Maize metacaspases modulate the defense response mediated by the NLR protein Rp1 $\epsilon$ 21 likely by affecting its subcellular localization. <i>Plant Journal</i> , 2021, 105, 151-166.	2.8	15
4	Maize Plants Chimeric for an Autoactive Resistance Gene Display a Cell-Autonomous Hypersensitive Response but Non-Cell Autonomous Defense Signaling. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 606-616.	1.4	2
5	Analysis of the transcriptomic, metabolomic, and gene regulatory responses to <i>Puccinia sorghi</i> in maize. <i>Molecular Plant Pathology</i> , 2021, 22, 465-479.	2.0	18
6	The maize ZmMIEL1 E3 ligase and ZmMYB83 transcription factor proteins interact and regulate the hypersensitive defence response. <i>Molecular Plant Pathology</i> , 2021, 22, 694-709.	2.0	10
7	Variation in Gene Expression between Two Sorghum bicolor Lines Differing in Innate Immunity Response. <i>Plants</i> , 2021, 10, 1536.	1.6	3
8	Microbe-dependent heterosis in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	42
9	Multi-Omics Analyses Reveal the Regulatory Network and the Function of ZmUGTs in Maize Defense Response. <i>Frontiers in Plant Science</i> , 2021, 12, 738261.	1.7	8
10	Analysis of leaf microbiome composition of near-isogenic maize lines differing in broad-spectrum disease resistance. <i>New Phytologist</i> , 2020, 225, 2152-2165.	3.5	42
11	<i>Herbaspirillum rubrisubalbicans</i> as a Phytopathogenic Model to Study the Immune System of <i>Sorghum bicolor</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 235-246.	1.4	15
12	A CRISPR/dCas9 toolkit for functional analysis of maize genes. <i>Plant Methods</i> , 2020, 16, 133.	1.9	21
13	Use of virus-induced gene silencing to characterize genes involved in modulating hypersensitive cell death in maize. <i>Molecular Plant Pathology</i> , 2020, 21, 1662-1676.	2.0	12
14	Genome-wide association analysis of the strength of the MAMP-elicited defense response and resistance to target leaf spot in sorghum. <i>Scientific Reports</i> , 2020, 10, 20817.	1.6	12
15	Genetic and Physiological Characterization of a Calcium Deficiency Phenotype in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1963-1970.	0.8	7
16	What are the Top 10 Unanswered Questions in Molecular Plant-Microbe Interactions?. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1354-1365.	1.4	47
17	Multiple insertions of COIN , a novel maize Foldback transposable element, in the Conring gene cause a spontaneous progressive cell death phenotype. <i>Plant Journal</i> , 2020, 104, 581-595.	2.8	0
18	Heterosis of leaf and rhizosphere microbiomes in field-grown maize. <i>New Phytologist</i> , 2020, 228, 1055-1069.	3.5	66

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19	Fine-Tuning Immunity: Players and Regulators for Plant NLRs. <i>Trends in Plant Science</i> , 2020, 25, 695-713.	4.3	77
20	Genotypic and phenotypic characterization of a large, diverse population of maize near-isogenic lines. <i>Plant Journal</i> , 2020, 103, 1246-1255.	2.8	12
21	A maize polygalacturonase functions as a suppressor of programmed cell death in plants. <i>BMC Plant Biology</i> , 2019, 19, 310.	1.6	17
22	The plant hypersensitive response: concepts, control and consequences. <i>Molecular Plant Pathology</i> , 2019, 20, 1163-1178.	2.0	369
23	Dominant, Heritable Resistance to Stewart's Wilt in Maize Is Associated with an Enhanced Vascular Defense Response to Infection with <i>Pantoea stewartii</i> . <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1581-1597.	1.4	11
24	A maize cytochrome <i>b</i> c1 complex subunit protein ZmQCR7 controls variation in the hypersensitive response. <i>Planta</i> , 2019, 249, 1477-1485.	1.6	10
25	Diverse Components of Resistance to <i>Fusarium verticillioides</i> Infection and Fumonisin Contamination in Four Maize Recombinant Inbred Families. <i>Toxins</i> , 2019, 11, 86.	1.5	18
26	Validation and Characterization of Maize Multiple Disease Resistance QTL. G3: Genes, Genomes, Genetics, 2019, 9, 2905-2912.	0.8	18
27	Identification of QTL for Target Leaf Spot resistance in <i>Sorghum bicolor</i> and investigation of relationships between disease resistance and variation in the MAMP response. <i>Scientific Reports</i> , 2019, 9, 18285.	1.6	13
28	Using Maize Chromosome Segment Substitution Line Populations for the Identification of Loci Associated with Multiple Disease Resistance. G3: Genes, Genomes, Genetics, 2019, 9, 189-201.	0.8	39
29	Quantifying MAMP-induced Production of Reactive Oxygen Species in <i>Sorghum</i> and Maize. <i>Bio-protocol</i> , 2019, 9, .	0.2	10
30	Semiautomated confocal imaging of fungal pathogenesis on plants: Microscopic analysis of macroscopic specimens. <i>Microscopy Research and Technique</i> , 2018, 81, 141-152.	1.2	17
31	Navigating complexity to breed disease-resistant crops. <i>Nature Reviews Genetics</i> , 2018, 19, 21-33.	7.7	321
32	Identification of Quantitative Trait Loci for Goss's Wilt of Maize. <i>Crop Science</i> , 2018, 58, 1192-1200.	0.8	15
33	Identification of a locus in maize controlling response to a host-selective toxin derived from <i>Cochliobolus heterostrophus</i> , causal agent of southern leaf blight. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2601-2612.	1.8	3
34	Large Scale Field Inoculation and Scoring of Maize Southern Leaf Blight and Other Maize Foliar Fungal Diseases. <i>Bio-protocol</i> , 2018, 8, e2745.	0.2	9
35	Quantitative Disease Resistance: Dissection and Adoption in Maize. <i>Molecular Plant</i> , 2017, 10, 402-413.	3.9	91
36	Fine mapping of a quantitative resistance gene for gray leaf spot of maize ( <i>Zea mays</i> L.) derived from teosinte ( <i>Z. mays</i> ssp. <i>parviglumis</i> ). <i>Theoretical and Applied Genetics</i> , 2017, 130, 1285-1295.	1.8	26

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37	Genetic dissection of the maize ( <i>Zea mays</i> L.) MAMP response. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1155-1168.	1.8	23
38	A gene encoding maize caffeoyl-CoA O-methyltransferase confers quantitative resistance to multiple pathogens. <i>Nature Genetics</i> , 2017, 49, 1364-1372.	9.4	199
39	Identification of Teosinte Alleles for Resistance to Southern Leaf Blight in Near Isogenic Maize Lines. <i>Crop Science</i> , 2017, 57, 1973-1983.	0.8	23
40	Identification of Alleles Conferring Resistance to Gray Leaf Spot in Maize Derived from its Wild Progenitor Species Teosinte. <i>Crop Science</i> , 2016, 56, 209-218.	0.8	36
41	Maize Homologs of CCoAOMT and HCT, Two Key Enzymes in Lignin Biosynthesis, Form Complexes with the NLR Rp1 Protein to Modulate the Defense Response. <i>Plant Physiology</i> , 2016, 171, 2166-2177.	2.3	80
42	Expanding Maize Genetic Resources with Predomestication Alleles: Maize's Teosinte Introgression Populations. <i>Plant Genome</i> , 2016, 9, plantgenome2015.07.0053.	1.6	43
43	The Genetics of Leaf Flecking in Maize and Its Relationship to Plant Defense and Disease Resistance. <i>Plant Physiology</i> , 2016, 172, 1787-1803.	2.3	25
44	A Genome-Wide Association Study for Partial Resistance to Maize Common Rust. <i>Phytopathology</i> , 2016, 106, 745-751.	1.1	51
45	Cytoplasmic and Nuclear Localizations Are Important for the Hypersensitive Response Conferred by Maize Autoactive Rp1-D21 Protein. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 1023-1031.	1.4	28
46	New insight into a complex plant-fungal pathogen interaction. <i>Nature Genetics</i> , 2015, 47, 101-103.	9.4	6
47	Molecular and Functional Analyses of a Maize Autoactive NB-LRR Protein Identify Precise Structural Requirements for Activity. <i>PLoS Pathogens</i> , 2015, 11, e1004674.	2.1	110
48	Maize Homologs of HCT, a Key Enzyme in Lignin Biosynthesis, Bind the NLR Rp1 Proteins to Modulate the Defense Response. <i>Plant Physiology</i> , 2015, 169, pp.00703.2015.	2.3	48
49	QTL Mapping Using High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2015, 1284, 257-285.	0.4	24
50	Yield Effects of Two Southern Leaf Blight Resistance Loci in Maize Hybrids. <i>Crop Science</i> , 2014, 54, 882-894.	0.8	8
51	Southern leaf blight disease severity is correlated with decreased maize leaf epiphytic bacterial species richness and the phyllosphere bacterial diversity decline is enhanced by nitrogen fertilization. <i>Frontiers in Plant Science</i> , 2014, 5, 403.	1.7	58
52	A Genome-Wide Association Study of the Maize Hypersensitive Defense Response Identifies Genes That Cluster in Related Pathways. <i>PLoS Genetics</i> , 2014, 10, e1004562.	1.5	62
53	Limits on the reproducibility of marker associations with southern leaf blight resistance in the maize nested association mapping population. <i>BMC Genomics</i> , 2014, 15, 1068.	1.2	35
54	Characterization of temperature and light effects on the defense response phenotypes associated with the maize Rp1-D21 autoactive resistance gene. <i>BMC Plant Biology</i> , 2013, 13, 106.	1.6	35

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55	A Connected Set of Genes Associated with Programmed Cell Death Implicated in Controlling the Hypersensitive Response in Maize. <i>Genetics</i> , 2013, 193, 609-620.	1.2	50
56	PhenoPhyte: a flexible affordable method to quantify 2D phenotypes from imagery. <i>Plant Methods</i> , 2012, 8, 45.	1.9	70
57	Multivariate Mixed Linear Model Analysis of Longitudinal Data: An Information-Rich Statistical Technique for Analyzing Plant Disease Resistance. <i>Phytopathology</i> , 2012, 102, 1016-1025.	1.1	8
58	Analysis of quantitative disease resistance to southern leaf blight and of multiple disease resistance in maize, using near-isogenic lines. <i>Theoretical and Applied Genetics</i> , 2012, 124, 433-445.	1.8	44
59	The Wheat Puroindoline Genes Confer Fungal Resistance in Transgenic Corn. <i>Journal of Phytopathology</i> , 2011, 159, 188-190.	0.5	17
60	Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. <i>Nature Genetics</i> , 2011, 43, 163-168.	9.4	553
61	Targeted discovery of quantitative trait loci for resistance to northern leaf blight and other diseases of maize. <i>Theoretical and Applied Genetics</i> , 2011, 123, 307-326.	1.8	45
62	Use of mutant-assisted gene identification and characterization (MAGIC) to identify novel genetic loci that modify the maize hypersensitive response. <i>Theoretical and Applied Genetics</i> , 2011, 123, 985-997.	1.8	27
63	A novel genetic framework for studying response to artificial selection. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 281-283.	0.4	9
64	Multivariate analysis of maize disease resistances suggests a pleiotropic genetic basis and implicates a <i>GST</i> gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7339-7344.	3.3	157
65	Mapping QTL Controlling Southern Leaf Blight Resistance by Joint Analysis of Three Related Recombinant Inbred Line Populations. <i>Crop Science</i> , 2011, 51, 1571-1579.	0.8	32
66	Mapping Resistance Quantitative Trait Loci for Three Foliar Diseases in a Maize Recombinant Inbred Line Population—Evidence for Multiple Disease Resistance?. <i>Phytopathology</i> , 2010, 100, 72-79.	1.1	87
67	Resistance loci affecting distinct stages of fungal pathogenesis: use of introgression lines for QTL mapping and characterization in the maize - <i>Setosphaeria turcica</i> pathosystem. <i>BMC Plant Biology</i> , 2010, 10, 103.	1.6	87
68	Joint Analysis of Near-Isogenic and Recombinant Inbred Line Populations Yields Precise Positional Estimates for Quantitative Trait Loci. <i>Plant Genome</i> , 2010, 3, .	1.6	16
69	Use of a Maize Advanced Intercross Line for Mapping of QTL for Northern Leaf Blight Resistance and Multiple Disease Resistance. <i>Crop Science</i> , 2010, 50, 458-466.	0.8	48
70	Identification of a Maize Locus That Modulates the Hypersensitive Defense Response, Using Mutant-Assisted Gene Identification and Characterization. <i>Genetics</i> , 2010, 184, 813-825.	1.2	52
71	Genetic Control of Photoperiod Sensitivity in Maize Revealed by Joint Multiple Population Analysis. <i>Genetics</i> , 2010, 184, 799-812.	1.2	112
72	Maize Leaf Epiphytic Bacteria Diversity Patterns Are Genetically Correlated with Resistance to Fungal Pathogen Infection. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 473-484.	1.4	107

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73	Use of selection with recurrent backcrossing and QTL mapping to identify loci contributing to southern leaf blight resistance in a highly resistant maize line. <i>Theoretical and Applied Genetics</i> , 2009, 118, 911-925.	1.8	39
74	Shades of gray: the world of quantitative disease resistance. <i>Trends in Plant Science</i> , 2009, 14, 21-29.	4.3	588
75	Maize Disease Resistance. , 2009, , 229-250.		30
76	IDENTIFYING MAIZE GERMPLASM WITH RESISTANCE TO AFLATOXIN ACCUMULATION. <i>Toxin Reviews</i> , 2008, 27, 319-345.	1.5	19
77	Mining and Harnessing Natural Variation: A Little MAGIC. <i>Crop Science</i> , 2008, 48, 2066-2073.	0.8	36
78	Use of an Advanced Intercross Line Population for Precise Mapping of Quantitative Trait Loci for Gray Leaf Spot Resistance in Maize. <i>Crop Science</i> , 2008, 48, 1696-1704.	0.8	41
79	Precise Mapping of Quantitative Trait Loci for Resistance to Southern Leaf Blight, Caused by <i>Cochliobolus heterostrophus</i> Race O, and Flowering Time Using Advanced Intercross Maize Lines. <i>Genetics</i> , 2007, 176, 645-657.	1.2	107
80	Disruption of a Maize 9-Lipoxygenase Results in Increased Resistance to Fungal Pathogens and Reduced Levels of Contamination with Mycotoxin Fumonisin. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 922-933.	1.4	167
81	The Genetic Architecture of Disease Resistance in Maize: A Synthesis of Published Studies. <i>Phytopathology</i> , 2006, 96, 120-129.	1.1	233
82	QTL Mapping for Fusarium Ear Rot and Fumonisin Contamination Resistance in Two Maize Populations. <i>Crop Science</i> , 2006, 46, 1734-1743.	0.8	120
83	Inverted repeat of a heterologous 3' untranslated region for high-efficiency, high-throughput gene silencing. <i>Plant Journal</i> , 2003, 33, 793-800.	2.8	42
84	Agrobacterium?-mediated transformation of embryogenic cell suspensions of the banana cultivar Rasthali (AAB). <i>Plant Cell Reports</i> , 2001, 20, 157-162.	2.8	173
85	Fruit-specific lectins from banana and plantain. <i>Planta</i> , 2000, 211, 546-554.	1.6	103
86	Characterization of the Tomato Cf-4 Gene for Resistance to <i>Cladosporium fulvum</i> Identifies Sequences That Determine Recognitional Specificity in Cf-4 and Cf-9. <i>Plant Cell</i> , 1997, 9, 2209.	3.1	67
87	Development and Use of a Seedling Growth Retardation Assay to Quantify and Map Loci Underlying Variation in the Maize Basal Defense Response. <i>PhytoFrontiers</i> , 0, , PHYTOFR-12-20-0.	0.8	4