

# Peter J Balint-Kurti

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4270680/publications.pdf>

Version: 2024-02-01

88  
papers

5,601  
citations

94433

37  
h-index

88630

70  
g-index

94  
all docs

94  
docs citations

94  
times ranked

5710  
citing authors

#	ARTICLE	IF	CITATIONS
1	Shades of gray: the world of quantitative disease resistance. <i>Trends in Plant Science</i> , 2009, 14, 21-29.	8.8	588
2	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.	21.4	553
3	The plant hypersensitive response: concepts, control and consequences. <i>Molecular Plant Pathology</i> , 2019, 20, 1163-1178.	4.2	369
4	Navigating complexity to breed disease-resistant crops. <i>Nature Reviews Genetics</i> , 2018, 19, 21-33.	16.8	321
5	The Genetic Architecture of Disease Resistance in Maize: A Synthesis of Published Studies. <i>Phytopathology</i> , 2006, 96, 120-129.	2.2	233
6	A gene encoding maize caffeoyl-CoA O-methyltransferase confers quantitative resistance to multiple pathogens. <i>Nature Genetics</i> , 2017, 49, 1364-1372.	21.4	199
7	Agrobacterium?-mediated transformation of embryogenic cell suspensions of the banana cultivar Rasthali (AAB). <i>Plant Cell Reports</i> , 2001, 20, 157-162.	5.6	173
8	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.	2.6	167
9	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.	7.1	157
10	QTL Mapping for Fusarium Ear Rot and Fumonisin Contamination Resistance in Two Maize Populations. <i>Crop Science</i> , 2006, 46, 1734-1743.	1.8	120
11	Genetic Control of Photoperiod Sensitivity in Maize Revealed by Joint Multiple Population Analysis. <i>Genetics</i> , 2010, 184, 799-812.	2.9	112
12	Molecular and Functional Analyses of a Maize Autoactive NB-LRR Protein Identify Precise Structural Requirements for Activity. <i>PLoS Pathogens</i> , 2015, 11, e1004674.	4.7	110
13	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.	2.9	107
14	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.	2.6	107
15	Fruit-specific lectins from banana and plantain. <i>Planta</i> , 2000, 211, 546-554.	3.2	103
16	Quantitative Disease Resistance: Dissection and Adoption in Maize. <i>Molecular Plant</i> , 2017, 10, 402-413.	8.3	91
17	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.	2.2	87
18	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.	3.6	87

#	ARTICLE	IF	CITATIONS
19	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.	4.8	80
20	Fine-Tuning Immunity: Players and Regulators for Plant NLRs. <i>Trends in Plant Science</i> , 2020, 25, 695-713.	8.8	77
21	PhenoPhyte: a flexible affordable method to quantify 2D phenotypes from imagery. <i>Plant Methods</i> , 2012, 8, 45.	4.3	70
22	Characterization of the Tomato Cf-4 Gene for Resistance to <i>Cladosporium fulvum</i> Identifies Sequences That Determine Recognition Specificity in Cf-4 and Cf-9. <i>Plant Cell</i> , 1997, 9, 2209.	6.6	67
23	Heterosis of leaf and rhizosphere microbiomes in field-grown maize. <i>New Phytologist</i> , 2020, 228, 1055-1069.	7.3	66
24	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.	3.5	62
25	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.	3.6	58
26	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.	2.9	52
27	A Genome-Wide Association Study for Partial Resistance to Maize Common Rust. <i>Phytopathology</i> , 2016, 106, 745-751.	2.2	51
28	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.	2.9	50
29	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.	1.8	48
30	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.	4.8	48
31	What are the Top 10 Unanswered Questions in Molecular Plant-Microbe Interactions?. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1354-1365.	2.6	47
32	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.	3.6	45
33	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.	3.6	44
34	Expanding Maize Genetic Resources with Predomestication Alleles: Maize's Teosinte Introgression Populations. <i>Plant Genome</i> , 2016, 9, plantgenome2015.07.0053.	2.8	43
35	Inverted repeat of a heterologous 3'-untranslated region for high-efficiency, high-throughput gene silencing. <i>Plant Journal</i> , 2003, 33, 793-800.	5.7	42
36	Analysis of leaf microbiome composition of near-isogenic maize lines differing in broad-spectrum disease resistance. <i>New Phytologist</i> , 2020, 225, 2152-2165.	7.3	42

#	ARTICLE	IF	CITATIONS
37	Microbe-dependent heterosis in maize. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	42
38	Use of an Advanced Intercross Line Population for Precise Mapping of Quantitative Trait Loci for Gray Leaf Spot Resistance in Maize. Crop Science, 2008, 48, 1696-1704.	1.8	41
39	Use of selection with recurrent backcrossing and QTL mapping to identify loci contributing to southern leaf blight resistance in a highly resistant maize line. Theoretical and Applied Genetics, 2009, 118, 911-925.	3.6	39
40	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.	1.8	39
41	Mining and Harnessing Natural Variation: A Little MAGIC. Crop Science, 2008, 48, 2066-2073.	1.8	36
42	Identification of Alleles Conferring Resistance to Gray Leaf Spot in Maize Derived from its Wild Progenitor Species Teosinte. Crop Science, 2016, 56, 209-218.	1.8	36
43	Characterization of temperature and light effects on the defense response phenotypes associated with the maize Rp1-D21 autoactive resistance gene. BMC Plant Biology, 2013, 13, 106.	3.6	35
44	Limits on the reproducibility of marker associations with southern leaf blight resistance in the maize nested association mapping population. BMC Genomics, 2014, 15, 1068.	2.8	35
45	Mapping QTL Controlling Southern Leaf Blight Resistance by Joint Analysis of Three Related Recombinant Inbred Line Populations. Crop Science, 2011, 51, 1571-1579.	1.8	32
46	Maize Disease Resistance. , 2009, , 229-250.		30
47	Cytoplasmic and Nuclear Localizations Are Important for the Hypersensitive Response Conferred by Maize Autoactive Rp1-D21 Protein. Molecular Plant-Microbe Interactions, 2015, 28, 1023-1031.	2.6	28
48	Use of mutant-assisted gene identification and characterization (MAGIC) to identify novel genetic loci that modify the maize hypersensitive response. Theoretical and Applied Genetics, 2011, 123, 985-997.	3.6	27
49	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> ). Theoretical and Applied Genetics, 2017, 130, 1285-1295.	3.6	26
50	The Genetics of Leaf Flecking in Maize and Its Relationship to Plant Defense and Disease Resistance. Plant Physiology, 2016, 172, 1787-1803.	4.8	25
51	QTL Mapping Using High-Throughput Sequencing. Methods in Molecular Biology, 2015, 1284, 257-285.	0.9	24
52	Genetic dissection of the maize ( <i>Zea mays</i> L.) MAMP response. Theoretical and Applied Genetics, 2017, 130, 1155-1168.	3.6	23
53	Identification of Teosinte Alleles for Resistance to Southern Leaf Blight in Near Isogenic Maize Lines. Crop Science, 2017, 57, 1973-1983.	1.8	23
54	A CRISPR/dCas9 toolkit for functional analysis of maize genes. Plant Methods, 2020, 16, 133.	4.3	21

#	ARTICLE	IF	CITATIONS
55	IDENTIFYING MAIZE GERMPLOSM WITH RESISTANCE TO AFLATOXIN ACCUMULATION. <i>Toxin Reviews</i> , 2008, 27, 319-345.	3.4	19
56	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.	3.4	18
57	Validation and Characterization of Maize Multiple Disease Resistance QTL. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2905-2912.	1.8	18
58	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.	4.2	18
59	The Wheat Puroindoline Genes Confer Fungal Resistance in Transgenic Corn. <i>Journal of Phytopathology</i> , 2011, 159, 188-190.	1.0	17
60	Semiatomated confocal imaging of fungal pathogenesis on plants: Microscopic analysis of macroscopic specimens. <i>Microscopy Research and Technique</i> , 2018, 81, 141-152.	2.2	17
61	A maize polygalacturonase functions as a suppressor of programmed cell death in plants. <i>BMC Plant Biology</i> , 2019, 19, 310.	3.6	17
62	Joint Analysis of Near-Isogenic and Recombinant Inbred Line Populations Yields Precise Positional Estimates for Quantitative Trait Loci. <i>Plant Genome</i> , 2010, 3, .	2.8	16
63	Identification of Quantitative Trait Loci for Goss's Wilt of Maize. <i>Crop Science</i> , 2018, 58, 1192-1200.	1.8	15
64	<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.	2.6	15
65	Maize metacaspases modulate the defense response mediated by the NLR protein Rp1-21 likely by affecting its subcellular localization. <i>Plant Journal</i> , 2021, 105, 151-166.	5.7	15
66	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.	3.3	13
67	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.	4.2	12
68	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.	3.3	12
69	Genotypic and phenotypic characterization of a large, diverse population of maize near-isogenic lines. <i>Plant Journal</i> , 2020, 103, 1246-1255.	5.7	12
70	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.	2.6	11
71	A maize cytochrome <i>b</i> -c1 complex subunit protein ZmQCR7 controls variation in the hypersensitive response. <i>Planta</i> , 2019, 249, 1477-1485.	3.2	10
72	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.	4.2	10

#	ARTICLE	IF	CITATIONS
73	Quantifying MAMP-induced Production of Reactive Oxygen Species in Sorghum and Maize. Bio-protocol, 2019, 9, .	0.4	10
74	A novel genetic framework for studying response to artificial selection. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 281-283.	0.8	9
75	Large Scale Field Inoculation and Scoring of Maize Southern Leaf Blight and Other Maize Foliar Fungal Diseases. Bio-protocol, 2018, 8, e2745.	0.4	9
76	Multivariate Mixed Linear Model Analysis of Longitudinal Data: An Information-Rich Statistical Technique for Analyzing Plant Disease Resistance. Phytopathology, 2012, 102, 1016-1025.	2.2	8
77	Yield Effects of Two Southern Leaf Blight Resistance Loci in Maize Hybrids. Crop Science, 2014, 54, 882-894.	1.8	8
78	Multi-Omics Analyses Reveal the Regulatory Network and the Function of ZmUGTs in Maize Defense Response. Frontiers in Plant Science, 2021, 12, 738261.	3.6	8
79	Genetic and Physiological Characterization of a Calcium Deficiency Phenotype in Maize. G3: Genes, Genomes, Genetics, 2020, 10, 1963-1970.	1.8	7
80	New insight into a complex plant-fungal pathogen interaction. Nature Genetics, 2015, 47, 101-103.	21.4	6
81	Development and Use of a Seedling Growth Retardation Assay to Quantify and Map Loci Underlying Variation in the Maize Basal Defense Response. PhytoFrontiers, 0, , PHYTOFR-12-20-0.	1.6	4
82	Genome-wide association study for morphological traits and resistance to <i>Peryonella pinodes</i> in the USDA pea single plant plus collection. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	4
83	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. Theoretical and Applied Genetics, 2018, 131, 2601-2612.	3.6	3
84	Variation in Gene Expression between Two Sorghum bicolor Lines Differing in Innate Immunity Response. Plants, 2021, 10, 1536.	3.5	3
85	Maize Plants Chimeric for an Autoactive Resistance Gene Display a Cell-Autonomous Hypersensitive Response but Non-Cell Autonomous Defense Signaling. Molecular Plant-Microbe Interactions, 2021, 34, 606-616.	2.6	2
86	Development of a transformation system for <i>Mycosphaerella</i> pathogens of banana: a tool for the study of host/pathogen interactions. FEMS Microbiology Letters, 2001, 195, 9-15.	1.8	1
87	Multiple insertions of COIN , a novel maize Foldback transposable element, in the Conring gene cause a spontaneous progressive cell death phenotype. Plant Journal, 2020, 104, 581-595.	5.7	0
88	Close encounters in the corn field. Molecular Plant, 2022, , .	8.3	0