

Jim Holland

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4474684/publications.pdf>

Version: 2024-02-01

129
papers

16,492
citations

50170

46
h-index

18606

119
g-index

143
all docs

143
docs citations

143
times ranked

11537
citing authors

#	ARTICLE	IF	CITATIONS
1	A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. <i>Nature Genetics</i> , 2006, 38, 203-208.	9.4	3,622
2	The Genetic Architecture of Maize Flowering Time. <i>Science</i> , 2009, 325, 714-718.	6.0	1,284
3	Genome-wide association study of leaf architecture in the maize nested association mapping population. <i>Nature Genetics</i> , 2011, 43, 159-162.	9.4	987
4	Genetic Properties of the Maize Nested Association Mapping Population. <i>Science</i> , 2009, 325, 737-740.	6.0	959
5	Genetic Design and Statistical Power of Nested Association Mapping in Maize. <i>Genetics</i> , 2008, 178, 539-551.	1.2	939
6	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	9.4	577
7	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
8	Comprehensive genotyping of the USA national maize inbred seed bank. <i>Genome Biology</i> , 2013, 14, R55.	3.8	458
9	Increased Food and Ecosystem Security via Perennial Grains. <i>Science</i> , 2010, 328, 1638-1639.	6.0	397
10	Genetic architecture of complex traits in plants. <i>Current Opinion in Plant Biology</i> , 2007, 10, 156-161.	3.5	372
11	The Genetic Architecture Of Maize Height. <i>Genetics</i> , 2014, 196, 1337-1356.	1.2	329
12	Genetic Architecture of Maize Kernel Composition in the Nested Association Mapping and Inbred Association Panels. <i>Plant Physiology</i> , 2012, 158, 824-834.	2.3	307
13	<i>ZmCCT</i> and the genetic basis of day-length adaptation underlying the postdomestication spread of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1913-21.	3.3	290
14	Estimating Genotypic Correlations and Their Standard Errors Using Multivariate Restricted Maximum Likelihood Estimation with SAS Proc MIXED. <i>Crop Science</i> , 2006, 46, 642-654.	0.8	262
15	Distinct Genetic Architectures for Male and Female Inflorescence Traits of Maize. <i>PLoS Genetics</i> , 2011, 7, e1002383.	1.5	231
16	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , 2017, 357, 512-515.	6.0	169
17	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
18	A heritability-adjusted GGE biplot for test environment evaluation. <i>Euphytica</i> , 2010, 171, 355-369.	0.6	149

#	ARTICLE	IF	CITATIONS
19	Genetic Data Analysis for Plant and Animal Breeding. , 2017, , .		144
20	The relationship between parental genetic or phenotypic divergence and progeny variation in the maize nested association mapping population. <i>Heredity</i> , 2012, 108, 490-499.	1.2	128
21	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
22	Genetic Control of Photoperiod Sensitivity in Maize Revealed by Joint Multiple Population Analysis. <i>Genetics</i> , 2010, 184, 799-812.	1.2	112
23	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
24	QTL mapping with near-isogenic lines in maize. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1211-1228.	1.8	107
25	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	5.8	105
26	Heritabilities and Correlations of Fusarium Ear Rot Resistance and Fumonisin Contamination Resistance in Two Maize Populations. <i>Crop Science</i> , 2006, 46, 353-361.	0.8	103
27	A Genome-Wide Association Study Reveals Genes Associated with Fusarium Ear Rot Resistance in a Maize Core Diversity Panel. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2095-2104.	0.8	98
28	Modifications to a <i>LATE MERISTEM IDENTITY1</i> gene are responsible for the major leaf shapes of Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E57-E66.	3.3	96
29	Panzea: a database and resource for molecular and functional diversity in the maize genome. <i>Nucleic Acids Research</i> , 2006, 34, D752-D757.	6.5	89
30	Climatic Adaptation and Ecological Descriptors of 42 Mexican Maize Races. <i>Crop Science</i> , 2008, 48, 1502-1512.	0.8	88
31	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
32	Genome-wide association study of Fusarium ear rot disease in the U.S.A. maize inbred line collection. <i>BMC Plant Biology</i> , 2014, 14, 372.	1.6	85
33	Training population selection and use of fixed effects to optimize genomic predictions in a historical USA winter wheat panel. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1247-1261.	1.8	78
34	Enhancing genomic prediction with genome-wide association studies in multiparental maize populations. <i>Heredity</i> , 2017, 118, 585-593.	1.2	77
35	Joint-multiple family linkage analysis predicts within-family variation better than single-family analysis of the maize nested association mapping population. <i>Heredity</i> , 2015, 114, 552-563.	1.2	74
36	Genome-wide association study reveals a set of genes associated with resistance to the Mediterranean corn borer (<i>Sesamia nonagrioides</i> L.) in a maize diversity panel. <i>BMC Plant Biology</i> , 2015, 15, 35.	1.6	73

#	ARTICLE	IF	CITATIONS
37	Ecogeography of teosinte. PLoS ONE, 2018, 13, e0192676.	1.1	67
38	Molecular Characterization of Maize Inbreds with Expired U.S. Plant Variety Protection. Crop Science, 2008, 48, 1673-1685.	0.8	66
39	Heterosis of leaf and rhizosphere microbiomes in field-grown maize. New Phytologist, 2020, 228, 1055-1069.	3.5	66
40	Genomic regions controlling vernalization and photoperiod responses in oat. Theoretical and Applied Genetics, 2002, 105, 113-126.	1.8	64
41	Diallel Analysis of Resistance to Fusarium Ear Rot and Fumonisin Contamination in Maize. Crop Science, 2012, 52, 2173-2181.	0.8	63
42	Optimal Designs for Genomic Selection in Hybrid Crops. Molecular Plant, 2019, 12, 390-401.	3.9	63
43	A Genome-Wide Association Study of the Maize Hypersensitive Defense Response Identifies Genes That Cluster in Related Pathways. PLoS Genetics, 2014, 10, e1004562.	1.5	62
44	The genetic architecture of teosinte catalyzed and constrained maize domestication. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5643-5652.	3.3	59
45	Genetic Improvement for Yield and Fertility of Alfalfa Cultivars Representing Different Eras of Breeding. Crop Science, 1994, 34, 953-957.	0.8	56
46	Inheritance of resistance to southern corn rust in tropical-by-corn-belt maize populations. Theoretical and Applied Genetics, 1998, 96, 232-241.	1.8	54
47	Relationships Among Resistances to Fusarium and Aspergillus Ear Rots and Contamination by Fumonisin and Aflatoxin in Maize. Phytopathology, 2007, 97, 311-317.	1.1	52
48	The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	52
49	Confirming quantitative trait loci for aflatoxin resistance from Mp313E in different genetic backgrounds. Molecular Breeding, 2013, 32, 15-26.	1.0	50
50	A Connected Set of Genes Associated with Programmed Cell Death Implicated in Controlling the Hypersensitive Response in Maize. Genetics, 2013, 193, 609-620.	1.2	50
51	Mapping resistance to Southern rust in a tropical by temperate maize recombinant inbred topcross population. Theoretical and Applied Genetics, 2007, 114, 659-667.	1.8	48
52	Title is missing!. Euphytica, 2001, 122, 69-79.	0.6	46
53	BREEDING FOR IMPROVED RESISTANCE TO FUMONISIN CONTAMINATION IN MAIZE. Toxin Reviews, 2008, 27, 371-389.	1.5	45
54	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. Frontiers in Genetics, 2020, 11, 592769.	1.1	44

#	ARTICLE	IF	CITATIONS
55	Identification of Quantitative Trait Loci for Resistance to Southern Leaf Blight and Days to Anthesis in a Maize Recombinant Inbred Line Population. <i>Phytopathology</i> , 2006, 96, 1067-1071.	1.1	40
56	Genetic Architecture of Domestication-Related Traits in Maize. <i>Genetics</i> , 2016, 204, 99-113.	1.2	39
57	Selection for water-soluble carbohydrate accumulation and investigation of genetic–environment interactions in an elite wheat breeding population. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2445-2461.	1.8	39
58	Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. <i>Genetics</i> , 2014, 198, 409-421.	1.2	38
59	Maize genomes to fields (G2F): 2014–2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. <i>BMC Research Notes</i> , 2020, 13, 71.	0.6	38
60	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
61	Dominance Effects and Functional Enrichments Improve Prediction of Agronomic Traits in Hybrid Maize. <i>Genetics</i> , 2020, 215, 215-230.	1.2	35
62	A Genome Wide Association Study Reveals Markers and Genes Associated with Resistance to <i>Fusarium verticillioides</i> Infection of Seedlings in a Maize Diversity Panel. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 571-579.	0.8	34
63	Genetic Relationships of Crown Rust Resistance, Grain Yield, Test Weight, and Seed Weight in Oat. <i>Crop Science</i> , 2001, 41, 1041-1050.	0.8	33
64	Selection for Reduced Fusarium Ear Rot and Fumonisin Content in Advanced Backcross Maize Lines and Their Topcross Hybrids. <i>Crop Science</i> , 2010, 50, 2249-2260.	0.8	33
65	Direct mapping of density response in a population of B73 × Mo17 recombinant inbred lines of maize (<i>Zea Mays</i> L.). <i>Heredity</i> , 2010, 104, 583-599.	1.2	32
66	Three new teosintes (<i>Zea</i> spp., Poaceae) from Mexico. <i>American Journal of Botany</i> , 2011, 98, 1537-1548.	0.8	32
67	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
68	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. <i>Plant Cell</i> , 2021, 33, 882-900.	3.1	31
69	Hallauer's Tus3n: a decade of selection for tropical-to-temperate phenological adaptation in maize. <i>Heredity</i> , 2015, 114, 229-240.	1.2	30
70	MAGIC maize: a new resource for plant genetics. <i>Genome Biology</i> , 2015, 16, 163.	3.8	28
71	The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. <i>PLoS Genetics</i> , 2020, 16, e1008791.	1.5	27
72	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

#	ARTICLE	IF	CITATIONS
73	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. <i>BMC Research Notes</i> , 2018, 11, 452.	0.6	25
74	Mining Natural Variation for Maize Improvement: Selection on Phenotypes and Genes. , 2014, , 615-649.		24
75	QTL Mapping Using High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2015, 1284, 257-285.	0.4	24
76	Genomic-wide Association Study of Popping Expansion in Tropical Popcorn and Field Corn Germplasm. <i>Crop Science</i> , 2019, 59, 2007-2019.	0.8	23
77	The Genomic Basis for Short-Term Evolution of Environmental Adaptation in Maize. <i>Genetics</i> , 2019, 213, 1479-1494.	1.2	23
78	Environment-specific genomic prediction ability in maize using environmental covariates depends on environmental similarity to training data. <i>G3: Genes, Genomes, Genetics</i> , 2021, , .	0.8	23
79	Mapping Density Response in Maize: A Direct Approach for Testing Genotype and Treatment Interactions. <i>Genetics</i> , 2006, 173, 331-348.	1.2	22
80	Genotypic Correlation and Multivariate QTL Analyses for Cell Wall Components and Resistance to Stalk Tunneling by the European Corn Borer in Maize. <i>Crop Science</i> , 2007, 47, 485-488.	0.8	22
81	Relationships of Resistance to Fusarium Ear Rot and Fumonisin Contamination with Agronomic Performance of Maize. <i>Crop Science</i> , 2007, 47, 1770-1778.	0.8	22
82	Genome-Wide Associations for Water-Soluble Carbohydrate Concentration and Relative Maturity in Wheat Using SNP and DArT Marker Arrays. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2821-2830.	0.8	22
83	Seed Dormancy in Mexican Teosinte. <i>Crop Science</i> , 2011, 51, 2056-2066.	0.8	21
84	Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. <i>Crop Science</i> , 2020, 60, 62-81.	0.8	21
85	Mapping reciprocal effects and interactions with plant density stress in <i>Zea mays</i> L.. <i>Heredity</i> , 2007, 99, 14-30.	1.2	20
86	Genomic prediction for resistance to Fusarium ear rot and fumonisin contamination in maize. <i>Crop Science</i> , 2020, 60, 1863-1875.	0.8	20
87	Defining the Role of the MADS-Box Gene, <i>Zea</i> <i>Agamous-like1</i> , a Target of Selection During Maize Domestication. <i>Journal of Heredity</i> , 2018, 109, 333-338.	1.0	19
88	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
89	Validation and Characterization of Maize Multiple Disease Resistance QTL. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2905-2912.	0.8	18
90	Allelic Effect Variation at Key Photoperiod Response Quantitative Trait Loci in Maize. <i>Crop Science</i> , 2011, 51, 1036-1049.	0.8	17

#	ARTICLE	IF	CITATIONS
91	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
92	Responses to Selection for Partial Resistance to Crown Rust in Oat. <i>Crop Science</i> , 2006, 46, 1260-1265.	0.8	15
93	Comparison of Conventional, Modified Single Seed Descent, and Doubled Haploid Breeding Methods for Maize Inbred Line Development Using Germplasm Enhancement of Maize Breeding Crosses. <i>Crop Science</i> , 2011, 51, 1534-1543.	0.8	15
94	Quantitative Trait Loci and Epistasis for Crown Freezing Tolerance in the "Kanota" – "Ogle" Hexaploid Oat Mapping Population. <i>Crop Science</i> , 2008, 48, 149-157.	0.8	14
95	Responses to Recurrent Index Selection for Reduced Fusarium Ear Rot and Lodging and for Increased Yield in Maize. <i>Crop Science</i> , 2016, 56, 85-94.	0.8	14
96	Dissecting Symptomatology and Fumonisin Contamination Produced by <i>Fusarium verticillioides</i> in Maize Ears. <i>Phytopathology</i> , 2018, 108, 1475-1485.	1.1	13
97	A Genome-Wide Association Study To Understand the Effect of <i>Fusarium verticillioides</i> Infection on Seedlings of a Maize Diversity Panel. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1685-1696.	0.8	13
98	Accounting for Genotype-by-Environment Interactions and Residual Genetic Variation in Genomic Selection for Water-Soluble Carbohydrate Concentration in Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1909-1919.	0.8	12
99	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
100	Characterizing the oligogenic architecture of plant growth phenotypes informs genomic selection approaches in a common wheat population. <i>BMC Genomics</i> , 2021, 22, 402.	1.2	12
101	Correlated Responses to Selection for Greater β -Glucan Content in Two Oat Populations. <i>Crop Science</i> , 2002, 42, 730.	0.8	11
102	High-Throughput Resequencing of Maize Landraces at Genomic Regions Associated with Flowering Time. <i>PLoS ONE</i> , 2017, 12, e0168910.	1.1	10
103	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
104	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
105	Yield Effects of Two Southern Leaf Blight Resistance Loci in Maize Hybrids. <i>Crop Science</i> , 2014, 54, 882-894.	0.8	8
106	Association mapping and genomic prediction for ear rot disease caused by <i>Fusarium verticillioides</i> in a tropical maize germplasm. <i>Crop Science</i> , 2020, 60, 2867-2881.	0.8	8
107	Johnsongrass (<i>Sorghum halepense</i>) Pollen Expresses Accase Target-site Resistance. <i>Weed Technology</i> , 2007, 21, 384-388.	0.4	7
108	Harnessing Maize Biodiversity. <i>Compendium of Plant Genomes</i> , 2018, , 335-366.	0.3	7

#	ARTICLE	IF	CITATIONS
109	QTL Controlling Masculinization of Ear Tips in a Maize (<i>Zea mays</i> L.) Intraspecific Cross. G3: Genes, Genomes, Genetics, 2011, 1, 337-341.	0.8	6
110	New insight into a complex plant-fungal pathogen interaction. Nature Genetics, 2015, 47, 101-103.	9.4	6
111	Ensemble Learning of QTL Models Improves Prediction of Complex Traits. G3: Genes, Genomes, Genetics, 2015, 5, 2073-2084.	0.8	6
112	Effects of artificial inoculation on trait correlations with resistance to Fusarium ear rot and fumonisin contamination in maize. Crop Science, 2021, 61, 2522.	0.8	6
113	Domestication reshaped the genetic basis of inbreeding depression in a maize landrace compared to its wild relative, teosinte. PLoS Genetics, 2021, 17, e1009797.	1.5	5
114	Protein Profiling Reveals Novel Proteins in Pollen and Pistil of W22 (<i>ga1; Ga1</i>) in Maize. Proteomes, 2014, 2, 258-271.	1.7	4
115	Prediction ability of genome-wide markers in <i>Pinus taeda</i> L. within and between population is affected by relatedness to the training population and trait genetic architecture. G3: Genes, Genomes, Genetics, 2021, , .	0.8	4
116	Outlook for Implementation of Genomics-Based Selection in Public Cotton Breeding Programs. Plants, 2022, 11, 1446.	1.6	4
117	Genomic Relationships and GBLUP. , 2017, , 311-354.		3
118	Increasing Yield. , 2009, , 469-482.		3
119	Registration of tropical populations of maize selected in parallel for early flowering time across the United States. Journal of Plant Registrations, 2022, 16, 100-108.	0.4	3
120	Empirical comparison of genomic and phenotypic selection for resistance to Fusarium ear rot and fumonisin contamination in maize. Theoretical and Applied Genetics, 2022, 135, 2799-2816.	1.8	2
121	Plant Genetics: Two Steps on the Path to Maize Adaptation. Current Biology, 2018, 28, R1098-R1101.	1.8	1
122	A conserved genetic architecture among populations of the maize progenitor, teosinte, was radically altered by domestication. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	1
123	Genomic Selection. , 2017, , 355-384.		0
124	Imputing Missing Genotypes. , 2017, , 287-309.		0
125	Multivariate Models. , 2017, , 165-201.		0
126	Genetic variation for response to mixed triazole and strobilurin application in diverse maize. , 2020, 3, e20054.		0

#	ARTICLE	IF	CITATIONS
127	The potential to breed a low-protein maize for protein-restricted diets. <i>Crop Science</i> , 0, , .	0.8	0
128	Harnessing quantitative genetics and genomics for understanding and improving complex traits in crops. , 2009, , 123-136.		0
129	Enhancing Crop Breeding Using Population Genomics Approaches. <i>Population Genomics</i> , 2020, , 1.	0.2	0