

Jim Holland

List of Publications by Year in descending order

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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	Registration of tropical populations of maize selected in parallel for early flowering time across the United States. <i>Journal of Plant Registrations</i> , 2022, 16, 100-108.	0.4	3
2	Outlook for Implementation of Genomics-Based Selection in Public Cotton Breeding Programs. <i>Plants</i> , 2022, 11, 1446.	1.6	4
3	Empirical comparison of genomic and phenotypic selection for resistance to Fusarium ear rot and fumonisin contamination in maize. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2799-2816.	1.8	2
4	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
5	Effects of artificial inoculation on trait correlations with resistance to Fusarium ear rot and fumonisin contamination in maize. <i>Crop Science</i> , 2021, 61, 2522.	0.8	6
6	The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	52
7	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
8	A conserved genetic architecture among populations of the maize progenitor, teosinte, was radically altered by domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	1
9	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. <i>G3: Genes, Genomes, Genetics</i> , 2021, , .	0.8	4
10	Domestication reshaped the genetic basis of inbreeding depression in a maize landrace compared to its wild relative, teosinte. <i>PLoS Genetics</i> , 2021, 17, e1009797.	1.5	5
11	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
12	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
13	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
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	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
16	Heterosis of leaf and rhizosphere microbiomes in field-grown maize. <i>New Phytologist</i> , 2020, 228, 1055-1069.	3.5	66
17	Genetic variation for response to mixed triazole and strobilurin application in diverse maize. , 2020, 3, e20054.		0
18	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

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19	Genomic prediction for resistance to Fusarium ear rot and fumonisin contamination in maize. <i>Crop Science</i> , 2020, 60, 1863-1875.	0.8	20
20	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
21	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. <i>Frontiers in Genetics</i> , 2020, 11, 592769.	1.1	44
22	Dominance Effects and Functional Enrichments Improve Prediction of Agronomic Traits in Hybrid Maize. <i>Genetics</i> , 2020, 215, 215-230.	1.2	35
23	Enhancing Crop Breeding Using Population Genomics Approaches. <i>Population Genomics</i> , 2020, , 1.	0.2	0
24	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
25	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
26	Optimal Designs for Genomic Selection in Hybrid Crops. <i>Molecular Plant</i> , 2019, 12, 390-401.	3.9	63
27	The genetic architecture of teosinte catalyzed and constrained maize domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5643-5652.	3.3	59
28	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
29	The Genomic Basis for Short-Term Evolution of Environmental Adaptation in Maize. <i>Genetics</i> , 2019, 213, 1479-1494.	1.2	23
30	Validation and Characterization of Maize Multiple Disease Resistance QTL. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2905-2912.	0.8	18
31	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
32	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
33	Defining the Role of the MADS-Box Gene, <i>Zea Agamous-like1</i> , a Target of Selection During Maize Domestication. <i>Journal of Heredity</i> , 2018, 109, 333-338.	1.0	19
34	Plant Genetics: Two Steps on the Path to Maize Adaptation. <i>Current Biology</i> , 2018, 28, R1098-R1101.	1.8	1
35	Dissecting Symptomatology and Fumonisin Contamination Produced by <i>Fusarium verticillioides</i> in Maize Ears. <i>Phytopathology</i> , 2018, 108, 1475-1485.	1.1	13
36	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

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37	Ecogeography of teosinte. PLoS ONE, 2018, 13, e0192676.	1.1	67
38	Harnessing Maize Biodiversity. Compendium of Plant Genomes, 2018, , 335-366.	0.3	7
39	Enhancing genomic prediction with genome-wide association studies in multiparental maize populations. Heredity, 2017, 118, 585-593.	1.2	77
40	Modifications to a <i>LATE MERISTEM IDENTITY1</i> gene are responsible for the major leaf shapes of Upland cotton (<i>Gossypium hirsutum</i> L.). Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E57-E66.	3.3	96
41	Selection for water-soluble carbohydrate accumulation and investigation of genetic—environment interactions in an elite wheat breeding population. Theoretical and Applied Genetics, 2017, 130, 2445-2461.	1.8	39
42	Genomic Relationships and GBLUP. , 2017, , 311-354.		3
43	Genomic Selection. , 2017, , 355-384.		0
44	Imputing Missing Genotypes. , 2017, , 287-309.		0
45	Multivariate Models. , 2017, , 165-201.		0
46	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. Science, 2017, 357, 512-515.	6.0	169
47	The effect of artificial selection on phenotypic plasticity in maize. Nature Communications, 2017, 8, 1348.	5.8	105
48	Genome-Wide Associations for Water-Soluble Carbohydrate Concentration and Relative Maturity in Wheat Using SNP and DArT Marker Arrays. G3: Genes, Genomes, Genetics, 2017, 7, 2821-2830.	0.8	22
49	High-Throughput Resequencing of Maize Landraces at Genomic Regions Associated with Flowering Time. PLoS ONE, 2017, 12, e0168910.	1.1	10
50	Genetic Data Analysis for Plant and Animal Breeding. , 2017, , .		144
51	Responses to Recurrent Index Selection for Reduced Fusarium Ear Rot and Lodging and for Increased Yield in Maize. Crop Science, 2016, 56, 85-94.	0.8	14
52	The Genetics of Leaf Flecking in Maize and Its Relationship to Plant Defense and Disease Resistance. Plant Physiology, 2016, 172, 1787-1803.	2.3	25
53	Genetic Architecture of Domestication-Related Traits in Maize. Genetics, 2016, 204, 99-113.	1.2	39
54	MAGIC maize: a new resource for plant genetics. Genome Biology, 2015, 16, 163.	3.8	28

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55	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
56	New insight into a complex plant-fungal pathogen interaction. <i>Nature Genetics</i> , 2015, 47, 101-103.	9.4	6
57	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
58	Ensemble Learning of QTL Models Improves Prediction of Complex Traits. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2073-2084.	0.8	6
59	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
60	QTL Mapping Using High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2015, 1284, 257-285.	0.4	24
61	Yield Effects of Two Southern Leaf Blight Resistance Loci in Maize Hybrids. <i>Crop Science</i> , 2014, 54, 882-894.	0.8	8
62	Protein Profiling Reveals Novel Proteins in Pollen and Pistil of W22 (ga1; Ga1) in Maize. <i>Proteomes</i> , 2014, 2, 258-271.	1.7	4
63	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
64	Mining Natural Variation for Maize Improvement: Selection on Phenotypes and Genes. , 2014, , 615-649.		24
65	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
66	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
67	The Genetic Architecture Of Maize Height. <i>Genetics</i> , 2014, 196, 1337-1356.	1.2	329
68	Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. <i>Genetics</i> , 2014, 198, 409-421.	1.2	38
69	Comprehensive genotyping of the USA national maize inbred seed bank. <i>Genome Biology</i> , 2013, 14, R55.	3.8	458
70	Confirming quantitative trait loci for aflatoxin resistance from Mp313E in different genetic backgrounds. <i>Molecular Breeding</i> , 2013, 32, 15-26.	1.0	50
71	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
72	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

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73	Diallel Analysis of Resistance to Fusarium Ear Rot and Fumonisin Contamination in Maize. <i>Crop Science</i> , 2012, 52, 2173-2181.	0.8	63
74	<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
75	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
76	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
77	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
78	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	9.4	577
79	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
80	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
81	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
82	Three new teosintes (<i>Zea</i> spp., Poaceae) from Mxico. <i>American Journal of Botany</i> , 2011, 98, 1537-1548.	0.8	32
83	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
84	Distinct Genetic Architectures for Male and Female Inflorescence Traits of Maize. <i>PLoS Genetics</i> , 2011, 7, e1002383.	1.5	231
85	Allelic Effect Variation at Key Photoperiod Response Quantitative Trait Loci in Maize. <i>Crop Science</i> , 2011, 51, 1036-1049.	0.8	17
86	Seed Dormancy in Mexican Teosinte. <i>Crop Science</i> , 2011, 51, 2056-2066.	0.8	21
87	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
88	QTL Controlling Masculinization of Ear Tips in a Maize (<i>Zea mays</i> L.) Intraspecific Cross. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 337-341.	0.8	6
89	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
90	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

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91	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
92	A heritability-adjusted GGE biplot for test environment evaluation. <i>Euphytica</i> , 2010, 171, 355-369.	0.6	149
93	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
94	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
95	Increased Food and Ecosystem Security via Perennial Grains. <i>Science</i> , 2010, 328, 1638-1639.	6.0	397
96	Genetic Control of Photoperiod Sensitivity in Maize Revealed by Joint Multiple Population Analysis. <i>Genetics</i> , 2010, 184, 799-812.	1.2	112
97	Genetic Properties of the Maize Nested Association Mapping Population. <i>Science</i> , 2009, 325, 737-740.	6.0	959
98	The Genetic Architecture of Maize Flowering Time. <i>Science</i> , 2009, 325, 714-718.	6.0	1,284
99	Increasing Yield. , 2009, , 469-482.		3
100	Harnessing quantitative genetics and genomics for understanding and improving complex traits in crops. , 2009, , 123-136.		0
101	BREEDING FOR IMPROVED RESISTANCE TO FUMONISIN CONTAMINATION IN MAIZE. <i>Toxin Reviews</i> , 2008, 27, 371-389.	1.5	45
102	Genetic Design and Statistical Power of Nested Association Mapping in Maize. <i>Genetics</i> , 2008, 178, 539-551.	1.2	939
103	Molecular Characterization of Maize Inbreds with Expired U.S. Plant Variety Protection. <i>Crop Science</i> , 2008, 48, 1673-1685.	0.8	66
104	Climatic Adaptation and Ecological Descriptors of 42 Mexican Maize Races. <i>Crop Science</i> , 2008, 48, 1502-1512.	0.8	88
105	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
106	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
107	Relationships Among Resistances to <i>Fusarium</i> and <i>Aspergillus</i> Ear Rots and Contamination by Fumonisin and Aflatoxin in Maize. <i>Phytopathology</i> , 2007, 97, 311-317.	1.1	52
108	Johnsongrass (<i>Sorghum halepense</i>) Pollen Expresses Accase Target-site Resistance. <i>Weed Technology</i> , 2007, 21, 384-388.	0.4	7

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109	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
110	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
111	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
112	Genetic architecture of complex traits in plants. <i>Current Opinion in Plant Biology</i> , 2007, 10, 156-161.	3.5	372
113	Mapping resistance to Southern rust in a tropical by temperate maize recombinant inbred topcross population. <i>Theoretical and Applied Genetics</i> , 2007, 114, 659-667.	1.8	48
114	QTL mapping with near-isogenic lines in maize. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1211-1228.	1.8	107
115	Mapping Density Response in Maize: A Direct Approach for Testing Genotype and Treatment Interactions. <i>Genetics</i> , 2006, 173, 331-348.	1.2	22
116	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
117	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
118	Responses to Selection for Partial Resistance to Crown Rust in Oat. <i>Crop Science</i> , 2006, 46, 1260-1265.	0.8	15
119	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
120	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
121	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
122	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
123	Genomic regions controlling vernalization and photoperiod responses in oat. <i>Theoretical and Applied Genetics</i> , 2002, 105, 113-126.	1.8	64
124	Correlated Responses to Selection for Greater β -Glucan Content in Two Oat Populations. <i>Crop Science</i> , 2002, 42, 730.	0.8	11
125	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
126	Title is missing!. <i>Euphytica</i> , 2001, 122, 69-79.	0.6	46

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127	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
128	Genetic Improvement for Yield and Fertility of Alfalfa Cultivars Representing Different Eras of Breeding. Crop Science, 1994, 34, 953-957.	0.8	56
129	The potential to breed a low-protein maize for protein-restricted diets. Crop Science, 0, , .	0.8	0