

Jim Holland

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

133
papers

12,084
citations

42
h-index

109
g-index

143
ext. papers

14,904
ext. citations

6.8
avg. IF

6.1
L-index

#	Paper	IF	Citations
133	A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. <i>Nature Genetics</i> , 2006 , 38, 203-8	36.3	2595
132	The genetic architecture of maize flowering time. <i>Science</i> , 2009 , 325, 714-8	33.3	1043
131	Genetic properties of the maize nested association mapping population. <i>Science</i> , 2009 , 325, 737-40	33.3	775
130	Genetic design and statistical power of nested association mapping in maize. <i>Genetics</i> , 2008 , 178, 539-514		753
129	Genome-wide association study of leaf architecture in the maize nested association mapping population. <i>Nature Genetics</i> , 2011 , 43, 159-62	36.3	746
128	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012 , 44, 803-7	36.3	470
127	Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. <i>Nature Genetics</i> , 2011 , 43, 163-8	36.3	444
126	Comprehensive genotyping of the USA national maize inbred seed bank. <i>Genome Biology</i> , 2013 , 14, R55	18.3	337
125	Genetic architecture of complex traits in plants. <i>Current Opinion in Plant Biology</i> , 2007 , 10, 156-61	9.9	310
124	Agriculture. Increased food and ecosystem security via perennial grains. <i>Science</i> , 2010 , 328, 1638-9	33.3	303
123	Genetic architecture of maize kernel composition in the nested association mapping and inbred association panels. <i>Plant Physiology</i> , 2012 , 158, 824-34	6.6	242
122	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	2.4	230
121	ZmCCT 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, E1913-215	11.5	226
120	The genetic architecture of maize height. <i>Genetics</i> , 2014 , 196, 1337-56	4	211
119	Distinct genetic architectures for male and female inflorescence traits of maize. <i>PLoS Genetics</i> , 2011 , 7, e1002383	6	175
118	Estimating and Interpreting Heritability for Plant Breeding: An Update 2010 , 9-112		140
117	Multivariate analysis of maize disease resistances suggests a pleiotropic genetic basis and implicates a GST gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 7339-44	11.5	115

116	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , 2017 , 357, 512-515	33.3	110
115	QTL Mapping for Fusarium Ear Rot and Fumonisin Contamination Resistance in Two Maize Populations. <i>Crop Science</i> , 2006 , 46, 1734-1743	2.4	101
114	A heritability-adjusted GGE biplot for test environment evaluation. <i>Euphytica</i> , 2010 , 171, 355-369	2.1	97
113	The relationship between parental genetic or phenotypic divergence and progeny variation in the maize nested association mapping population. <i>Heredity</i> , 2012 , 108, 490-9	3.6	96
112	QTL mapping with near-isogenic lines in maize. <i>Theoretical and Applied Genetics</i> , 2007 , 114, 1211-28	6	93
111	Genetic control of photoperiod sensitivity in maize revealed by joint multiple population analysis. <i>Genetics</i> , 2010 , 184, 799-812	4	88
110	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, 645-57	4	88
109	Heritabilities and Correlations of Fusarium Ear Rot Resistance and Fumonisin Contamination Resistance in Two Maize Populations. <i>Crop Science</i> , 2006 , 46, 353-361	2.4	88
108	Genetic Data Analysis for Plant and Animal Breeding 2017 ,		85
107	Panzea: a database and resource for molecular and functional diversity in the maize genome. <i>Nucleic Acids Research</i> , 2006 , 34, D752-7	20.1	74
106	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, 72-9	3.8	73
105	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, 2095-104	3.2	64
104	Climatic Adaptation and Ecological Descriptors of 42 Mexican Maize Races. <i>Crop Science</i> , 2008 , 48, 1502-1512	17.4	64
103	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	5.3	62
102	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017 , 8, 1348	17.4	58
101	Molecular Characterization of Maize Inbreds with Expired U.S. Plant Variety Protection. <i>Crop Science</i> , 2008 , 48, 1673-1685	2.4	57
100	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	5.3	55
99	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, 552-63	3.6	55

98	Genomic regions controlling vernalization and photoperiod responses in oat. <i>Theoretical and Applied Genetics</i> , 2002 , 105, 113-126	6	54
97	Modifications to a LATE MERISTEM IDENTITY1 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	11.5	48
96	Genetic Improvement for Yield and Fertility of Alfalfa Cultivars Representing Different Eras of Breeding. <i>Crop Science</i> , 1994 , 34, 953-957	2.4	47
95	Diallel Analysis of Resistance to Fusarium Ear Rot and Fumonisin Contamination in Maize. <i>Crop Science</i> , 2012 , 52, 2173-2181	2.4	46
94	Relationships among resistances to fusarium and Aspergillus ear rots and contamination by fumonisin and aflatoxin in maize. <i>Phytopathology</i> , 2007 , 97, 311-7	3.8	44
93	Enhancing genomic prediction with genome-wide association studies in multiparental maize populations. <i>Heredity</i> , 2017 , 118, 585-593	3.6	43
92	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	6	43
91	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	6	41
90	Optimal Designs for Genomic Selection in Hybrid Crops. <i>Molecular Plant</i> , 2019 , 12, 390-401	14.4	41
89	BREEDING FOR IMPROVED RESISTANCE TO FUMONISIN CONTAMINATION IN MAIZE. <i>Toxin Reviews</i> , 2008 , 27, 371-389	2.3	41
88	A connected set of genes associated with programmed cell death implicated in controlling the hypersensitive response in maize. <i>Genetics</i> , 2013 , 193, 609-20	4	40
87	Confirming quantitative trait loci for aflatoxin resistance from Mp313E in different genetic backgrounds. <i>Molecular Breeding</i> , 2013 , 32, 15-26	3.4	38
86	Ecogeography of teosinte. <i>PLoS ONE</i> , 2018 , 13, e0192676	3.7	36
85	Inheritance of resistance to southern corn rust in tropical-by-corn-belt maize populations. <i>Theoretical and Applied Genetics</i> , 1998 , 96, 232-241	6	36
84	Correlated responses of fatty acid composition, grain quality, and agronomic traits to nine cycles of recurrent selection for increased oil content in oat. <i>Euphytica</i> , 2001 , 122, 69-79	2.1	36
83	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	11.5	34
82	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, 1067-71	3.8	33
81	Genetic Architecture of Domestication-Related Traits in Maize. <i>Genetics</i> , 2016 , 204, 99-113	4	31

80	Mapping resistance to Southern rust in a tropical by temperate maize recombinant inbred topcross population. <i>Theoretical and Applied Genetics</i> , 2007 , 114, 659-67	6	31
79	Genetic Relationships of Crown Rust Resistance, Grain Yield, Test Weight, and Seed Weight in Oat. <i>Crop Science</i> , 2001 , 41, 1041-1050	2.4	28
78	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	6	26
77	Heterosis of leaf and rhizosphere microbiomes in field-grown maize. <i>New Phytologist</i> , 2020 , 228, 1055-1069	9.69	25
76	Insights into the effects of long-term artificial selection on seed size in maize. <i>Genetics</i> , 2014 , 198, 409-24	24	25
75	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	4.5	25
74	Direct mapping of density response in a population of B73 x Mo17 recombinant inbred lines of maize (<i>Zea Mays</i> L.). <i>Heredity</i> , 2010 , 104, 583-99	3.6	25
73	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	2.4	25
72	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	2.4	25
71	MAGIC maize: a new resource for plant genetics. <i>Genome Biology</i> , 2015 , 16, 163	18.3	24
70	Three new teosintes (<i>Zea</i> spp., Poaceae) from Mexico. <i>American Journal of Botany</i> , 2011 , 98, 1537-48	2.7	22
69	Hallauer's Tusū: a decade of selection for tropical-to-temperate phenological adaptation in maize. <i>Heredity</i> , 2015 , 114, 229-40	3.6	19
68	Relationships of Resistance to Fusarium Ear Rot and Fumonisin Contamination with Agronomic Performance of Maize. <i>Crop Science</i> , 2007 , 47, 1770-1778	2.4	19
67	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	2.4	18
66	Mapping density response in maize: a direct approach for testing genotype and treatment interactions. <i>Genetics</i> , 2006 , 173, 331-48	4	18
65	QTL mapping using high-throughput sequencing. <i>Methods in Molecular Biology</i> , 2015 , 1284, 257-85	1.4	18
64	The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. <i>PLoS Genetics</i> , 2020 , 16, e1008791	6	17
63	Mining Natural Variation for Maize Improvement: Selection on Phenotypes and Genes 2014 , 615-649		17

62	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	2.3	16
61	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	2.3	16
60	Allelic Effect Variation at Key Photoperiod Response Quantitative Trait Loci in Maize. <i>Crop Science</i> , 2011 , 51, 1036-1049	2.4	16
59	A Genome Wide Association Study Reveals Markers and Genes Associated with Resistance to Infection of Seedlings in a Maize Diversity Panel. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 571-579	3.2	16
58	Defining the Role of the MADS-Box Gene, <i>Zea</i> Agamous-like1, a Target of Selection During Maize Domestication. <i>Journal of Heredity</i> , 2018 , 109, 333-338	2.4	15
57	Seed Dormancy in Mexican Teosinte. <i>Crop Science</i> , 2011 , 51, 2056-2066	2.4	15
56	Genomic-Wide Association Study of Popping Expansion in Tropical Popcorn and Field Corn Germplasm. <i>Crop Science</i> , 2019 , 59, 2007-2019	2.4	14
55	Mapping reciprocal effects and interactions with plant density stress in <i>Zea mays</i> L. <i>Heredity</i> , 2007 , 99, 14-30	3.6	14
54	The Genetics of Leaf Flecking in Maize and Its Relationship to Plant Defense and Disease Resistance. <i>Plant Physiology</i> , 2016 , 172, 1787-1803	6.6	14
53	Epistasis and Plant Breeding		14
52	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	3.2	13
51	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	2.4	13
50	Joint Analysis of Near-Isogenic and Recombinant Inbred Line Populations Yields Precise Positional Estimates for Quantitative Trait Loci. <i>Plant Genome</i> , 2010 , 3,	4.4	12
49	Responses to Selection for Partial Resistance to Crown Rust in Oat. <i>Crop Science</i> , 2006 , 46, 1260-1265	2.4	12
48	Dominance Effects and Functional Enrichments Improve Prediction of Agronomic Traits in Hybrid Maize. <i>Genetics</i> , 2020 , 215, 215-230	4	12
47	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,	3.2	12
46	Diverse Components of Resistance to Infection and Fumonisin Contamination in Four Maize Recombinant Inbred Families. <i>Toxins</i> , 2019 , 11,	4.9	11
45	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	4.5	11

44	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	2.4	11
43	The Genomic Basis for Short-Term Evolution of Environmental Adaptation in Maize. <i>Genetics</i> , 2019 , 213, 1479-1494	4	11
42	Genomic prediction for resistance to Fusarium ear rot and fumonisin contamination in maize. <i>Crop Science</i> , 2020 , 60, 1863-1875	2.4	10
41	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	2.4	10
40	Correlated Responses to Selection for Greater β -Glucan Content in Two Oat Populations. <i>Crop Science</i> , 2002 , 42, 730	2.4	10
39	Dissecting Symptomatology and Fumonisin Contamination Produced by <i>Fusarium verticillioides</i> in Maize Ears. <i>Phytopathology</i> , 2018 , 108, 1475-1485	3.8	9
38	Marker-Assisted Breeding for Host Resistance to Mycotoxin Contamination. <i>Food Additives</i> , 2005 , 423-436		9
37	High-Throughput Resequencing of Maize Landraces at Genomic Regions Associated with Flowering Time. <i>PLoS ONE</i> , 2017 , 12, e0168910	3.7	8
36	A novel genetic framework for studying response to artificial selection. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011 , 9, 281-283	1	8
35	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	3.2	7
34	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	2.4	7
33	Validation and Characterization of Maize Multiple Disease Resistance QTL. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2905-2912	3.2	7
32	Ensemble Learning of QTL Models Improves Prediction of Complex Traits. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 2073-84	3.2	6
31	New insight into a complex plant-fungal pathogen interaction. <i>Nature Genetics</i> , 2015 , 47, 101-3	36.3	6
30	Johnsongrass (<i>Sorghum halepense</i>) Pollen Expresses Accase Target-site Resistance. <i>Weed Technology</i> , 2007 , 21, 384-388	1.4	6
29	QTL Controlling Masculinization of Ear Tips in a Maize (<i>Zea mays</i> L.) Intraspecific Cross. <i>G3: Genes, Genomes, Genetics</i> , 2011 , 1, 337-41	3.2	5
28	Harnessing Maize Biodiversity. <i>Compendium of Plant Genomes</i> , 2018 , 335-366	0.8	5
27	Multivariate mixed linear model analysis of longitudinal data: an information-rich statistical technique for analyzing plant disease resistance. <i>Phytopathology</i> , 2012 , 102, 1016-25	3.8	4

26	Genetic Analysis of Lodging in Diverse Maize Hybrids		4
25	Yield Effects of Two Southern Leaf Blight Resistance Loci in Maize Hybrids. <i>Crop Science</i> , 2014 , 54, 882-894		3
24	Protein Profiling Reveals Novel Proteins in Pollen and Pistil of W22 (ga1; Ga1) in Maize. <i>Proteomes</i> , 2014 , 2, 258-271	4.6	3
23	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. <i>Plant Cell</i> , 2021 , 33, 882-900	11.6	3
22	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	2.4	3
21	Characterizing the oligogenic architecture of plant growth phenotypes informs genomic selection approaches in a common wheat population. <i>BMC Genomics</i> , 2021 , 22, 402	4.5	3
20	Genomic Relationships and GBLUP 2017 , 311-354		2
19	Heterosis of leaf and rhizosphere microbiomes in field-grown maize		2
18	Eleven biosynthetic genes explain the majority of natural variation for carotenoid levels in maize grain		2
17	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	4.9	2
16	A Genome-Wide Association Study To Understand the Effect of Infection on Seedlings of a Maize Diversity Panel. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 1685-1696	3.2	2
15	Environment-specific genomic prediction ability in maize using environmental covariates depends on environmental similarity to training data.. <i>G3: Genes, Genomes, Genetics</i> , 2021 ,	3.2	2
14	Plant Genetics: Two Steps on the Path to Maize Adaptation. <i>Current Biology</i> , 2018 , 28, R1098-R1101	6.3	1
13	Increasing Yield 2009 , 469-482		1
12	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	6	1
11	Outlook for Implementation of Genomics-Based Selection in Public Cotton Breeding Programs. <i>Plants</i> , 2022 , 11, 1446	4.5	1
10	Effects of artificial inoculation on trait correlations with resistance to <i>Fusarium</i> ear rot and fumonisin contamination in maize. <i>Crop Science</i> , 2021 , 61, 2522	2.4	0
9	Genetic variation for response to mixed triazole and strobilurin application in diverse maize 2020 , 3, e20054		

8 Genomic Selection **2017**, 355-384

7 Imputing Missing Genotypes **2017**, 287-309

6 Multivariate Models **2017**, 165-201

5 Charles W. Stuber: Maize Geneticist and Pioneer of Marker-Assisted Selection **2015**, 1-22

4 Charles W. Stuber: Maize Geneticist and Pioneer of Marker-Assisted Selection **2015**, 1-22

3 Enhancing Crop Breeding Using Population Genomics Approaches. *Population Genomics*, **2020**, 1 1.4

2 Harnessing quantitative genetics and genomics for understanding and improving complex traits in crops **2009**, 123-136

1 Dedication: Major M. Goodman: Maize Geneticist and Breeder 1-29