

# H-P Piepho

## List of Publications by Year in descending order

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474  
papers

18,070  
citations

15504

65  
h-index

29157

104  
g-index

495  
all docs

495  
docs citations

495  
times ranked

14440  
citing authors

#	ARTICLE	IF	CITATIONS
1	BLUP for phenotypic selection in plant breeding and variety testing. <i>Euphytica</i> , 2008, 161, 209-228.	1.2	569
2	Computing Heritability and Selection Response From Unbalanced Plant Breeding Trials. <i>Genetics</i> , 2007, 177, 1881-1888.	2.9	483
3	Statistical Analysis of Yield Trials by AMMI and GGE: Further Considerations. <i>Crop Science</i> , 2008, 48, 866-889.	1.8	347
4	An Algorithm for a Letter-Based Representation of All-Pairwise Comparisons. <i>Journal of Computational and Graphical Statistics</i> , 2004, 13, 456-466.	1.7	313
5	The Area Under the Disease Progress Stairs: Calculation, Advantage, and Application. <i>Phytopathology</i> , 2012, 102, 381-389.	2.2	288
6	A Hitchhiker's Guide to Mixed Models for Randomized Experiments. <i>Journal of Agronomy and Crop Science</i> , 2003, 189, 310-322.	3.5	282
7	Comparison of Mixed-Model Approaches for Association Mapping. <i>Genetics</i> , 2008, 178, 1745-1754.	2.9	273
8	Genomic selection using regularized linear regression models: ridge regression, lasso, elastic net and their extensions. <i>BMC Proceedings</i> , 2012, 6, S10.	1.6	245
9	Extreme Wildlife Declines and Concurrent Increase in Livestock Numbers in Kenya: What Are the Causes?. <i>PLoS ONE</i> , 2016, 11, e0163249.	2.5	239
10	Ridge Regression and Extensions for Genomewide Selection in Maize. <i>Crop Science</i> , 2009, 49, 1165-1176.	1.8	234
11	What's normal anyway? Residual plots are more telling than significance tests when checking <sc>ANOVA</sc> assumptions. <i>Journal of Agronomy and Crop Science</i> , 2018, 204, 86-98.	3.5	227
12	Methods for Comparing the Yield Stability of Cropping Systems. <i>Journal of Agronomy and Crop Science</i> , 1998, 180, 193-213.	3.5	221
13	Continuing wildlife population declines and range contraction in the Mara region of Kenya during 1977â€“2009. <i>Journal of Zoology</i> , 2011, 285, 99-109.	1.7	191
14	Comparison of Weighting in Twoâ€“Stage Analysis of Plant Breeding Trials. <i>Crop Science</i> , 2009, 49, 1977-1988.	1.8	183
15	Analyzing Genotype-Environment Data by Mixed Models with Multiplicative Terms. <i>Biometrics</i> , 1997, 53, 761.	1.4	170
16	A comparison of random forests, boosting and support vector machines for genomic selection. <i>BMC Proceedings</i> , 2011, 5, S11.	1.6	169
17	A Mixed Modelling Approach for Randomized Experiments with Repeated Measures. <i>Journal of Agronomy and Crop Science</i> , 2004, 190, 230-247.	3.5	154
18	Empirical best linear unbiased prediction in cultivar trials using factor-analytic variance-covariance structures. <i>Theoretical and Applied Genetics</i> , 1998, 97, 195-201.	3.6	152

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19	A Quick Method for Computing Approximate Thresholds for Quantitative Trait Loci Detection. Genetics, 2001, 157, 425-432.	2.9	150
20	A stage-wise approach for the analysis of multi-environment trials. Biometrical Journal, 2012, 54, 844-860.	1.0	145
21	Variation explained in mixed-model association mapping. Heredity, 2010, 105, 333-340.	2.6	133
22	Breeding progress, environmental variation and correlation of winter wheat yield and quality traits in German official variety trials and on-farm during 1983–2014. Theoretical and Applied Genetics, 2017, 130, 223-245.	3.6	133
23	Yield stability of hybrids versus lines in wheat, barley, and triticale. Theoretical and Applied Genetics, 2014, 127, 309-316.	3.6	130
24	Dynamics of Mara's Serengeti ungulates in relation to land use changes. Journal of Zoology, 2009, 278, 1-14.	1.7	129
25	The Role of Epistasis in the Manifestation of Heterosis: A Systems-Oriented Approach. Genetics, 2007, 177, 1815-1825.	2.9	125
26	Best Linear Unbiased Prediction (BLUP) for regional yield trials: a comparison to additive main effects and multiplicative interaction (AMMI) analysis. Theoretical and Applied Genetics, 1994, 89, 647-654.	3.6	119
27	Current statistical issues in Weed Research. Weed Research, 2010, 50, 5-24.	1.7	118
28	Stability Analysis Using the SAS System. Agronomy Journal, 1999, 91, 154-160.	1.8	116
29	Rainfall influences on ungulate population abundance in the Mara's Serengeti ecosystem. Journal of Animal Ecology, 2008, 77, 814-829.	2.8	115
30	Assessing the importance of genotype–environment interaction for root traits in rice using a mapping population II: conventional QTL analysis. Theoretical and Applied Genetics, 2006, 113, 953-964.	3.6	113
31	Comparison of Maize ( <i>Zea mays</i> L.) F1-Hybrid and Parental Inbred Line Primary Root Transcriptomes Suggests Organ-Specific Patterns of Nonadditive Gene Expression and Conserved Expression Trends. Genetics, 2008, 179, 1275-1283.	2.9	111
32	Genetic and non-genetic long-term trends of 12 different crops in German official variety performance trials and on-farm yield trends. Theoretical and Applied Genetics, 2014, 127, 2599-2617.	3.6	111
33	Augmented p-rep designs. Biometrical Journal, 2011, 53, 19-27.	1.0	109
34	Efficient phosphorus application strategies for increased crop production in sub-Saharan West Africa. Field Crops Research, 2001, 72, 1-15.	5.1	104
35	Manifestation of heterosis during early maize ( <i>Zea mays</i> L.) root development. Theoretical and Applied Genetics, 2006, 112, 421-429.	3.6	104
36	Effects of soybean variety and Bradyrhizobium strains on yield, protein content and biological nitrogen fixation under cool growing conditions in Germany. European Journal of Agronomy, 2016, 72, 38-46.	4.1	104

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37	Enviromics in breeding: applications and perspectives on envirotypic-assisted selection. Theoretical and Applied Genetics, 2021, 134, 95-112.	3.6	103
38	Effect of supplementation of xylanase and phospholipase to a wheat-based diet for weanling pigs on nutrient digestibility and concentrations of microbial metabolites in ileal digesta and feces1. Journal of Animal Science, 2004, 82, 2647-2656.	0.5	102
39	Analysis of Unbalanced Data by Mixed Linear Models Using the mixed Procedure of the SAS System. Journal of Agronomy and Crop Science, 2005, 191, 47-54.	3.5	97
40	Comparative expression profiling in meristems of inbred-hybrid triplets of maize based on morphological investigations of heterosis for plant height. Plant Molecular Biology, 2006, 63, 21-34.	3.9	97
41	Association mapping reveals gene action and interactions in the determination of flowering time in barley. Theoretical and Applied Genetics, 2009, 118, 259-273.	3.6	96
42	Genetic Basis of Heterosis for Growth-Related Traits in Arabidopsis Investigated by Testcross Progenies of Near-Isogenic Lines Reveals a Significant Role of Epistasis. Genetics, 2007, 177, 1827-1837.	2.9	95
43	Heritability in Plant Breeding on a Genotype-Difference Basis. Genetics, 2019, 212, 991-1008.	2.9	94
44	Data Transformation in Statistical Analysis of Field Trials with Changing Treatment Variance. Agronomy Journal, 2009, 101, 865-869.	1.8	93
45	Drought yield index to select high yielding rice lines under different drought stress severities. Rice, 2012, 5, 31.	4.0	92
46	A Mixed-Model Approach to Mapping Quantitative Trait Loci in Barley on the Basis of Multiple Environment Data. Genetics, 2000, 156, 2043-2050.	2.9	91
47	Genome-based prediction of maize hybrid performance across genetic groups, testers, locations, and years. Theoretical and Applied Genetics, 2014, 127, 1375-1386.	3.6	90
48	El Niño and Southern Oscillation, rainfall, temperature and Normalized Difference Vegetation Index fluctuations in the Mara-Serengeti ecosystem. African Journal of Ecology, 2008, 46, 132-143.	0.9	88
49	Simultaneous improvement of grain yield and protein content in durum wheat by different phenotypic indices and genomic selection. Theoretical and Applied Genetics, 2018, 131, 1315-1329.	3.6	87
50	Influence of coastal vegetation on the 2004 tsunami wave impact in west Aceh. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18612-18617.	7.1	86
51	Selection in Cultivar Trials—Is It Ignorable?. Crop Science, 2006, 46, 192-201.	1.8	85
52	Model training across multiple breeding cycles significantly improves genomic prediction accuracy in rye (Secale cereale L.). Theoretical and Applied Genetics, 2016, 129, 2043-2053.	3.6	84
53	Best Linear Unbiased Prediction of Cultivar Effects for Subdivided Target Regions. Crop Science, 2005, 45, 1151-1159.	1.8	81
54	Statistical Models and Methods for Network Meta-Analysis. Phytopathology, 2016, 106, 792-806.	2.2	81

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55	Comparing the performance of cereal varieties in organic and non-organic cropping systems in different European countries. <i>Euphytica</i> , 2008, 163, 417-433.	1.2	80
56	Nonsyntenic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. <i>Plant Cell</i> , 2014, 26, 3939-3948.	6.6	80
57	Outlier detection methods for generalized lattices: a case study on the transition from ANOVA to REML. <i>Theoretical and Applied Genetics</i> , 2016, 129, 787-804.	3.6	80
58	Heterosis in early seed development: a comparative study of F1 embryo and endosperm tissues 6Âdays after fertilization. <i>Theoretical and Applied Genetics</i> , 2010, 120, 389-400.	3.6	78
59	Extensive tissue-specific transcriptomic plasticity in maize primary roots upon water deficit. <i>Journal of Experimental Botany</i> , 2016, 67, 1095-1107.	4.8	78
60	A coefficient of determination ( $R^2$ ) for generalized linear mixed models. <i>Biometrical Journal</i> , 2019, 61, 860-872.	1.0	77
61	Molecular marker-based prediction of hybrid performance in maize using unbalanced data from multiple experiments with factorial crosses. <i>Theoretical and Applied Genetics</i> , 2009, 118, 741-751.	3.6	76
62	Development of Heterotic Groups in Triticale. <i>Crop Science</i> , 2010, 50, 584-590.	1.8	76
63	Corn hybrids display lower metabolite variability and complex metabolite inheritance patterns. <i>Plant Journal</i> , 2011, 68, 326-336.	5.7	75
64	Robustness of statistical tests for multiplicative terms in the additive main effects and multiplicative interaction model for cultivar trials. <i>Theoretical and Applied Genetics</i> , 1995, 90, 438-443.	3.6	74
65	One Step at a Time: Stage-Wise Analysis of a Series of Experiments. <i>Agronomy Journal</i> , 2017, 109, 845-857.	1.8	71
66	Breeding progress, variation, and correlation of grain and quality traits in winter rye hybrid and population varieties and national on-farm progress in Germany over 26 years. <i>Theoretical and Applied Genetics</i> , 2017, 130, 981-998.	3.6	71
67	Prediction of hybrid performance in maize using molecular markers and joint analyses of hybrids and parental inbreds. <i>Theoretical and Applied Genetics</i> , 2010, 120, 451-461.	3.6	70
68	Influence of land-use intensity on the spatial distribution of N-cycling microorganisms in grassland soils. <i>FEMS Microbiology Ecology</i> , 2011, 77, 95-106.	2.7	70
69	Agronomic improvements can make future cereal systems in South Asia far more productive and result in a lower environmental footprint. <i>Global Change Biology</i> , 2016, 22, 1054-1074.	9.5	70
70	Marker Pair Selection for Mapping Quantitative Trait Loci. <i>Genetics</i> , 2001, 157, 433-444.	2.9	70
71	Transcriptomic complexity in young maize primary roots in response to low water potentials. <i>BMC Genomics</i> , 2014, 15, 741.	2.8	69
72	Genomic Selection using Multiple Populations. <i>Crop Science</i> , 2012, 52, 2453-2461.	1.8	68

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73	Energy crop production in double-cropping systems: Results from an experiment at seven sites. <i>European Journal of Agronomy</i> , 2013, 51, 120-129.	4.1	68
74	Comparative changes in density and demography of large herbivores in the Masai Mara Reserve and its surrounding human-dominated pastoral ranches in Kenya. <i>Biodiversity and Conservation</i> , 2012, 21, 1509-1530.	2.6	67
75	Dissecting genetic and non-genetic sources of long-term yield trend in German official variety trials. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1009-1018.	3.6	67
76	Analysis of a Triple Testcross Design With Recombinant Inbred Lines Reveals a Significant Role of Epistasis in Heterosis for Biomass-Related Traits in <i>Arabidopsis</i> . <i>Genetics</i> , 2007, 175, 2009-2017.	2.9	65
77	A High-Resolution Tissue-Specific Proteome and Phosphoproteome Atlas of Maize Primary Roots Reveals Functional Gradients along the Root Axes. <i>Plant Physiology</i> , 2015, 168, 233-246.	4.8	64
78	Rainfall trends and variation in the Maasai Mara ecosystem and their implications for animal population and biodiversity dynamics. <i>PLoS ONE</i> , 2018, 13, e0202814.	2.5	61
79	Efficiency of strip- and line-transect surveys of African savanna mammals. <i>Journal of Zoology</i> , 2006, 269, 060303002124001-???	1.7	59
80	A tutorial on the statistical analysis of factorial experiments with qualitative and quantitative treatment factor levels. <i>Journal of Agronomy and Crop Science</i> , 2018, 204, 429-455.	3.5	59
81	Modelling expectation and variance for genotype by environment data. <i>Heredity</i> , 1997, 79, 162-171.	2.6	58
82	The Use of Two-Way Linear Mixed Models in Multitreatment Meta-Analysis. <i>Biometrics</i> , 2012, 68, 1269-1277.	1.4	58
83	Modeling Effective Dosages in Hormetic Dose-Response Studies. <i>PLoS ONE</i> , 2012, 7, e33432.	2.5	58
84	Multi-trait association mapping in sugar beet ( <i>Beta vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 117, 947-954.	3.6	57
85	Analysis of nonadditive protein accumulation in young primary roots of a maize ( <i>Zea mays</i> L.) inbred line. <i>Journal of Experimental Botany</i> , 2010, 61, 3882-3894.	2.2	57
86	Mineral NPK and manure fertilisation affecting the yield stability of winter wheat: Results from a long-term field experiment. <i>European Journal of Agronomy</i> , 2019, 102, 14-22.	4.1	57
87	Specification of Cortical Parenchyma and Stele of Maize Primary Roots by Asymmetric Levels of Auxin, Cytokinin, and Cytokinin-Regulated Proteins. <i>Plant Physiology</i> , 2009, 152, 4-18.	4.8	56
88	Estimating Broad-Sense Heritability with Unbalanced Data from Agricultural Cultivar Trials. <i>Crop Science</i> , 2019, 59, 525-536.	1.8	56
89	Heterosis for Biomass-Related Traits in <i>Arabidopsis</i> Investigated by Quantitative Trait Loci Analysis of the Triple Testcross Design With Recombinant Inbred Lines. <i>Genetics</i> , 2007, 177, 1839-1850.	2.9	55
90	Meta-Analysis of the Relative Efficiency of Methionine-Hydroxy-Analogue-Free-Acid Compared with dl-Methionine in Broilers Using Nonlinear Mixed Models. <i>Poultry Science</i> , 2008, 87, 2023-2031.	3.4	55

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91	The distribution of large herbivore hotspots in relation to environmental and anthropogenic correlates in the Mara region of Kenya. <i>Journal of Animal Ecology</i> , 2012, 81, 1268-1287.	2.8	55
92	Dynamics of ungulates in relation to climatic and land use changes in an insularized African savanna ecosystem. <i>Biodiversity and Conservation</i> , 2012, 21, 1033-1053.	2.6	55
93	Livestock Diversification: an Adaptive Strategy to Climate and Rangeland Ecosystem Changes in Southern Ethiopia. <i>Human Ecology</i> , 2014, 42, 509-520.	1.4	55
94	Factors controlling the variability of organic matter in the top- and subsoil of a sandy Dystric Cambisol under beech forest. <i>Geoderma</i> , 2018, 311, 37-44.	5.1	55
95	Nearest Neighbour Adjustment and Linear Variance Models in Plant Breeding Trials. <i>Biometrical Journal</i> , 2008, 50, 164-189.	1.0	53
96	Large herbivore responses to water and settlements in savannas. <i>Ecological Monographs</i> , 2010, 80, 241-266.	5.4	52
97	Comparisons of single-stage and two-stage approaches to genomic selection. <i>Theoretical and Applied Genetics</i> , 2013, 126, 69-82.	3.6	51
98	Genomic selection allowing for marker-by-environment interaction. <i>Plant Breeding</i> , 2013, 132, 532-538.	1.9	51
99	The importance of phenotypic data analysis for genomic prediction - a case study comparing different spatial models in rye. <i>BMC Genomics</i> , 2014, 15, 646.	2.8	51
100	A simulation study on tests of hypotheses and confidence intervals for fixed effects in mixed models for blocked experiments with missing data. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2005, 10, 374-389.	1.4	50
101	Validation of candidate genes putatively associated with resistance to SCMV and MDMV in maize ( <i>Zea mays</i> ) Tj ETQq1 1.0, 784314, rgBT / Over	3.6	50
102	Linear variance models for plant breeding trials. <i>Plant Breeding</i> , 2010, 129, 1-8.	1.9	50
103	Large herbivore responses to surface water and land use in an East African savanna: implications for conservation and human-wildlife conflicts. <i>Biodiversity and Conservation</i> , 2014, 23, 573-596.	2.6	50
104	Single-Parent Expression Is a General Mechanism Driving Extensive Complementation of Non-syntenic Genes in Maize Hybrids. <i>Current Biology</i> , 2018, 28, 431-437.e4.	3.9	50
105	Strategies to Subdivide a Target Population of Environments: Results from the CIMMYT-led Maize Hybrid Testing Programs in Africa. <i>Crop Science</i> , 2012, 52, 2143-2152.	1.8	49
106	Impacts of climate change and variability on cattle production in southern Ethiopia: Perceptions and empirical evidence. <i>Agricultural Systems</i> , 2014, 130, 23-34.	6.1	49
107	REML approach for adjusting the Fusarium head blight rating to a phenological date in inoculated selection experiments of wheat. <i>Theoretical and Applied Genetics</i> , 2008, 117, 65-73.	3.6	48
108	High-yielding, drought-tolerant, stable rice genotypes for the shallow rainfed lowland drought-prone ecosystem. <i>Field Crops Research</i> , 2012, 133, 37-47.	5.1	48

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109	Network-meta analysis made easy: detection of inconsistency using factorial analysis-of-variance models. BMC Medical Research Methodology, 2014, 14, 61.	3.1	48
110	Long-Term Experiments with cropping systems: Case studies on data analysis. European Journal of Agronomy, 2016, 77, 223-235.	4.1	48
111	Population structure and phenotypic variation of a spring barley world collection set up for association studies. Plant Breeding, 2010, 129, 271-279.	1.9	47
112	REML-Based Diallel Analysis. Crop Science, 2011, 51, 470-478.	1.8	47
113	Chemical composition and standardised ileal digestibilities of crude protein and amino acids in grain legumes for growing pigs. Livestock Science, 2011, 138, 229-243.	1.6	47
114	Response of soil fertility indices to long-term application of biogas and raw slurry under organic farming. Applied Soil Ecology, 2015, 96, 99-107.	4.3	47
115	Codominant Analysis of Banding Data From a Dominant Marker System by Normal Mixtures. Genetics, 2000, 155, 1459-1468.	2.9	47
116	Statistical aspects of on-farm experimentation. Crop and Pasture Science, 2011, 62, 721.	1.5	46
117	Hippopotamus and livestock grazing: influences on riparian vegetation and facilitation of other herbivores in the Mara Region of Kenya. Landscape and Ecological Engineering, 2013, 9, 47-58.	1.5	46
118	Genetic parameters for feather pecking and aggressive behavior in a large F2-cross of laying hens using generalized linear mixed models. Poultry Science, 2014, 93, 810-817.	3.4	46
119	Higher grain yield and higher grain protein deviation underline the potential of hybrid wheat for a sustainable agriculture. Plant Breeding, 2018, 137, 326-337.	1.9	46
120	Digesta characteristics of dorsal, middle and ventral rumen of cows fed with different hay qualities and concentrate levels. Archives of Animal Nutrition, 2004, 58, 325-342.	1.8	45
121	Efficiency of augmented p-rep designs in multi-environmental trials. Theoretical and Applied Genetics, 2014, 127, 1049-1060.	3.6	45
122	Influence of elevated soil temperature and biochar application on organic matter associated with aggregate-size and density fractions in an arable soil. Agriculture, Ecosystems and Environment, 2017, 241, 79-87.	5.3	45
123	Letters in Mean Comparisons: What They Do and Don't Mean. Agronomy Journal, 2018, 110, 431-434.	1.8	45
124	Soil microbial community structure and function mainly respond to indirect effects in a multifactorial climate manipulation experiment. Soil Biology and Biochemistry, 2020, 142, 107704.	8.8	45
125	Trends in genetic variance components during 30 years of hybrid maize breeding at the University of Hohenheim. Plant Breeding, 2008, 127, 446-451.	1.9	44
126	Integrating a simple shading algorithm into CERES-wheat and CERES-maize with particular regard to a changing microclimate within a relay-intercropping system. Field Crops Research, 2011, 121, 274-285.	5.1	44



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127	Herbivore Dynamics and Range Contraction in Kajiado County Kenya: Climate and Land Use Changes, Population Pressures, Governance, Policy and Human-wildlife Conflicts. Open Ecology Journal, 2014, 7, 9-31.	2.0	44
128	The Effect of Feather Eating on Feed Passage in Laying Hens. Poultry Science, 2006, 85, 21-25.	3.4	43
129	Power to Detect Higher-Order Epistatic Interactions in a Metabolic Pathway Using a New Mapping Strategy. Genetics, 2007, 176, 563-570.	2.9	43
130	Analysing disease incidence data from designed experiments by generalized linear mixed models. Plant Pathology, 1999, 48, 668-674.	2.4	42
131	Optimal marker density for interval mapping in a backcross population. Heredity, 2000, 84, 437-440.	2.6	42
132	Testcross performance of rye introgression lines developed by marker-assisted backcrossing using an Iranian accession as donor. Theoretical and Applied Genetics, 2009, 118, 1225-1238.	3.6	42
133	Nonadditive Protein Accumulation Patterns in Maize (Zea maysL.) Hybrids during Embryo Development. Journal of Proteome Research, 2010, 9, 6511-6522.	3.7	42
134	Efficient Computation of Ridgeâ€Regression Best Linear Unbiased Prediction in Genomic Selection in Plant Breeding. Crop Science, 2012, 52, 1093-1104.	1.8	42
135	Crop yield evaluation under controlled drainage in Ohio, United States. Journal of Soils and Water Conservation, 2012, 67, 465-473.	1.6	42
136	Transcriptomic reprogramming of barley seminal roots by combined water deficit and salt stress. BMC Genomics, 2019, 20, 325.	2.8	42
137	Wildlife Population Dynamics in Human-Dominated Landscapes under Community-Based Conservation: The Example of Nakuru Wildlife Conservancy, Kenya. PLoS ONE, 2017, 12, e0169730.	2.5	42
138	Selection Strategy for Sorghum Targeting Phosphorusâ€Limited Environments in West Africa: Analysis of Multiâ€Environment Experiments. Crop Science, 2012, 52, 2517-2527.	1.8	41
139	Similar spatial patterns of soil quality indicators in three poplar-based silvo-arable alley cropping systems in Germany. Biology and Fertility of Soils, 2019, 55, 1-14.	4.3	41
140	Statistical tests for QTL and QTL-by-environment effects in segregating populations derived from line crosses. Theoretical and Applied Genetics, 2005, 110, 561-566.	3.6	39
141	Molecular marker assisted broadening of the Central European heterotic groups in rye with Eastern European germplasm. Theoretical and Applied Genetics, 2010, 120, 291-299.	3.6	39
142	MULTI-SITE TIME-TREND ANALYSIS OF SOIL FERTILITY MANAGEMENT EFFECTS ON CROP PRODUCTION IN SUB-SAHARAN WEST AFRICA. Experimental Agriculture, 2002, 38, 163-183.	0.9	38
143	Occurrence and Distribution of 13 Trichothecene Toxins in Naturally Contaminated Maize Plants in Germany. Toxins, 2012, 4, 778-787.	3.4	38
144	Evaluation of approaches for estimating the accuracy of genomic prediction in plant breeding. BMC Genomics, 2013, 14, 860.	2.8	38

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145	Assessing the importance of genotype x environment interaction for root traits in rice using a mapping population. I: a soil-filled box screen. Theoretical and Applied Genetics, 2006, 113, 977-986.	3.6	37
146	Regularized group regression methods for genomic prediction: Bridge, MCP, SCAD, group bridge, group lasso, sparse group lasso, group MCP and group SCAD. BMC Proceedings, 2014, 8, S7.	1.6	37
147	A turbidity-based method to continuously monitor sediment, carbon and nitrogen flows in mountainous watersheds. Journal of Hydrology, 2014, 513, 45-57.	5.4	37
148	Genetic gain for rice yield in rainfed environments in India. Field Crops Research, 2021, 260, 107977.	5.1	37
149	Stability of Single-Parent Gene Expression Complementation in Maize Hybrids upon Water Deficit Stress. Plant Physiology, 2017, 173, 1247-1257.	4.8	36
150	Analysis of series of variety trials with perennial crops. Grass and Forage Science, 2014, 69, 431-440.	2.9	35
151	Breeding progress, genotypic and environmental variation and correlation of quality traits in malting barley in German official variety trials between 1983 and 2015. Theoretical and Applied Genetics, 2017, 130, 2411-2429.	3.6	35
152	Decoupling of impact factors reveals the response of German winter wheat yields to climatic changes. Global Change Biology, 2020, 26, 3601-3626.	9.5	35
153	A comparison of experimental designs for selection in breeding trials with nested treatment structure. Theoretical and Applied Genetics, 2006, 113, 1505-1513.	3.6	34
154	DNA polymorphisms and haplotype patterns of transcription factors involved in barley endosperm development are associated with key agronomic traits. BMC Plant Biology, 2010, 10, 5.	3.6	34
155	Stability analysis of farmer participatory trials for conservation agriculture using mixed models. Field Crops Research, 2011, 121, 450-459.	5.1	34
156	Integration of genotypic, hyperspectral, and phenotypic data to improve biomass yield prediction in hybrid rye. Theoretical and Applied Genetics, 2020, 133, 3001-3015.	3.6	34
157	Rank correlation among parametric and nonparametric measures of phenotypic stability. Euphytica, 1992, 64, 221-225.	1.2	33
158	A simple procedure for yield component analysis. Euphytica, 1995, 84, 43-48.	1.2	33
159	The folded exponential transformation for proportions. Journal of the Royal Statistical Society: Series D (the Statistician), 2003, 52, 575-589.	0.2	33
160	A new test for family-based association mapping with inbred lines from plant breeding programs. Theoretical and Applied Genetics, 2006, 113, 1121-1130.	3.6	33
161	Prediction of single-cross hybrid performance in maize using haplotype blocks associated with QTL for grain yield. Theoretical and Applied Genetics, 2007, 114, 1345-1355.	3.6	33
162	An on-farm approach to quantify yield variation and to derive decision rules for site-specific weed management. Precision Agriculture, 2008, 9, 133-146.	6.0	33

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163	Predicting biphasic responses in binary mixtures: Pelargonic acid versus glyphosate. Chemosphere, 2017, 178, 88-98.	8.2	33
164	Do we need more drought for better nutrition? The effect of precipitation on nutrient concentration in East African food crops. Science of the Total Environment, 2019, 658, 405-415.	8.0	33
165	A general method for controlling the genome-wide type I error rate in linkage and association mapping experiments in plants. Heredity, 2011, 106, 825-831.	2.6	32
166	Production objectives and breeding goals of Sahiwal cattle keepers in Kenya and implications for a breeding programme. Tropical Animal Health and Production, 2012, 44, 519-530.	1.4	32
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