Fred A Van Eeuwijk

List of Publications by Year
in descending order

156 papers	8,676 citations	43973 48 h-index	54797 84 g-index
169 all docs	169 docs citations	169 times ranked	8883 citing authors

#	Article	IF	Citations
1	Linkage Disequilibrium Mapping of Yield and Yield Stability in Modern Spring Barley Cultivars. Genetics, 2004, 168, 435-446.	1.2	375
2	Models for navigating biological complexity in breeding improved crop plants. Trends in Plant Science, 2006, 11, 587-593.	4.3	364
3	The statistical analysis of multi-environment data: modeling genotype-by-environment interaction and its genetic basis. Frontiers in Physiology, 2013, 4, 44.	1.3	349
4	Tracing the ancestry of modern bread wheats. Nature Genetics, 2019, 51, 905-911.	9.4	230
5	A Mixed-Model Quantitative Trait Loci (QTL) Analysis for Multiple-Environment Trial Data Using Environmental Covariables for QTL-by-Environment Interactions, With an Example in Maize. Genetics, 2007, 177, 1801-1813.	1.2	201
6	Natural variation for seed dormancy in Arabidopsis is regulated by additive genetic and molecular pathways. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4264-4269.	3.3	194
7	Marker-Based Estimation of Heritability in Immortal Populations. Genetics, 2015, 199, 379-398.	1.2	192
8	Correcting for spatial heterogeneity in plant breeding experiments with P-splines. Spatial Statistics, 2018, 23, 52-71.	0.9	180
9	What Should Students in Plant Breeding Know About the Statistical Aspects of Genotype Ã— Environment Interactions?. Crop Science, 2016, 56, 2119-2140.	0.8	175
10	Modelling strategies for assessing and increasing the effectiveness of new phenotyping techniques in plant breeding. Plant Science, 2019, 282, 23-39.	1.7	173
11	Improved batch correction in untargeted MS-based metabolomics. Metabolomics, 2016, 12, 88.	1.4	167
12	Root phenotyping: from component trait in the lab to breeding: Table 1.. Journal of Experimental Botany, 2015, 66, 5389-5401.	2.4	163
13	Multi-environment QTL mixed models for drought stress adaptation in wheat. Theoretical and Applied Genetics, 2008, 117, 1077-1091.	1.8	160
14	Evaluation of LD decay and various LD-decay estimators in simulated and SNP-array data of tetraploid potato. Theoretical and Applied Genetics, 2017, 130, 123-135.	1.8	158
15	Genomic prediction of maize yield across European environmental conditions. Nature Genetics, 2019, 51, 952-956.	9.4	157
16	Modeling QTL for complex traits: detection and context for plant breeding. Current Opinion in Plant Biology, 2009, 12, 231-240.	3.5	153
17	Detection and use of QTL for complex traits in multiple environments. Current Opinion in Plant Biology, 2010, 13, 193-205.	3.5	146
18	Genetic architecture of plant stress resistance: multiâ€trait genomeâ€wide association mapping. New Phytologist, 2017, 213, 1346-1362.	3.5	144

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19	Genome-wide analysis of yield in Europe: allelic effects as functions of drought and heat scenarios. Plant Physiology, 2016, 172, pp.00621.2016.	2.3	140
20	Analysis of natural allelic variation in <i>Arabidopsis</i> using a multiparent recombinant inbred line population. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4488-4493.	3.3	137
21	A multi-trait multi-environment QTL mixed model with an application to drought and nitrogen stress trials in maize (Zea maysÂL.). Euphytica, 2008, 161, 241-257.	0.6	134
22	Quality of core collections for effective utilisation of genetic resources review, discussion and interpretation. Theoretical and Applied Genetics, 2013, 126, 289-305.	1.8	134
23	Accuracy of imputation to whole-genome sequence data in Holstein Friesian cattle. Genetics Selection Evolution, 2014, 46, 41.	1.2	128
24	Natural DNA variation at candidate loci is associated with potato chip color, tuber starch content, yield and starch yield. Theoretical and Applied Genetics, 2008, 116, 1167-1181.	1.8	121
25	Using Partial Least Squares Regression, Factorial Regression, and AMMI Models for Interpreting Genotype Ã— Environment Interaction. Crop Science, 1999, 39, 955-967.	0.8	120
26	Genetic Analysis of Variation in Gene Expression in Arabidopsis thaliana. Genetics, 2005, 171, 1267-1275.	1.2	116
27	Mapping QTLs and QTLÂÃ—Âenvironment interaction for CIMMYT maize drought stress program using factorial regression and partial least squares methods. Theoretical and Applied Genetics, 2006, 112, 1009-1023.	1.8	114
28	Natural Variation for Seed Longevity and Seed Dormancy Are Negatively Correlated in Arabidopsis Â Â. Plant Physiology, 2012, 160, 2083-2092.	2.3	114
29	QTL analysis and QTL-based prediction of flowering phenology in recombinant inbred lines of barley. Journal of Experimental Botany, 2005, 56, 967-976.	2.4	112
30	Population structure and linkage disequilibrium unravelled in tetraploid potato. Theoretical and Applied Genetics, 2010, 121, 1151-1170.	1.8	107
31	Genomic prediction using imputed whole-genome sequence data in Holstein Friesian cattle. Genetics Selection Evolution, 2015, 47, 71.	1.2	104
32	Association mapping of quality traits in potato (Solanum tuberosum L.). Euphytica, 2008, 161, 47-60.	0.6	98
33	Modelling spatial trends in sorghum breeding field trials using a two-dimensional P-spline mixed model. Theoretical and Applied Genetics, 2017, 130, 1375-1392.	1.8	92
34	Statistical models for genotype by environment data: from conventional ANOVA models to eco-physiological QTL models. Australian Journal of Agricultural Research, 2005, 56, 883.	1.5	91
35	Predicting Responses in Multiple Environments: Issues in Relation to Genotype Ã— Environment Interactions. Crop Science, 2016, 56, 2210-2222.	0.8	91
36	Association mapping of leaf traits, flowering time, and phytate content in Brassica rapa. Genome, 2007, 50, 963-973.	0.9	89

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37	SPICY: towards automated phenotyping of large pepper plants in the greenhouse. Functional Plant Biology, 2012, 39, 870.	1.1	86
38	A correlation network approach to metabolic data analysis for tomato fruits. Euphytica, 2008, 161, 181.	0.6	79
39	QTLs for barley yield adaptation to Mediterranean environments in the 'Nure'×'Tremois' biparental population. Euphytica, 2014, 197, 73-86.	0.6	74
40	Determinants of barley grain yield in a wide range of Mediterranean environments. Field Crops Research, 2011, 120, 169-178.	2.3	73
41	Genetic variability in duration of pre-heading phases and relationships with leaf appearance and tillering dynamics in a barley population. Field Crops Research, 2009, 113, 95-104.	2.3	68
42	Identification of agronomically important QTL in tetraploid potato cultivars using a marker–trait association analysis. Theoretical and Applied Genetics, 2014, 127, 731-748.	1.8	66
43	Combining Crop Growth Modeling and Statistical Genetic Modeling to Evaluate Phenotyping Strategies. Frontiers in Plant Science, 2019, 10, 1491.	1.7	65
44	On the increase of predictive performance with high-level data fusion. Analytica Chimica Acta, 2011, 705, 41-47.	2.6	59
45	Reconstruction of Genome Ancestry Blocks in Multiparental Populations. Genetics, 2015, 200, 1073-1087.	1.2	59
46	Modelling expectation and variance for genotype by environment data. Heredity, 1997, 79, 162-171.	1.2	58
47	Gene Regulatory Networks from Multifactorial Perturbations Using Graphical Lasso: Application to the DREAM4 Challenge. PLoS ONE, 2010, 5, e14147.	1.1	54
48	Imputation to whole-genome sequence using multiple pig populations and its use in genome-wide association studies. Genetics Selection Evolution, 2019, 51, 2.	1.2	54
49	Multiplicative Interaction in Generalized Linear Models. Biometrics, 1995, 51, 1017.	0.8	53
50	Gene and QTL detection in a three-way barley cross under selection by a mixed model with kinship information using SNPs. Theoretical and Applied Genetics, 2011, 122, 1605-1616.	1.8	53
51	Genetic control of pre-heading phases and other traits related to development in a double-haploid barley (Hordeum vulgare L.) population. Field Crops Research, 2010, 119, 36-47.	2.3	51
52	Genome-Wide Association Mapping for Kernel and Malting Quality Traits Using Historical European Barley Records. PLoS ONE, 2014, 9, e110046.	1.1	51
53	Modelling of Genotype by Environment Interaction and Prediction of Complex Traits across Multiple Environments as a Synthesis of Crop Growth Modelling, Genetics and Statistics. , 2016, , 55-82.		51
54	Exome sequences and multi‐environment field trials elucidate the genetic basis of adaptation in barley. Plant Journal, 2019, 99, 1172-1191.	2.8	50

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55	Multi-trait and multi-environment QTL analyses of yield and a set of physiological traits in pepper. Theoretical and Applied Genetics, 2013, 126, 2597-2625.	1.8	48
56	Genomic Prediction of Grain Yield and Drought-Adaptation Capacity in Sorghum Is Enhanced by Multi-Trait Analysis. Frontiers in Plant Science, 2019, 10, 997.	1.7	48
57	Interpreting Treatment Ã— Environment Interaction in Agronomy Trials. Agronomy Journal, 2001, 93, 949-960.	0.9	47
58	A Weighted AMMI Algorithm to Study Genotypeâ€byâ€Environment Interaction and QTLâ€byâ€Environment Interaction. Crop Science, 2014, 54, 1555-1570.	0.8	47
59	Statistical epistasis between candidate gene alleles for complex tuber traits in an association mapping population of tetraploid potato. Theoretical and Applied Genetics, 2010, 121, 1303-1310.	1.8	46
60	CGIAR modeling approaches for resourceâ€constrained scenarios: I. Accelerating crop breeding for a changing climate. Crop Science, 2020, 60, 547-567.	0.8	45
61	Reciprocal cybrids reveal how organellar genomes affect plant phenotypes. Nature Plants, 2020, 6, 13-21.	4.7	40
62	Calibration of Multivariate Scatter plots for Exploratory Analysis of Relations Within and Between Sets of Variables in Genomic Research. Biometrical Journal, 2005, 47, 863-879.	0.6	39
63	Using crop growth model stress covariates and AMMI decomposition to better predict genotype-by-environment interactions. Theoretical and Applied Genetics, 2019, 132, 3399-3411.	1.8	38
64	The establishment of â€˜essential derivationâ€™ among rose varieties, using AFLP. Theoretical and Applied Genetics, 2004, 109, 1718-1725.	1.8	37
65	Accurate Genotype Imputation in Multiparental Populations from Low-Coverage Sequence. Genetics, 2018, 210, 71-82.	1.2	37
66	A New Method to Infer Causal Phenotype Networks Using QTL and Phenotypic Information. PLoS ONE, 2014, 9, e103997.	1.1	35
67	Natural variation of YELLOW SEEDLING1 affects photosynthetic acclimation of Arabidopsis thaliana. Nature Communications, 2017, 8, 1421.	5.8	35
68	Genes and gene clusters related to genotype and drought-induced variation in saccharification potential, lignin content and wood anatomical traits in Populus nigraâ€. Tree Physiology, 2018, 38, 320-339.	1.4	35
69	The genetic and functional analysis of flavor in commercial tomato: the <i>FLORAL4</i> gene underlies a QTL for floral aroma volatiles in tomato fruit. Plant Journal, 2020, 103, 1189-1204.	2.8	35
70	Imputation of 3 million SNPs in the Arabidopsis regional mapping population. Plant Journal, 2020, 102, 872-882.	2.8	34
71	Significance testing and genomic inflation factor using highâ€density genotypes or wholeâ€genome sequence data. Journal of Animal Breeding and Genetics, 2019, 136, 418-429.	0.8	33
72	From QTLs to Adaptation Landscapes: Using Genotype-To-Phenotype Models to Characterize GÃ—E Over Time. Frontiers in Plant Science, 2019, 10, 1540.	1.7	33

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73	Metabolomics reveals organ-specific metabolic rearrangements during early tomato seedling development. Metabolomics, 2014, 10, 958-974.	1.4	32
74	Improvement of Predictive Ability by Uniform Coverage of the Target Genetic Space. G3: Genes, Genomes, Genetics, 2016, 6, 3733-3747.	0.8	32
75	How do the type of QTL effect and the form of the residual term influence QTL detection in multi-parent populations? A case study in the maize EU-NAM population. Theoretical and Applied Genetics, 2017, 130, 1753-1764.	1.8	32
76	Mixed model approaches for the identification of QTLs within a maize hybrid breeding program. Theoretical and Applied Genetics, 2010, 120, 429-440.	1.8	31
77	Development of Genomic Prediction in Sorghum. Crop Science, 2018, 58, 690-700.	0.8	31
78	Variation in Broccoli Cultivar Phytochemical Content under Organic and Conventional Management Systems: Implications in Breeding for Nutrition. PLoS ONE, 2014, 9, e95683.	1.1	31
79	Combining pedigree and genomic information to improve prediction quality: an example in sorghum. Theoretical and Applied Genetics, 2019, 132, 2055-2067.	1.8	30
80	Back to Acid Soil Fields: The Citrate Transporter SbMATE Is a Major Asset for Sustainable Grain Yield for Sorghum Cultivated on Acid Soils. G3: Genes, Genomes, Genetics, 2016, 6, 475-484.	0.8	29
81	Dynamics of senescence-related QTLs in potato. Euphytica, 2012, 183, 289-302.	0.6	28
82	Natural Variation in Portuguese Common Bean Germplasm Reveals New Sources of Resistance Against *Fusarium oxysporum* f. sp. *phaseoli* and Resistance-Associated Candidate Genes. Phytopathology, 2020, 110, 633-647.	1.1	28
83	Genetic and QTL analyses of yield and a set of physiological traits in pepper. Euphytica, 2013, 190, 181-201.	0.6	25
84	Genotype–phenotype modeling considering intermediate level of biological variation: a case study involving sensory traits, metabolites and QTLs in ripe tomatoes. Molecular BioSystems, 2015, 11, 3101-3110.	2.9	25
85	Dietary Intakes of Vegetable Protein, Folate, and Vitamins B-6 and B-12 Are Partially Correlated with Physical Functioning of Dutch Older Adults Using Copula Graphical Models. Journal of Nutrition, 2020, 150, 634-643.	1.3	24
86	A mixed model QTL analysis for a complex cross population consisting of a half diallel of two-way hybrids in Arabidopsis thaliana: analysis of simulated data. Euphytica, 2008, 161, 107-114.	0.6	23
87	Statistical aspects of essential derivation, with illustrations based on lettuce and barley. Euphytica, 2004, 137, 129-137.	0.6	22
88	New Figures of Merit for Comprehensive Functional Genomics Data: The Metabolomics Case. Analytical Chemistry, 2011, 83, 3267-3274.	3.2	22
89	Improving Hierarchical Clustering of Genotypic Data via Principal Component Analysis. Crop Science, 2013, 53, 1546-1554.	0.8	22
90	QTL-based analysis of genotype-by-environment interaction for grain yield of rice in stress and non-stress environments. Euphytica, 2007, 156, 213-226.	0.6	21

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91	Another Look at Bayesian Analysis of AMMI Models for Genotype-Environment Data. Journal of Agricultural, Biological, and Environmental Statistics, 2014, 19, 240.	0.7	21
92	Genome-wide screening for cis-regulatory variation using a classical diallel crossing scheme. Nucleic Acids Research, 2006, 34, 3677-3686.	6.5	20
93	Maximizing genetic differentiation in core collections by PCA-based clustering of molecular marker data. Theoretical and Applied Genetics, 2013, 126, 763-772.	1.8	20
94	Genome-wide association study for kernel composition and flour pasting behavior in wholemeal maize flour. BMC Plant Biology, 2019, 19, 123.	1.6	19
95	Physiological adaptive traits are a potential allele reservoir for maize genetic progress under challenging conditions. Nature Communications, 2022, 13, .	5.8	19
96	Genetic diversity and linkage disequilibrium analysis in elite sugar beet breeding lines and wild beet accessions. Theoretical and Applied Genetics, 2014, 127, 559-571.	1.8	18
97	Understanding the Effectiveness of Genomic Prediction in Tetraploid Potato. Frontiers in Plant Science, 2021, 12, 672417.	1.7	18
98	Phenomics data processing: A plot-level model for repeated measurements to extract the timing of key stages and quantities at defined time points. Field Crops Research, 2021, 274, 108314.	2.3	18
99	A comparison of population types used for QTL mapping in *Arabidopsis thaliana*. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 185-188.	0.4	17
100	Determinants of barley grain yield in drought-prone Mediterranean environments. Italian Journal of Agronomy, 2013, 8, 1.	0.4	17
101	Constraint-based probabilistic learning of metabolic pathways from tomato volatiles. Metabolomics, 2009, 5, 419-428.	1.4	16
102	Codominant scoring of AFLP in association panels. Theoretical and Applied Genetics, 2010, 121, 337-351.	1.8	15
103	Use of Two-Part Regression Calibration Model to Correct for Measurement Error in Episodically Consumed Foods in a Single-Replicate Study Design: EPIC Case Study. PLoS ONE, 2014, 9, e113160.	1.1	15
104	Broccoli Cultivar Performance under Organic and Conventional Management Systems and Implications for Crop Improvement. Crop Science, 2014, 54, 1539-1554.	0.8	15
105	Phenotypic Analyses of Multi-Environment Data for Two Diverse Tetraploid Potato Collections: Comparing an Academic Panel with an Industrial Panel. Potato Research, 2011, 54, 157-181.	1.2	14
106	A General Modeling Framework for Genome Ancestral Origins in Multiparental Populations. Genetics, 2014, 198, 87-101.	1.2	14
107	Intercontinental prediction of soybean phenology via hybrid ensemble of knowledge-based and data-driven models. In Silico Plants, 2021, 3, .	0.8	14
108	Multi-environment analysis of sorghum breeding trials using additive and dominance genomic relationships. Theoretical and Applied Genetics, 2020, 133, 1009-1018.	1.8	13

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109	Common bean SNP alleles and candidate genes affecting photosynthesis under contrasting water regimes. Horticulture Research, 2021, 8, 4.	2.9	13
110	The use of general and specific combining abilities in a context of gene expression relevant to plant breeding. Euphytica, 2008, 161, 115-122.	0.6	12
111	A diversity of resistance sources to Fusarium oxysporum f. sp. pisi found within grass pea germplasm. Plant and Soil, 2021, 463, 19-38.	1.8	12
112	Grain Yield Variation in Malting Barley Cultivars in Uruguay and Its Consequences for the Design of a Trials Network. Crop Science, 2008, 48, 167-180.	0.8	11
113	Homoplasy corrected estimation of genetic similarity from AFLP bands, and the effect of the number of bands on the precision of estimation. Theoretical and Applied Genetics, 2009, 119, 397-416.	1.8	11
114	Construction of Genetic Linkage Maps in Multiparental Populations. Genetics, 2019, 212, 1031-1044.	1.2	11
115	QTL detection in a pedigreed breeding population of diploid potato. Euphytica, 2020, 216, 1.	0.6	10
116	Multi-parent multi-environment QTL analysis: an illustration with the EU-NAM Flint population. Theoretical and Applied Genetics, 2020, 133, 2627-2638.	1.8	10
117	Genotype by Environment Interaction and Adaptation. , 2018, , 1-44.		10
118	Optimal Plot Dimensions for Performance Testing of Hybrid Potato in the Field. Potato Research, 2022, 65, 417-434.	1.2	10
119	A two-stage approach for the spatio-temporal analysis of high-throughput phenotyping data. Scientific Reports, 2022, 12, 3177.	1.6	10
120	Penalized regression techniques for modeling relationships between metabolites and tomato taste attributes. Euphytica, 2012, 183, 379-387.	0.6	9
121	Evaluation of a two‐part regression calibration to adjust for dietary exposure measurement error in the Cox proportional hazards model: A simulation study. Biometrical Journal, 2016, 58, 766-782.	0.6	9
122	Estimation of metabolite networks with regard to a specific covariable: applications to plant and human data. Metabolomics, 2017, 13, 129.	1.4	9
123	An IBD-based mixed model approach for QTL mapping in multiparental populations. Theoretical and Applied Genetics, 2021, 134, 3643-3660.	1.8	9
124	Lessons from a GWAS study of a wheat pre-breeding program: pyramiding resistance alleles to Fusarium crown rot. Theoretical and Applied Genetics, 2021, 134, 897-908.	1.8	9
125	Genetic research in a public–private research consortium: prospects for indirect use of Elite breeding germplasm in academic research. Euphytica, 2008, 161, 293-300.	0.6	8
126	Assessment of heterosis in two Arabidopsis thaliana common-reference mapping populations. PLoS ONE, 2018, 13, e0205564.	1.1	8

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127	Recursive Algorithms for Modeling Genomic Ancestral Origins in a Fixed Pedigree. G3: Genes, Genomes, Genetics, 2018, 8, 3231-3245.	0.8	8
128	Semantic concept schema of the linear mixed model of experimental observations. Scientific Data, 2020, 7, 70.	2.4	8
129	Genotype-specific P-spline response surfaces assist interpretation of regional wheat adaptation to climate change. In Silico Plants, 2021, 3, .	0.8	8
130	Identification of environment types and adaptation zones with self-organizing maps; applications to sunflower multi-environment data in Europe. Theoretical and Applied Genetics, 2022, 135, 2059-2082.	1.8	8
131	Understanding the genetic basis of potato development using a multi-trait QTL analysis. Euphytica, 2015, 204, 229-241.	0.6	7
132	A model-based approach to analyse genetic variation in potato using standard cultivars and a segregating population. I. Canopy cover dynamics. Field Crops Research, 2019, 242, 107581.	2.3	7
133	Alleles to Enhance Antioxidant Content in Maizeâ€"A Genome-Wide Association Approach. Journal of Agricultural and Food Chemistry, 2020, 68, 4051-4061.	2.4	7
134	The influence of QTL allelic diversity on QTL detection in multi-parent populations: a simulation study in sugar beet. BMC Genomic Data, 2021, 22, 4.	0.7	7
135	Little heterosis found in diploid hybrid potato: The genetic underpinnings of a new hybrid crop. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	7
136	The potential of probabilistic graphical models in linkage map construction. Theoretical and Applied Genetics, 2017, 130, 433-444.	1.8	6
137	A model-based approach to analyse genetic variation in potato using standard cultivars and a segregating population. II. Tuber bulking and resource use efficiency. Field Crops Research, 2019, 242, 107582.	2.3	6
138	Volatilomeâ€"Genome-Wide Association Study on Wholemeal Maize Flour. Journal of Agricultural and Food Chemistry, 2020, 68, 7809-7818.	2.4	6
139	Reconstruction of Networks with Direct and Indirect Genetic Effects. Genetics, 2020, 214, 781-807.	1.2	6
140	Yield dissection models to improve yield: a case study in tomato. In Silico Plants, 2021, 3, .	0.8	6
141	A method for sensitivity analysis to assess the effects of measurement error in multiple exposure variables using external validation data. BMC Medical Research Methodology, 2016, 16, 139.	1.4	5
142	Genotype by Environment Interaction and Adaptation. , 2019, , 29-71.		5
143	An analysis of simulated yield data for pepper shows how genotype Ã— environment interaction in yield can be understood in terms of yield components and their QTLs. Crop Science, 2021, 61, 1826-1842.	0.8	5
144	Grass pea natural variation reveals oligogenic resistance to <i>Fusarium oxysporum</i> f. sp. <i>pisi</i>. Plant Genome, 2021, 14, e20154.	1.6	5

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145	Automated estimation of leaf area development in sweet pepper plants from image analysis. Functional Plant Biology, 2015, 42, 486.	1.1	4
146	Improvement of protoplast regeneration from a recalcitrant inbred line of Brassica oleracea: a morphogenic analysis. Plant Science, 1994, 98, 87-95.	1.7	3
147	How to dissect complex traits and how to choose suitable mapping resources for system genetics?. Physics of Life Reviews, 2015, 13, 186-189.	1.5	3
148	Genomic prediction for broad and specific adaptation in sorghum accommodating differential variances of SNP effects. Crop Science, 2020, 60, 2328-2342.	0.8	3
149	Improving Genomic Prediction Using High-Dimensional Secondary Phenotypes. Frontiers in Genetics, 2021, 12, 667358.	1.1	3
150	Review and simulation of homoplasy and collision in AFLP. Euphytica, 2012, 183, 389-400.	0.6	2
151	Validation of accelerometer for measuring physical activity in free-living individuals. Baltic Journal of Health and Physical Activity, 2018, 10, 7-21.	0.2	2
152	Special issue in honour of Prof. Reto J. StrasserÂ-ÂPhenotyping with fast fluorescence sensors approximates yield component measurements in pepper (Capsicum annuum L.). Photosynthetica, 2020, 58, 622-637.	0.9	1
153	XIVth meeting of the Eucarpia Section â€˜Biometrics in Plant Breedingâ€™. Euphytica, 2012, 183, 275-276.	0.6	0
154	Parameter estimation in tree graph metabolic networks. PeerJ, 2016, 4, e2417.	0.9	0
155	Training Set Construction for Genomic Prediction in Auto-Tetraploids: An Example in Potato. Frontiers in Plant Science, 2021, 12, 771075.	1.7	0
156	psBLUP: incorporating marker proximity for improving genomic prediction accuracy. Euphytica, 2022, 218, 1.	0.6	0