

# Fred A Van Eeuwijk

## List of Publications by Year in descending order

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156  
papers

8,676  
citations

43973

48  
h-index

54797

84  
g-index

169  
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169  
docs citations

169  
times ranked

8883  
citing authors

#	ARTICLE	IF	CITATIONS
1	Optimal Plot Dimensions for Performance Testing of Hybrid Potato in the Field. <i>Potato Research</i> , 2022, 65, 417-434.	1.2	10
2	A two-stage approach for the spatio-temporal analysis of high-throughput phenotyping data. <i>Scientific Reports</i> , 2022, 12, 3177.	1.6	10
3	psBLUP: incorporating marker proximity for improving genomic prediction accuracy. <i>Euphytica</i> , 2022, 218, 1.	0.6	0
4	Little heterosis found in diploid hybrid potato: The genetic underpinnings of a new hybrid crop. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
5	Identification of environment types and adaptation zones with self-organizing maps; applications to sunflower multi-environment data in Europe. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2059-2082.	1.8	8
6	Physiological adaptive traits are a potential allele reservoir for maize genetic progress under challenging conditions. <i>Nature Communications</i> , 2022, 13, .	5.8	19
7	Yield dissection models to improve yield: a case study in tomato. <i>In Silico Plants</i> , 2021, 3, .	0.8	6
8	Common bean SNP alleles and candidate genes affecting photosynthesis under contrasting water regimes. <i>Horticulture Research</i> , 2021, 8, 4.	2.9	13
9	Intercontinental prediction of soybean phenology via hybrid ensemble of knowledge-based and data-driven models. <i>In Silico Plants</i> , 2021, 3, .	0.8	14
10	A diversity of resistance sources to <i>Fusarium oxysporum</i> f. sp. <i>pisii</i> found within grass pea germplasm. <i>Plant and Soil</i> , 2021, 463, 19-38.	1.8	12
11	The influence of QTL allelic diversity on QTL detection in multi-parent populations: a simulation study in sugar beet. <i>BMC Genomic Data</i> , 2021, 22, 4.	0.7	7
12	An analysis of simulated yield data for pepper shows how genotype × environment interaction in yield can be understood in terms of yield components and their QTLs. <i>Crop Science</i> , 2021, 61, 1826-1842.	0.8	5
13	Improving Genomic Prediction Using High-Dimensional Secondary Phenotypes. <i>Frontiers in Genetics</i> , 2021, 12, 667358.	1.1	3
14	Genotype-specific P-spline response surfaces assist interpretation of regional wheat adaptation to climate change. <i>In Silico Plants</i> , 2021, 3, .	0.8	8
15	Understanding the Effectiveness of Genomic Prediction in Tetraploid Potato. <i>Frontiers in Plant Science</i> , 2021, 12, 672417.	1.7	18
16	An IBD-based mixed model approach for QTL mapping in multiparental populations. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3643-3660.	1.8	9
17	Grass pea natural variation reveals oligogenic resistance to <i>Fusarium oxysporum</i> f. sp. <i>pisii</i> . <i>Plant Genome</i> , 2021, 14, e20154.	1.6	5
18	Phenomics data processing: A plot-level model for repeated measurements to extract the timing of key stages and quantities at defined time points. <i>Field Crops Research</i> , 2021, 274, 108314.	2.3	18

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19	Lessons from a GWAS study of a wheat pre-breeding program: pyramiding resistance alleles to Fusarium crown rot. <i>Theoretical and Applied Genetics</i> , 2021, 134, 897-908.	1.8	9
20	Training Set Construction for Genomic Prediction in Auto-Tetraploids: An Example in Potato. <i>Frontiers in Plant Science</i> , 2021, 12, 771075.	1.7	0
21	Natural Variation in Portuguese Common Bean Germplasm Reveals New Sources of Resistance Against <i>Fusarium oxysporum</i> f. sp. <i>phaseoli</i> and Resistance-Associated Candidate Genes. <i>Phytopathology</i> , 2020, 110, 633-647.	1.1	28
22	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. <i>Journal of Nutrition</i> , 2020, 150, 634-643.	1.3	24
23	Imputation of 3 million SNPs in the Arabidopsis regional mapping population. <i>Plant Journal</i> , 2020, 102, 872-882.	2.8	34
24	Multi-environment analysis of sorghum breeding trials using additive and dominance genomic relationships. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1009-1018.	1.8	13
25	QTL detection in a pedigree breeding population of diploid potato. <i>Euphytica</i> , 2020, 216, 1.	0.6	10
26	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. <i>Plant Journal</i> , 2020, 103, 1189-1204.	2.8	35
27	Genomic prediction for broad and specific adaptation in sorghum accommodating differential variances of SNP effects. <i>Crop Science</i> , 2020, 60, 2328-2342.	0.8	3
28	Multi-parent multi-environment QTL analysis: an illustration with the EU-NAM Flint population. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2627-2638.	1.8	10
29	Volatilome—Genome-Wide Association Study on Wholemeal Maize Flour. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 7809-7818.	2.4	6
30	Alleles to Enhance Antioxidant Content in Maize—A Genome-Wide Association Approach. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 4051-4061.	2.4	7
31	Semantic concept schema of the linear mixed model of experimental observations. <i>Scientific Data</i> , 2020, 7, 70.	2.4	8
32	Reciprocal hybrids reveal how organellar genomes affect plant phenotypes. <i>Nature Plants</i> , 2020, 6, 13-21.	4.7	40
33	CGIAR modeling approaches for resource-constrained scenarios: I. Accelerating crop breeding for a changing climate. <i>Crop Science</i> , 2020, 60, 547-567.	0.8	45
34	Reconstruction of Networks with Direct and Indirect Genetic Effects. <i>Genetics</i> , 2020, 214, 781-807.	1.2	6
35	Special issue in honour of Prof. Reto J. Strasser—Phenotyping with fast fluorescence sensors approximates yield component measurements in pepper ( <i>Capsicum annuum</i> L.). <i>Photosynthetica</i> , 2020, 58, 622-637.	0.9	1
36	Modelling strategies for assessing and increasing the effectiveness of new phenotyping techniques in plant breeding. <i>Plant Science</i> , 2019, 282, 23-39.	1.7	173

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37	Genomic Prediction of Grain Yield and Drought-Adaptation Capacity in Sorghum Is Enhanced by Multi-Trait Analysis. <i>Frontiers in Plant Science</i> , 2019, 10, 997.	1.7	48
38	A model-based approach to analyse genetic variation in potato using standard cultivars and a segregating population. II. Tuber bulking and resource use efficiency. <i>Field Crops Research</i> , 2019, 242, 107582.	2.3	6
39	A model-based approach to analyse genetic variation in potato using standard cultivars and a segregating population. I. Canopy cover dynamics. <i>Field Crops Research</i> , 2019, 242, 107581.	2.3	7
40	Using crop growth model stress covariates and AMMI decomposition to better predict genotype-by-environment interactions. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3399-3411.	1.8	38
41	Imputation to whole-genome sequence using multiple pig populations and its use in genome-wide association studies. <i>Genetics Selection Evolution</i> , 2019, 51, 2.	1.2	54
42	Exome sequences and multi-environment field trials elucidate the genetic basis of adaptation in barley. <i>Plant Journal</i> , 2019, 99, 1172-1191.	2.8	50
43	Significance testing and genomic inflation factor using high-density genotypes or whole-genome sequence data. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 418-429.	0.8	33
44	Construction of Genetic Linkage Maps in Multiparental Populations. <i>Genetics</i> , 2019, 212, 1031-1044.	1.2	11
45	Genomic prediction of maize yield across European environmental conditions. <i>Nature Genetics</i> , 2019, 51, 952-956.	9.4	157
46	Combining pedigree and genomic information to improve prediction quality: an example in sorghum. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2055-2067.	1.8	30
47	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911.	9.4	230
48	Genotype by Environment Interaction and Adaptation. , 2019, , 29-71.		5
49	Genome-wide association study for kernel composition and flour pasting behavior in wholemeal maize flour. <i>BMC Plant Biology</i> , 2019, 19, 123.	1.6	19
50	Combining Crop Growth Modeling and Statistical Genetic Modeling to Evaluate Phenotyping Strategies. <i>Frontiers in Plant Science</i> , 2019, 10, 1491.	1.7	65
51	From QTLs to Adaptation Landscapes: Using Genotype-To-Phenotype Models to Characterize G×E Over Time. <i>Frontiers in Plant Science</i> , 2019, 10, 1540.	1.7	33
52	Correcting for spatial heterogeneity in plant breeding experiments with P-splines. <i>Spatial Statistics</i> , 2018, 23, 52-71.	0.9	180
53	Assessment of heterosis in two <i>Arabidopsis thaliana</i> common-reference mapping populations. <i>PLoS ONE</i> , 2018, 13, e0205564.	1.1	8
54	Recursive Algorithms for Modeling Genomic Ancestral Origins in a Fixed Pedigree. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3231-3245.	0.8	8

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55	Genes and gene clusters related to genotype and drought-induced variation in saccharification potential, lignin content and wood anatomical traits in <i>Populus nigra</i> . <i>Tree Physiology</i> , 2018, 38, 320-339.	1.4	35
56	Accurate Genotype Imputation in Multiparental Populations from Low-Coverage Sequence. <i>Genetics</i> , 2018, 210, 71-82.	1.2	37
57	Development of Genomic Prediction in Sorghum. <i>Crop Science</i> , 2018, 58, 690-700.	0.8	31
58	Genotype by Environment Interaction and Adaptation. , 2018, , 1-44.		10
59	Validation of accelerometer for measuring physical activity in free-living individuals. <i>Baltic Journal of Health and Physical Activity</i> , 2018, 10, 7-21.	0.2	2
60	Modelling spatial trends in sorghum breeding field trials using a two-dimensional P-spline mixed model. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1375-1392.	1.8	92
61	The potential of probabilistic graphical models in linkage map construction. <i>Theoretical and Applied Genetics</i> , 2017, 130, 433-444.	1.8	6
62	Estimation of metabolite networks with regard to a specific covariable: applications to plant and human data. <i>Metabolomics</i> , 2017, 13, 129.	1.4	9
63	Natural variation of <i>YELLOW SEEDLING1</i> affects photosynthetic acclimation of <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2017, 8, 1421.	5.8	35
64	Evaluation of LD decay and various LD-decay estimators in simulated and SNP-array data of tetraploid potato. <i>Theoretical and Applied Genetics</i> , 2017, 130, 123-135.	1.8	158
65	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. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1753-1764.	1.8	32
66	Genetic architecture of plant stress resistance: multi-trait genome-wide association mapping. <i>New Phytologist</i> , 2017, 213, 1346-1362.	3.5	144
67	Predicting Responses in Multiple Environments: Issues in Relation to Genotype $\times$ Environment Interactions. <i>Crop Science</i> , 2016, 56, 2210-2222.	0.8	91
68	What Should Students in Plant Breeding Know About the Statistical Aspects of Genotype $\times$ Environment Interactions?. <i>Crop Science</i> , 2016, 56, 2119-2140.	0.8	175
69	Genome-wide analysis of yield in Europe: allelic effects as functions of drought and heat scenarios. <i>Plant Physiology</i> , 2016, 172, pp.00621.2016.	2.3	140
70	Improvement of Predictive Ability by Uniform Coverage of the Target Genetic Space. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3733-3747.	0.8	32
71	A method for sensitivity analysis to assess the effects of measurement error in multiple exposure variables using external validation data. <i>BMC Medical Research Methodology</i> , 2016, 16, 139.	1.4	5
72	Evaluation of a two-part regression calibration to adjust for dietary exposure measurement error in the Cox proportional hazards model: A simulation study. <i>Biometrical Journal</i> , 2016, 58, 766-782.	0.6	9

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73	Improved batch correction in untargeted MS-based metabolomics. <i>Metabolomics</i> , 2016, 12, 88.	1.4	167
74	Back to Acid Soil Fields: The Citrate Transporter SbMATE Is a Major Asset for Sustainable Grain Yield for Sorghum Cultivated on Acid Soils. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 475-484.	0.8	29
75	Modelling of Genotype by Environment Interaction and Prediction of Complex Traits across Multiple Environments as a Synthesis of Crop Growth Modelling, <i>Genetics and Statistics</i> , , 2016, , 55-82.		51
76	Parameter estimation in tree graph metabolic networks. <i>PeerJ</i> , 2016, 4, e2417.	0.9	0
77	Automated estimation of leaf area development in sweet pepper plants from image analysis. <i>Functional Plant Biology</i> , 2015, 42, 486.	1.1	4
78	Marker-Based Estimation of Heritability in Immortal Populations. <i>Genetics</i> , 2015, 199, 379-398.	1.2	192
79	Root phenotyping: from component trait in the lab to breeding: Table 1.. <i>Journal of Experimental Botany</i> , 2015, 66, 5389-5401.	2.4	163
80	How to dissect complex traits and how to choose suitable mapping resources for system genetics?. <i>Physics of Life Reviews</i> , 2015, 13, 186-189.	1.5	3
81	Understanding the genetic basis of potato development using a multi-trait QTL analysis. <i>Euphytica</i> , 2015, 204, 229-241.	0.6	7
82	Genomic prediction using imputed whole-genome sequence data in Holstein Friesian cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 71.	1.2	104
83	Reconstruction of Genome Ancestry Blocks in Multiparental Populations. <i>Genetics</i> , 2015, 200, 1073-1087.	1.2	59
84	Genotype-phenotype modeling considering intermediate level of biological variation: a case study involving sensory traits, metabolites and QTLs in ripe tomatoes. <i>Molecular BioSystems</i> , 2015, 11, 3101-3110.	2.9	25
85	A New Method to Infer Causal Phenotype Networks Using QTL and Phenotypic Information. <i>PLoS ONE</i> , 2014, 9, e103997.	1.1	35
86	Genome-Wide Association Mapping for Kernel and Malting Quality Traits Using Historical European Barley Records. <i>PLoS ONE</i> , 2014, 9, e110046.	1.1	51
87	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. <i>PLoS ONE</i> , 2014, 9, e113160.	1.1	15
88	A Weighted AMMI Algorithm to Study Genotype-by-Environment Interaction and QTL-by-Environment Interaction. <i>Crop Science</i> , 2014, 54, 1555-1570.	0.8	47
89	Broccoli Cultivar Performance under Organic and Conventional Management Systems and Implications for Crop Improvement. <i>Crop Science</i> , 2014, 54, 1539-1554.	0.8	15
90	A General Modeling Framework for Genome Ancestral Origins in Multiparental Populations. <i>Genetics</i> , 2014, 198, 87-101.	1.2	14

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91	Accuracy of imputation to whole-genome sequence data in Holstein Friesian cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 41.	1.2	128
92	Identification of agronomically important QTL in tetraploid potato cultivars using a marker-trait association analysis. <i>Theoretical and Applied Genetics</i> , 2014, 127, 731-748.	1.8	66
93	Genetic diversity and linkage disequilibrium analysis in elite sugar beet breeding lines and wild beet accessions. <i>Theoretical and Applied Genetics</i> , 2014, 127, 559-571.	1.8	18
94	Metabolomics reveals organ-specific metabolic rearrangements during early tomato seedling development. <i>Metabolomics</i> , 2014, 10, 958-974.	1.4	32
95	Another Look at Bayesian Analysis of AMMI Models for Genotype-Environment Data. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2014, 19, 240.	0.7	21
96	QTLs for barley yield adaptation to Mediterranean environments in the Nure-Tremois biparental population. <i>Euphytica</i> , 2014, 197, 73-86.	0.6	74
97	Variation in Broccoli Cultivar Phytochemical Content under Organic and Conventional Management Systems: Implications in Breeding for Nutrition. <i>PLoS ONE</i> , 2014, 9, e95683.	1.1	31
98	Multi-trait and multi-environment QTL analyses of yield and a set of physiological traits in pepper. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2597-2625.	1.8	48
99	Genetic and QTL analyses of yield and a set of physiological traits in pepper. <i>Euphytica</i> , 2013, 190, 181-201.	0.6	25
100	Quality of core collections for effective utilisation of genetic resources review, discussion and interpretation. <i>Theoretical and Applied Genetics</i> , 2013, 126, 289-305.	1.8	134
101	Maximizing genetic differentiation in core collections by PCA-based clustering of molecular marker data. <i>Theoretical and Applied Genetics</i> , 2013, 126, 763-772.	1.8	20
102	The statistical analysis of multi-environment data: modeling genotype-by-environment interaction and its genetic basis. <i>Frontiers in Physiology</i> , 2013, 4, 44.	1.3	349
103	Improving Hierarchical Clustering of Genotypic Data via Principal Component Analysis. <i>Crop Science</i> , 2013, 53, 1546-1554.	0.8	22
104	Determinants of barley grain yield in drought-prone Mediterranean environments. <i>Italian Journal of Agronomy</i> , 2013, 8, 1.	0.4	17
105	Natural Variation for Seed Longevity and Seed Dormancy Are Negatively Correlated in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2012, 160, 2083-2092.	2.3	114
106	SPICY: towards automated phenotyping of large pepper plants in the greenhouse. <i>Functional Plant Biology</i> , 2012, 39, 870.	1.1	86
107	Review and simulation of homoplasy and collision in AFLP. <i>Euphytica</i> , 2012, 183, 389-400.	0.6	2
108	Penalized regression techniques for modeling relationships between metabolites and tomato taste attributes. <i>Euphytica</i> , 2012, 183, 379-387.	0.6	9

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109	Dynamics of senescence-related QTLs in potato. <i>Euphytica</i> , 2012, 183, 289-302.	0.6	28
110	XIVth meeting of the Eucarpia Section "Biometrics in Plant Breeding". <i>Euphytica</i> , 2012, 183, 275-276.	0.6	0
111	New Figures of Merit for Comprehensive Functional Genomics Data: The Metabolomics Case. <i>Analytical Chemistry</i> , 2011, 83, 3267-3274.	3.2	22
112	On the increase of predictive performance with high-level data fusion. <i>Analytica Chimica Acta</i> , 2011, 705, 41-47.	2.6	59
113	Determinants of barley grain yield in a wide range of Mediterranean environments. <i>Field Crops Research</i> , 2011, 120, 169-178.	2.3	73
114	A comparison of population types used for QTL mapping in <i>Arabidopsis thaliana</i> . <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 185-188.	0.4	17
115	Gene and QTL detection in a three-way barley cross under selection by a mixed model with kinship information using SNPs. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1605-1616.	1.8	53
116	Phenotypic Analyses of Multi-Environment Data for Two Diverse Tetraploid Potato Collections: Comparing an Academic Panel with an Industrial Panel. <i>Potato Research</i> , 2011, 54, 157-181.	1.2	14
117	Analysis of natural allelic variation in <i>Arabidopsis</i> using a multiparent recombinant inbred line population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4488-4493.	3.3	137
118	Mixed model approaches for the identification of QTLs within a maize hybrid breeding program. <i>Theoretical and Applied Genetics</i> , 2010, 120, 429-440.	1.8	31
119	Codominant scoring of AFLP in association panels. <i>Theoretical and Applied Genetics</i> , 2010, 121, 337-351.	1.8	15
120	Population structure and linkage disequilibrium unravelled in tetraploid potato. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1151-1170.	1.8	107
121	Statistical epistasis between candidate gene alleles for complex tuber traits in an association mapping population of tetraploid potato. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1303-1310.	1.8	46
122	Detection and use of QTL for complex traits in multiple environments. <i>Current Opinion in Plant Biology</i> , 2010, 13, 193-205.	3.5	146
123	Gene Regulatory Networks from Multifactorial Perturbations Using Graphical Lasso: Application to the DREAM4 Challenge. <i>PLoS ONE</i> , 2010, 5, e14147.	1.1	54
124	Natural variation for seed dormancy in <i>Arabidopsis</i> is regulated by additive genetic and molecular pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4264-4269.	3.3	194
125	Genetic control of pre-heading phases and other traits related to development in a double-haploid barley ( <i>Hordeum vulgare</i> L.) population. <i>Field Crops Research</i> , 2010, 119, 36-47.	2.3	51
126	Modeling QTL for complex traits: detection and context for plant breeding. <i>Current Opinion in Plant Biology</i> , 2009, 12, 231-240.	3.5	153



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127	Constraint-based probabilistic learning of metabolic pathways from tomato volatiles. <i>Metabolomics</i> , 2009, 5, 419-428.	1.4	16
128	Homoplasmy corrected estimation of genetic similarity from AFLP bands, and the effect of the number of bands on the precision of estimation. <i>Theoretical and Applied Genetics</i> , 2009, 119, 397-416.	1.8	11
129	Genetic variability in duration of pre-heading phases and relationships with leaf appearance and tillering dynamics in a barley population. <i>Field Crops Research</i> , 2009, 113, 95-104.	2.3	68
130	The use of general and specific combining abilities in a context of gene expression relevant to plant breeding. <i>Euphytica</i> , 2008, 161, 115-122.	0.6	12
131	Genetic research in a public-private research consortium: prospects for indirect use of Elite breeding germplasm in academic research. <i>Euphytica</i> , 2008, 161, 293-300.	0.6	8
132	Association mapping of quality traits in potato ( <i>Solanum tuberosum</i> L.). <i>Euphytica</i> , 2008, 161, 47-60.	0.6	98
133	A multi-trait multi-environment QTL mixed model with an application to drought and nitrogen stress trials in maize ( <i>Zea mays</i> L.). <i>Euphytica</i> , 2008, 161, 241-257.	0.6	134
134	A mixed model QTL analysis for a complex cross population consisting of a half diallel of two-way hybrids in <i>Arabidopsis thaliana</i> : analysis of simulated data. <i>Euphytica</i> , 2008, 161, 107-114.	0.6	23
135	A correlation network approach to metabolic data analysis for tomato fruits. <i>Euphytica</i> , 2008, 161, 181.	0.6	79
136	Natural DNA variation at candidate loci is associated with potato chip color, tuber starch content, yield and starch yield. <i>Theoretical and Applied Genetics</i> , 2008, 116, 1167-1181.	1.8	121
137	Multi-environment QTL mixed models for drought stress adaptation in wheat. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1077-1091.	1.8	160
138	Grain Yield Variation in Malting Barley Cultivars in Uruguay and Its Consequences for the Design of a Trials Network. <i>Crop Science</i> , 2008, 48, 167-180.	0.8	11
139	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. <i>Genetics</i> , 2007, 177, 1801-1813.	1.2	201
140	Association mapping of leaf traits, flowering time, and phytate content in <i>Brassica rapa</i> . <i>Genome</i> , 2007, 50, 963-973.	0.9	89
141	QTL-based analysis of genotype-by-environment interaction for grain yield of rice in stress and non-stress environments. <i>Euphytica</i> , 2007, 156, 213-226.	0.6	21
142	Models for navigating biological complexity in breeding improved crop plants. <i>Trends in Plant Science</i> , 2006, 11, 587-593.	4.3	364
143	Mapping QTLs and QTL-environment interaction for CIMMYT maize drought stress program using factorial regression and partial least squares methods. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1009-1023.	1.8	114
144	Genome-wide screening for cis-regulatory variation using a classical diallel crossing scheme. <i>Nucleic Acids Research</i> , 2006, 34, 3677-3686.	6.5	20

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145	Calibration of Multivariate Scatter plots for Exploratory Analysis of Relations Within and Between Sets of Variables in Genomic Research. <i>Biometrical Journal</i> , 2005, 47, 863-879.	0.6	39
146	QTL analysis and QTL-based prediction of flowering phenology in recombinant inbred lines of barley. <i>Journal of Experimental Botany</i> , 2005, 56, 967-976.	2.4	112
147	Genetic Analysis of Variation in Gene Expression in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2005, 171, 1267-1275.	1.2	116
148	Statistical models for genotype by environment data: from conventional ANOVA models to eco-physiological QTL models. <i>Australian Journal of Agricultural Research</i> , 2005, 56, 883.	1.5	91
149	Statistical aspects of essential derivation, with illustrations based on lettuce and barley. <i>Euphytica</i> , 2004, 137, 129-137.	0.6	22
150	The establishment of "essential derivation"™ among rose varieties, using AFLP. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1718-1725.	1.8	37
151	Linkage Disequilibrium Mapping of Yield and Yield Stability in Modern Spring Barley Cultivars. <i>Genetics</i> , 2004, 168, 435-446.	1.2	375
152	Interpreting Treatment × Environment Interaction in Agronomy Trials. <i>Agronomy Journal</i> , 2001, 93, 949-960.	0.9	47
153	Using Partial Least Squares Regression, Factorial Regression, and AMMI Models for Interpreting Genotype × Environment Interaction. <i>Crop Science</i> , 1999, 39, 955-967.	0.8	120
154	Modelling expectation and variance for genotype by environment data. <i>Heredity</i> , 1997, 79, 162-171.	1.2	58
155	Multiplicative Interaction in Generalized Linear Models. <i>Biometrics</i> , 1995, 51, 1017.	0.8	53
156	Improvement of protoplast regeneration from a recalcitrant inbred line of <i>Brassica oleracea</i> : a morphogenic analysis. <i>Plant Science</i> , 1994, 98, 87-95.	1.7	3