Jeffrey B Endelman

List of Publications by Year
in descending order

39 papers	4,166 citations	304368 22 h-index	301761 39 g-index
47 all docs	47 docs citations	47 times ranked	4247 citing authors

#	ARTICLE	IF	CITATIONS
1	Ridge Regression and Other Kernels for Genomic Selection with R Package rrBLUP. Plant Genome, 2011, 4, 250-255.	1.6	1,588
2	Shrinkage Estimation of the Realized Relationship Matrix. G3: Genes, Genomes, Genetics, 2012, 2, 1405-1413.	0.8	420
3	Software for Genome€Wide Association Studies in Autopolyploids and Its Application to Potato. Plant Genome, 2016, 9, plantgenome2015.08.0073.	1.6	191
4	The USDA Barley Core Collection: Genetic Diversity, Population Structure, and Potential for Genome-Wide Association Studies. PLoS ONE, 2014, 9, e94688.	1.1	188
5	Genomic Predictability of Interconnected Biparental Maize Populations. Genetics, 2013, 194, 493-503.	1.2	180
6	LPmerge: an R package for merging genetic maps by linear programming. Bioinformatics, 2014, 30, 1623-1624.	1.8	140
7	Library analysis of SCHEMA-guided protein recombination. Protein Science, 2003, 12, 1686-1693.	3.1	138
8	Structure-Guided Recombination Creates an Artificial Family of Cytochromes P450. PLoS Biology, 2006, 4, e112.	2.6	133
9	Genetic Variance Partitioning and Genome-Wide Prediction with Allele Dosage Information in Autotetraploid Potato. Genetics, 2018, 209, 77-87.	1.2	117
10	The use of unbalanced historical data for genomic selection in an international wheat breeding program. Field Crops Research, 2013, 154, 12-22.	2.3	100
11	Optimal Design of Preliminary Yield Trials with Genome€Wide Markers. Crop Science, 2014, 54, 48-59.	0.8	100
12	Functional Evolution and Structural Conservation in Chimeric Cytochromes P450. Chemistry and Biology, 2004, 11, 309-318.	6.2	97
13	Genetic mapping with an inbred line-derived F2 population in potato. Theoretical and Applied Genetics, 2016, 129, 935-943.	1.8	74
14	Phased, chromosome-scale genome assemblies of tetraploid potato reveal a complex genome, transcriptome, and predicted proteome landscape underpinning genetic diversity. Molecular Plant, 2022, 15, 520-536.	3.9	72
15	Site-directed protein recombination as a shortest-path problem. Protein Engineering, Design and Selection, 2004, 17, 589-594.	1.0	70
16	Automated tetraploid genotype calling by hierarchical clustering. Theoretical and Applied Genetics, 2017, 130, 717-726.	1.8	61
17	Genomic Prediction of Autotetraploids; Influence of Relationship Matrices, Allele Dosage, and Continuous Genotyping Calls in Phenotype Prediction. G3: Genes, Genomes, Genetics, 2019, 9, 1189-1198.	0.8	60
18	FIELDimageR: An R package to analyze orthomosaic images from agricultural fieldÂtrials. The Plant Phenome Journal, 2020, 3, e20005.	1.0	58

#	ARTICLE	IF	CITATIONS
19	Genome-wide distribution of genetic diversity and linkage disequilibrium in a mass-selected population of maritime pine. BMC Genomics, 2014, 15, 171.	1.2	41
20	On the accuracy of genomic prediction models considering multi-trait and allele dosage in Urochloa spp. interspecific tetraploid hybrids. Molecular Breeding, 2019, 39, 1.	1.0	37
21	Association mapping of grain hardness, polyphenol oxidase, total phenolics, amylose content, and Î²-glucan in US barley breeding germplasm. Molecular Breeding, 2014, 34, 1229-1243.	1.0	35
22	SCHEMA-Guided Protein Recombination. Methods in Enzymology, 2004, 388, 35-42.	0.4	31
23	Impact of dominance effects on autotetraploid genomic prediction. Crop Science, 2020, 60, 656-665.	0.8	28
24	Haplotype reconstruction in connected tetraploid F1 populations. Genetics, 2021, 219, .	1.2	26
25	Impact of Dominance Effects on Autotetraploid Genomic Prediction. Crop Science, 2019, .	0.8	25
26	Pedigree Reconstruction with Genome-Wide Markers in Potato. American Journal of Potato Research, 2017, 94, 184-190.	0.5	19
27	QTL mapping in outbred tetraploid (and diploid) diallel populations. Genetics, 2021, 219, .	1.2	15
28	New algorithm improves fine structure of the barley consensus SNP map. BMC Genomics, 2011, 12, 407.	1.2	13
29	Expected Genotype Quality and Diploidized Marker Data from Genotyping‑by‑Sequencing of <i>Urochloa</i> spp. Tetraploids. Plant Genome, 2019, 12, 1-9.	1.6	13
30	Image‑based phenotyping and genetic analysis of potato skin set and color. Crop Science, 2020, 60, 202-210.	0.8	13
31	A New Decay Series for Organic Crop Production. Agronomy Journal, 2010, 102, 457-463.	0.9	11
32	Reliability of Measurement and Genotype Ã— Environment Interaction for Potato Specific Gravity. Crop Science, 2017, 57, 1966-1972.	0.8	11
33	Evaluation of genetic diversity among Russet potato clones and varieties from breeding programs across the United States. PLoS ONE, 2018, 13, e0201415.	1.1	10
34	Compost carryover: nitrogen, phosphorus and FT-IR analysis of soil organic matter. Nutrient Cycling in Agroecosystems, 2015, 101, 317-331.	1.1	9
35	Acrylamide‑Forming Potential and Agronomic Properties of Elite US Potato Germplasm from the National Fry Processing Trial. Crop Science, 2016, 56, 30-39.	0.8	9
36	Genetic Covariance of Environments in the Potato National Chip Processing Trial. Crop Science, 2019, 59, 107-114.	0.8	6

#	Article	IF	Citations
37	Economically Optimal Compost Rates for Organic Crop Production. Agronomy Journal, 2010, 102, 1283-1289.	0.9	5
38	Characterization of a Late Blight Resistance Gene Homologous to R2 in Potato Variety Payette Russet. American Journal of Potato Research, 2021, 98, 78-84.	0.5	5
39	The genetic architectures of vine and skin maturity in tetraploid potato. Theoretical and Applied Genetics, 2022, 135, 2943-2951.	1.8	2