

Jeffrey B Endelman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7639619/publications.pdf>

Version: 2024-02-01

39
papers

4,166
citations

304743

22
h-index

302126

39
g-index

47
all docs

47
docs citations

47
times ranked

4247
citing authors

#	ARTICLE	IF	CITATIONS
1	Phased, chromosome-scale genome assemblies of tetraploid potato reveal a complex genome, transcriptome, and predicted proteome landscape underpinning genetic diversity. <i>Molecular Plant</i> , 2022, 15, 520-536.	8.3	72
2	The genetic architectures of vine and skin maturity in tetraploid potato. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2943-2951.	3.6	2
3	Characterization of a Late Blight Resistance Gene Homologous to R2 in Potato Variety Payette Russet. <i>American Journal of Potato Research</i> , 2021, 98, 78-84.	0.9	5
4	Haplotype reconstruction in connected tetraploid F1 populations. <i>Genetics</i> , 2021, 219, .	2.9	26
5	QTL mapping in outbred tetraploid (and diploid) diallel populations. <i>Genetics</i> , 2021, 219, .	2.9	15
6	FIELDimageR: An R package to analyze orthomosaic images from agricultural field trials. <i>The Plant Phenome Journal</i> , 2020, 3, e20005.	2.0	58
7	Image-based phenotyping and genetic analysis of potato skin set and color. <i>Crop Science</i> , 2020, 60, 202-210.	1.8	13
8	Impact of dominance effects on autotetraploid genomic prediction. <i>Crop Science</i> , 2020, 60, 656-665.	1.8	28
9	On the accuracy of genomic prediction models considering multi-trait and allele dosage in <i>Urochloa</i> spp. interspecific tetraploid hybrids. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	37
10	Genomic Prediction of Autotetraploids; Influence of Relationship Matrices, Allele Dosage, and Continuous Genotyping Calls in Phenotype Prediction. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1189-1198.	1.8	60
11	Impact of Dominance Effects on Autotetraploid Genomic Prediction. <i>Crop Science</i> , 2019, .	1.8	25
12	Expected Genotype Quality and Diploidized Marker Data from Genotyping-by-Sequencing of <i>Urochloa</i> spp. Tetraploids. <i>Plant Genome</i> , 2019, 12, 1-9.	2.8	13
13	Genetic Covariance of Environments in the Potato National Chip Processing Trial. <i>Crop Science</i> , 2019, 59, 107-114.	1.8	6
14	Genetic Variance Partitioning and Genome-Wide Prediction with Allele Dosage Information in Autotetraploid Potato. <i>Genetics</i> , 2018, 209, 77-87.	2.9	117
15	Evaluation of genetic diversity among Russet potato clones and varieties from breeding programs across the United States. <i>PLoS ONE</i> , 2018, 13, e0201415.	2.5	10
16	Automated tetraploid genotype calling by hierarchical clustering. <i>Theoretical and Applied Genetics</i> , 2017, 130, 717-726.	3.6	61
17	Pedigree Reconstruction with Genome-Wide Markers in Potato. <i>American Journal of Potato Research</i> , 2017, 94, 184-190.	0.9	19
18	Reliability of Measurement and Genotype \times Environment Interaction for Potato Specific Gravity. <i>Crop Science</i> , 2017, 57, 1966-1972.	1.8	11

#	ARTICLE	IF	CITATIONS
19	Acrylamide-Forming Potential and Agronomic Properties of Elite US Potato Germplasm from the National Fry Processing Trial. <i>Crop Science</i> , 2016, 56, 30-39.	1.8	9
20	Software for Genome-Wide Association Studies in Autopolyploids and Its Application to Potato. <i>Plant Genome</i> , 2016, 9, plantgenome2015.08.0073.	2.8	191
21	Genetic mapping with an inbred line-derived F2 population in potato. <i>Theoretical and Applied Genetics</i> , 2016, 129, 935-943.	3.6	74
22	Compost carryover: nitrogen, phosphorus and FT-IR analysis of soil organic matter. <i>Nutrient Cycling in Agroecosystems</i> , 2015, 101, 317-331.	2.2	9
23	Optimal Design of Preliminary Yield Trials with Genome-Wide Markers. <i>Crop Science</i> , 2014, 54, 48-59.	1.8	100
24	The USDA Barley Core Collection: Genetic Diversity, Population Structure, and Potential for Genome-Wide Association Studies. <i>PLoS ONE</i> , 2014, 9, e94688.	2.5	188
25	LPmerge: an R package for merging genetic maps by linear programming. <i>Bioinformatics</i> , 2014, 30, 1623-1624.	4.1	140
26	Association mapping of grain hardness, polyphenol oxidase, total phenolics, amylose content, and β -glucan in US barley breeding germplasm. <i>Molecular Breeding</i> , 2014, 34, 1229-1243.	2.1	35
27	Genome-wide distribution of genetic diversity and linkage disequilibrium in a mass-selected population of maritime pine. <i>BMC Genomics</i> , 2014, 15, 171.	2.8	41
28	Genomic Predictability of Interconnected Biparental Maize Populations. <i>Genetics</i> , 2013, 194, 493-503.	2.9	180
29	The use of unbalanced historical data for genomic selection in an international wheat breeding program. <i>Field Crops Research</i> , 2013, 154, 12-22.	5.1	100
30	Shrinkage Estimation of the Realized Relationship Matrix. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1405-1413.	1.8	420
31	Ridge Regression and Other Kernels for Genomic Selection with R Package rrBLUP. <i>Plant Genome</i> , 2011, 4, 250-255.	2.8	1,588
32	New algorithm improves fine structure of the barley consensus SNP map. <i>BMC Genomics</i> , 2011, 12, 407.	2.8	13
33	A New Decay Series for Organic Crop Production. <i>Agronomy Journal</i> , 2010, 102, 457-463.	1.8	11
34	Economically Optimal Compost Rates for Organic Crop Production. <i>Agronomy Journal</i> , 2010, 102, 1283-1289.	1.8	5
35	Structure-Guided Recombination Creates an Artificial Family of Cytochromes P450. <i>PLoS Biology</i> , 2006, 4, e112.	5.6	133
36	SCHEMA-Guided Protein Recombination. <i>Methods in Enzymology</i> , 2004, 388, 35-42.	1.0	31

#	ARTICLE	IF	CITATIONS
37	Functional Evolution and Structural Conservation in Chimeric Cytochromes P450. <i>Chemistry and Biology</i> , 2004, 11, 309-318.	6.0	97
38	Site-directed protein recombination as a shortest-path problem. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 589-594.	2.1	70
39	Library analysis of SCHEMA-guided protein recombination. <i>Protein Science</i> , 2003, 12, 1686-1693.	7.6	138