

Eric N Jellen

List of Publications by Year in descending order

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75
papers

3,414
citations

126907

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54
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all docs

79
docs citations

79
times ranked

2499
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of <i>Chenopodium quinoa</i> . <i>Nature</i> , 2017, 542, 307-312.	27.8	569
2	Genomic in situ hybridization differentiates between A/D- and C-genome chromatin and detects intergenomic translocations in polyploid oat species (genus <i>Avena</i>). <i>Genome</i> , 1994, 37, 613-618.	2.0	146
3	The Amaranth Genome: Genome, Transcriptome, and Physical Map Assembly. <i>Plant Genome</i> , 2016, 9, plantgenome2015.07.0062.	2.8	115
4	Single-molecule sequencing and Hi-C-based proximity-guided assembly of amaranth (<i>Amaranthus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.8	108
5	Characterization of <i>Salt Overly Sensitive 1</i> (<i>SOS1</i>) gene homoeologs in quinoa (<i>Chenopodium quinoa</i> Willd.). <i>Genome</i> , 2009, 52, 647-657.	2.0	96
6	Assessment of genetic diversity patterns in Chilean quinoa (<i>Chenopodium quinoa</i> Willd.) germplasm using multiplex fluorescent microsatellite markers. <i>Conservation Genetics</i> , 2009, 10, 369-377.	1.5	94
7	A genetic linkage map of quinoa (<i>Chenopodium quinoa</i>) based on AFLP, RAPD, and SSR markers. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1188-1195.	3.6	91
8	Assessment of genetic diversity in the USDA and CIP-FAO international nursery collections of quinoa (<i>Chenopodium quinoa</i> Willd.) using microsatellite markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2007, 5, 82-95.	0.8	85
9	A Consensus Map in Cultivated Hexaploid Oat Reveals Conserved Grass Synteny with Substantial Subgenome Rearrangement. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0102.	2.8	85
10	Model SNP development for complex genomes based on hexaploid oat using high-throughput 454 sequencing technology. <i>BMC Genomics</i> , 2011, 12, 77.	2.8	84
11	SNP Discovery via Genomic Reduction, Barcoding, and 454 Pyrosequencing in Amaranth. <i>Plant Genome</i> , 2009, 2, .	2.8	82
12	Development and Characterization of Microsatellite Markers for the Grain Amaranths. <i>Crop Science</i> , 2008, 48, 1098-1106.	1.8	75
13	SNP Discovery and Chromosome Anchoring Provide the First Physically-Anchored Hexaploid Oat Map and Reveal Synteny with Model Species. <i>PLoS ONE</i> , 2013, 8, e58068.	2.5	73
14	Development and Use of Microsatellite Markers for Germplasm Characterization in Quinoa () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222	1.8	72
15	The mosaic oat genome gives insights into a uniquely healthy cereal crop. <i>Nature</i> , 2022, 606, 113-119.	27.8	70
16	Simple sequence repeat marker development and genetic mapping in quinoa (<i>Chenopodium quinoa</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 67	6.7	67
17	C-banded karyotypes and polymorphisms in hexaploid oat accessions (<i>Avena</i> spp.) using Wright's stain. <i>Genome</i> , 1993, 36, 1129-1137.	2.0	65
18	Molecular and cytological characterization of ribosomal RNA genes in <i>Chenopodium quinoa</i> and <i>Chenopodium berlandieri</i> . <i>Genome</i> , 2006, 49, 825-839.	2.0	65

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19	A SNP Genotyping Array for Hexaploid Oat. <i>Plant Genome</i> , 2014, 7, plantgenome2014.03.0010.	2.8	63
20	Genomic insights from the first chromosome-scale assemblies of oat (<i>Avena</i> spp.) diploid species. <i>BMC Biology</i> , 2019, 17, 92.	3.8	58
21	High-density marker profiling confirms ancestral genomes of <i>Avena</i> species and identifies D-genome chromosomes of hexaploid oat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2133-2149.	3.6	56
22	The complete chloroplast genome sequences for four <i>Amaranthus</i> species (Amaranthaceae). <i>Applications in Plant Sciences</i> , 2016, 4, 1600063.	2.1	54
23	Geographical Distribution of a Chromosome 7C and 17 Intergenomic Translocation in Cultivated Oat. <i>Crop Science</i> , 2000, 40, 256-263.	1.8	50
24	<i>Chenopodium</i> polyploidy inferences from <i>Salt Overly Sensitive 1</i> (<i>SOS1</i>) data. <i>American Journal of Botany</i> , 2015, 102, 533-543.	1.7	50
25	Relationships between the Weedy <i>Amaranthus hybridus</i> (Amaranthaceae) and the Grain Amaranths. <i>Crop Science</i> , 2014, 54, 220-228.	1.8	49
26	Characterization of the hexaploid oat <i>Avena byzantina</i> cv. Kanota monosomic series using C-banding and RFLPs. <i>Genome</i> , 1993, 36, 962-970.	2.0	46
27	Development and use of an expressed sequenced tag library in quinoa (<i>Chenopodium quinoa</i> Willd.) for the discovery of single nucleotide polymorphisms. <i>Plant Science</i> , 2005, 168, 439-447.	3.6	46
28	A new chromosome nomenclature system for oat (<i>Avena sativa</i> L. and <i>A. byzantina</i> C. Koch) based on FISH analysis of monosomic lines. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1541-1552.	3.6	41
29	The introns in FLOWERING LOCUS T-LIKE (FTL) genes are useful markers for tracking paternity in tetraploid <i>Chenopodium quinoa</i> Willd.. <i>Genetic Resources and Crop Evolution</i> , 2015, 62, 913-925.	1.6	41
30	Single Nucleotide Polymorphism Identification, Characterization, and Linkage Mapping in Quinoa. <i>Plant Genome</i> , 2012, 5, .	2.8	40
31	Chromosomal localization and polymorphisms of ribosomal DNA in oat (<i>Avena</i> spp.). <i>Genome</i> , 1994, 37, 23-32.	2.0	38
32	Mitochondrial and chloroplast genomes provide insights into the evolutionary origins of quinoa (<i>Chenopodium quinoa</i> Willd.). <i>Scientific Reports</i> , 2019, 9, 185.	3.3	37
33	Chromosomal localization of two novel repetitive sequences isolated from the <i>Chenopodium quinoa</i> Willd. genome. <i>Genome</i> , 2011, 54, 710-717.	2.0	36
34	Construction of a quinoa (<i>Chenopodium quinoa</i> Willd.) BAC library and its use in identifying genes encoding seed storage proteins. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1593-1600.	3.6	35
35	Characterization of Sun II™ oat monosomics through C-banding and identification of eight new Sun II™ monosomics. <i>Theoretical and Applied Genetics</i> , 1997, 95, 1190-1195.	3.6	28
36	Assignment of RFLP linkage groups to chromosomes using monosomic F1 analysis in hexaploid oat. <i>Theoretical and Applied Genetics</i> , 2001, 102, 320-326.	3.6	28

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37	Distribution of 5S and 35S rRNA gene sites in 34 <i>Chenopodium</i> species (Amaranthaceae). <i>Botanical Journal of the Linnean Society</i> , 2012, 170, 220-231.	1.6	28
38	How genome size variation is linked with evolution within <i>Chenopodium sensu lato</i> . <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2016, 23, 18-32.	2.7	28
39	Expression and Evolutionary Relationships of the <i>Chenopodium quinoa</i> 11S Seed Storage Protein Gene. <i>International Journal of Plant Sciences</i> , 2008, 169, 281-291.	1.3	27
40	<i>Chenopodium</i> . , 2011, , 35-61.		27
41	New Diversity Arrays Technology (DART) markers for tetraploid oat (<i>Avena magna</i> Murphy et Terrell) provide the first complete oat linkage map and markers linked to domestication genes from hexaploid <i>A. sativa</i> L.. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1159-1171.	3.6	27
42	Identification of homoeologous chromosomes in hexaploid oat (<i>A. byzantina</i> cv Kanota) using monosomics and RFLP analysis. <i>Theoretical and Applied Genetics</i> , 1994, 89-89, 329-335.	3.6	23
43	Genome analysis in <i>Avena sativa</i> reveals hidden breeding barriers and opportunities for oat improvement. <i>Communications Biology</i> , 2022, 5, 474.	4.4	23
44	Assessment of Genetic Diversity in Peruvian Amaranth (<i>Amaranthus caudatus</i> and <i>A. Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 46</i>)	1.8	22
45	Giemsa C-banding in <i>Avena insularis</i> Ladizinsky. <i>Genetic Resources and Crop Evolution</i> , 2000, 47, 227-230.	1.6	21
46	Elevated Genetic Diversity in an F2:6 Population of Quinoa (<i>Chenopodium quinoa</i>) Developed through an Inter-ecotype Cross. <i>Frontiers in Plant Science</i> , 2016, 7, 1222.	3.6	20
47	C-banding variation in the Moroccan oat species <i>Avena agadiriana</i> (2n=4x=28). <i>Theoretical and Applied Genetics</i> , 1996, 92, 726-732.	3.6	19
48	The genome of <i>Chenopodium pallidicaule</i> : An emerging Andean super grain. <i>Applications in Plant Sciences</i> , 2019, 7, e11300.	2.1	19
49	A new genetic linkage map of barley (<i>Hordeum vulgare</i> L.) facilitates genetic dissection of height and spike length and angle. <i>Field Crops Research</i> , 2013, 154, 91-99.	5.1	18
50	Molecular genetic identification of <i>Avena</i> chromosomes related to the group 1 chromosomes of the Triticeae. <i>Genome</i> , 1995, 38, 185-189.	2.0	17
51	Quantitative Trait Loci and Epistasis for Oat Winter Hardiness Component Traits. <i>Crop Science</i> , 2009, 49, 1989-1998.	1.8	17
52	Identification of mixed linkage ð²â€glucan quantitative trait loci and evaluation of <i>AsCslF6</i> homoeologs in hexaploid oat. <i>Crop Science</i> , 2020, 60, 914-933.	1.8	16
53	A Cytological Marker Associated with Winterhardiness in Oat. <i>Crop Science</i> , 2006, 46, 203-208.	1.8	14
54	A survey of <i>Penstemon</i> genome size. <i>Genome</i> , 2011, 54, 160-173.	2.0	14

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55	Selection of Expression Reference Genes with Demonstrated Stability in Barley among a Diverse Set of Tissues and Cultivars. <i>Crop Science</i> , 2018, 58, 332-341.	1.8	13
56	Quantitative trait loci of barley malting quality trait components in the Stellar/01Ab8219 mapping population. <i>Molecular Breeding</i> , 2014, 34, 59-73.	2.1	12
57	Characterization of the Granule-Bound Starch Synthase I Gene in <i>Chenopodium</i> . <i>Plant Genome</i> , 2015, 8, eplantgenome2014.09.0051.	2.8	11
58	A Chromosome-Scale Assembly of the Garden Orach (<i>Atriplex hortensis</i> L.) Genome Using Oxford Nanopore Sequencing. <i>Frontiers in Plant Science</i> , 2020, 11, 624.	3.6	11
59	Development and use of microsatellite markers for genetic diversity analysis of cañahua (<i>Chenopodium pallidicaule</i> Aellen). <i>Genetic Resources and Crop Evolution</i> , 2011, 58, 727-739.	1.6	10
60	An Intergenomic Reciprocal Translocation Associated with Oat Winter Hardiness Component Traits. <i>Crop Science</i> , 2007, 47, 1832-1840.	1.8	9
61	Genetic diversity and crown rust resistance of oat landraces from various locations throughout Turkey. <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2016, 40, 262-268.	2.1	9
62	Title is missing!. <i>Euphytica</i> , 2000, 111, 175-184.	1.2	8
63	An Algorithm for Analyzing Linkages Affected by Heterozygous Translocations: QuadMap. <i>Journal of Heredity</i> , 2006, 97, 62-66.	2.4	8
64	The art of attrition: development of robust oat microsatellites. <i>Plant Breeding</i> , 2016, 135, 323-334.	1.9	8
65	C-banding variation in the Moroccan oat species <i>Avena agadiriana</i> . <i>Theoretical and Applied Genetics</i> , 1996, 92, 726-732.	3.6	7
66	C-Banding of Plant Chromosomes. <i>Methods in Molecular Biology</i> , 2016, 1429, 1-5.	0.9	5
67	C-Banding and Localization of 18S-5.8S-26S rDNA in Tall Oatgrass Species. <i>Crop Science</i> , 2003, 43, 32.	1.8	5
68	New seed collections of North American pitseed goosefoot (<i>Chenopodium berlandieri</i>) and efforts to identify its diploid ancestors through whole-genome sequencing. , 2019, 46, 187-196.		5
69	Cytogenetic affinities between populations of <i>Avena insularis</i> Ladizinsky from Sicily and Tunisia. <i>Genetic Resources and Crop Evolution</i> , 2003, 50, 11-15.	1.6	4
70	Prospects for Quinoa (<i>Chenopodium Quinoa</i> Willd.) Improvement Through Biotechnology. , 2013, , 173-201.		4
71	C-Banding and Localization of 18S-5.8S-26S rDNA in Tall Oatgrass Species. <i>Crop Science</i> , 2003, 43, 32.	1.8	3
72	Improving phylogenetic resolution of the Lamiales using the complete plastome sequences of six <i>Penstemon</i> species. <i>PLoS ONE</i> , 2021, 16, e0261143.	2.5	3

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73	Genetic variation of the granule-bound starch synthase I (GBSSI) genes in waxy and non-waxy accessions of <i>Chenopodium berlandieri</i> ssp. <i>nuttalliae</i> from Central Mexico. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2016, 14, 57-66.	0.8	2
74	Botanical Context for Domestication in North America. <i>Compendium of Plant Genomes</i> , 2021, , 33-49.	0.5	1
75	Genomic Reduction Assisted Single Nucleotide Polymorphism Discovery Using 454-Pyrosequencing. <i>Methods in Molecular Biology</i> , 2015, 1245, 169-182.	0.9	1