

Nicholas A Tinker

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

2,937
citations

186265

28
h-index

175258

52
g-index

70
all docs

70
docs citations

70
times ranked

2133
citing authors

#	ARTICLE	IF	CITATIONS
1	Random amplified polymorphic DNA and pedigree relationships in spring barley. <i>Theoretical and Applied Genetics</i> , 1993, 85, 976-984.	3.6	223
2	An Integrated Biplot Analysis System for Displaying, Interpreting, and Exploring Genotype × Environment Interaction. <i>Crop Science</i> , 2005, 45, 1004-1016.	1.8	213
3	Regions of the Genome that Affect Agronomic Performance in Two-Row Barley. <i>Crop Science</i> , 1996, 36, 1053-1062.	1.8	191
4	Using Genotyping-By-Sequencing (GBS) for Genomic Discovery in Cultivated Oat. <i>PLoS ONE</i> , 2014, 9, e102448.	2.5	147
5	New DArT markers for oat provide enhanced map coverage and global germplasm characterization. <i>BMC Genomics</i> , 2009, 10, 39.	2.8	135
6	A molecular marker map in 'Kanota' × 'Ogle' hexaploid oat (<i>Avena</i> spp.) enhanced by additional markers and a robust framework. <i>Genome</i> , 2003, 46, 28-47.	2.0	107
7	Haplotype-based genotyping-by-sequencing in oat genome research. <i>Plant Biotechnology Journal</i> , 2018, 16, 1452-1463.	8.3	86
8	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
9	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
10	Genomic, Marker-Assisted, and Pedigree-BLUP Selection Methods for β-Glucan Concentration in Elite Oat. <i>Crop Science</i> , 2013, 53, 1894-1906.	1.8	84
11	Genetic diversity among oat varieties of worldwide origin and associations of AFLP markers with quantitative traits. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1041-1053.	3.6	79
12	Population structure and linkage disequilibrium in oat (<i>Avena sativa</i> L.): implications for genome-wide association studies. <i>Theoretical and Applied Genetics</i> , 2011, 122, 623-632.	3.6	79
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	The mosaic oat genome gives insights into a uniquely healthy cereal crop. <i>Nature</i> , 2022, 606, 113-119.	27.8	70
15	A molecular linkage map with associated QTLs from a hulless × covered spring oat population. <i>Theoretical and Applied Genetics</i> , 2004, 108, 1285-1298.	3.6	69
16	A SNP Genotyping Array for Hexaploid Oat. <i>Plant Genome</i> , 2014, 7, plantgenome2014.03.0010.	2.8	63
17	Population structure and linkage disequilibrium in barley assessed by DArT markers. <i>Theoretical and Applied Genetics</i> , 2009, 119, 43-52.	3.6	58
18	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

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19	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
20	An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. <i>Molecular Plant</i> , 2021, 14, 874-887.	8.3	56
21	Population Genomics Related to Adaptation in Elite Oat Germplasm. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0103.	2.8	55
22	Genome size variation in the genus <i>Avena</i> . <i>Genome</i> , 2016, 59, 209-220.	2.0	55
23	KIN: Software for Computing Kinship Coefficients. <i>Journal of Heredity</i> , 1993, 84, 238-238.	2.4	52
24	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	50
25	Haplotag: Software for Haplotype-Based Genotyping-by-Sequencing Analysis. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 857-863.	1.8	49
26	Multivariate Genome-Wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (<i>Avena sativa</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2963-2975.	1.8	44
27	Marker-Based Selection of QTL Affecting Grain and Malt Quality in Two-Row Barley. <i>Crop Science</i> , 2000, 40, 1426-1433.	1.8	42
28	Discovery, localization, and sequence characterization of molecular markers for the crown rust resistance genes Pc38, Pc39, and Pc48 in cultivated oat (<i>Avena sativa</i> L.). <i>Molecular Breeding</i> , 2004, 14, 349-361.	2.1	40
29	Genome-Wide Association Mapping of Crown Rust Resistance in Oat Elite Germplasm. <i>Plant Genome</i> , 2017, 10, plantgenome2016.10.0107.	2.8	29
30	Associations Among Oat Traits and Their Responses to the Environment. <i>Journal of Crop Improvement</i> , 2007, 20, 1-29.	1.7	28
31	Verifications of a Quantitative Trait Locus Affecting Agronomic Traits in Two-Row Barley. <i>Crop Science</i> , 1999, 39, 248-252.	1.8	27
32	Comparative linkage mapping of diploid, tetraploid, and hexaploid <i>Avena</i> species suggests extensive chromosome rearrangement in ancestral diploids. <i>Scientific Reports</i> , 2019, 9, 12298.	3.3	26
33	Loci affecting flowering time in oat under short-day conditions. <i>Genome</i> , 2006, 49, 1528-1538.	2.0	25
34	Phosphoproteome profile of <i>Fusarium graminearum</i> grown in vitro under nonlimiting conditions. <i>Proteomics</i> , 2012, 12, 1002-1005.	2.2	25
35	Quantitative Trait Loci Affecting Oil Content, Oil Composition, and Other Agronomically Important Traits in Oat. <i>Plant Genome</i> , 2012, 5, .	2.8	24
36	Tagging and mapping candidate loci for vernalization and flower initiation in hexaploid oat. <i>Molecular Breeding</i> , 2012, 30, 1295-1312.	2.1	23

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37	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
38	A Curated Internet Database of Oat Pedigrees. <i>Crop Science</i> , 2005, 45, 2269-2272.	1.8	21
39	A Set of New Simple Sequence Repeat and Avenin DNA Markers Suitable for Mapping and Fingerprinting Studies in Oat (<i>Avena</i> spp.). <i>Crop Science</i> , 2010, 50, 1207-1218.	1.8	21
40	A biplot approach for investigating QTL-by-environment patterns. <i>Molecular Breeding</i> , 2005, 15, 31-43.	2.1	20
41	Genetic variation and associations involving <i>Fusarium</i> head blight and deoxynivalenol accumulation in cultivated oat (<i>Avena sativa</i> L.). <i>Plant Breeding</i> , 2017, 136, 620-636.	1.9	20
42	A genetic linkage map in southern European spring oat identifies multiple quantitative trait loci for adaptation and rust resistance. <i>Plant Breeding</i> , 2019, 138, 82-94.	1.9	17
43	Centromeric position and genomic allocation of a repetitive sequence isolated from chromosome 18D of hexaploid oat, <i>Avena sativa</i> L. <i>Genetic Resources and Crop Evolution</i> , 2015, 62, 1-4.	1.6	15
44	Phylogeny and maternal donor of <i>Kengyilia</i> species (Poaceae: Triticeae) based on three cpDNA (matK, Tj ETQq0 0 0 rgBT /Overlock 10 T	1.8	14
45	Comparative analysis of genetic diversity in Canadian barley assessed by SSR, DarT, and pedigree data. <i>Genome</i> , 2013, 56, 351-358.	2.0	13
46	Genetic diversity and genome-wide association analysis in Chinese hulless oat germplasm. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3365-3380.	3.6	12
47	Phylogenetic relationships in the genus <i>Avena</i> based on the nuclear <i>Pgk1</i> gene. <i>PLoS ONE</i> , 2018, 13, e0200047.	2.5	11
48	Mapping of the stem rust resistance gene <i>Pg13</i> in cultivated oat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 259-270.	3.6	11
49	Implementing within-cross genomic prediction to reduce oat breeding costs. <i>Plant Genome</i> , 2020, 13, e20004.	2.8	11
50	Improvement of Oat as a Winter Forage Crop in the Southern United States. <i>Crop Science</i> , 2014, 54, 1336-1346.	1.8	10
51	A targeted genotyping-by-sequencing tool (Rapture) for genomics-assisted breeding in oat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 653-664.	3.6	10
52	Population genomics of Mediterranean oat (<i>A. sativa</i>) reveals high genetic diversity and three loci for heading date. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2063-2077.	3.6	10
53	Groat yield of naked and covered oat. <i>Canadian Journal of Plant Science</i> , 2001, 81, 727-729.	0.9	9
54	Oat. , 2006, , 211-242.		9

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55	Mapping of the Oat Crown Rust Resistance Gene Pc39 Relative to Single Nucleotide Polymorphism Markers. <i>Plant Disease</i> , 2020, 104, 1507-1513.	1.4	9
56	Discovery, localization, and sequence characterization of molecular markers for the crown rust resistance genes Pc38, Pc39, and Pc48 in cultivated oat (<i>Avena sativa</i> L.). <i>Molecular Breeding</i> , 2005, 14, 349-361.	2.1	8
57	QTL Identification, Mega-Environment Classification, and Strategy Development for Marker-Based Selection Using Biplots. <i>Journal of Crop Improvement</i> , 2005, 14, 299-324.	1.7	7
58	The Genetic Architecture of Milling Quality in Spring Oat Lines of the Collaborative Oat Research Enterprise. <i>Foods</i> , 2021, 10, 2479.	4.3	7
59	Genome Assembly of the Canadian two-row Malting Barley cultivar AAC Synergy. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	6
60	Characterization of chromosome-specific genomic DNA from hexaploid oat. <i>Genome</i> , 2012, 55, 265-268.	2.0	5
61	Suitable dose of ^{60}Co γ -ray for mutation in <i>Roegneria</i> seeds. <i>Journal of Radioanalytical and Nuclear Chemistry</i> , 2013, 295, 1129-1134.	1.5	5
62	Genotyping-by-sequencing empowered genetic diversity analysis of Jordanian oat wild relative <i>Avena sterilis</i> . <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 2069-2082.	1.6	5
63	SPAGHETTI: Simulation Software to Test Genetic Mapping Programs. <i>Journal of Heredity</i> , 2010, 101, 257-259.	2.4	4
64	Genetic mapping and a new PCR-based marker linked to a dwarfing gene in oat (<i>Avena sativa</i> L.). <i>Genome</i> , 2018, 61, 497-503.	2.0	3
65	Comparative sequencing and SNP marker validation for oat stem rust resistance gene Pg6 in a diverse collection of <i>Avena</i> accessions. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1307-1318.	3.6	2
66	Toward the development of Ac/Ds transposon-mediated gene tagging system for functional genomics in oat (<i>Avena sativa</i> L.). <i>Functional and Integrative Genomics</i> , 2022, 22, 669-681.	3.5	2
67	Localization of the Stem Rust Resistance Gene <i>Pg2</i> to Linkage Group Mrg20 in Cultivated Oat (<i>Avena sativa</i>). <i>Phytopathology</i> , 2020, 110, 1721-1726.	2.2	1