

Nicholas A Tinker

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

2,937
citations

185998

28
h-index

174990

52
g-index

70
all docs

70
docs citations

70
times ranked

2133
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative sequencing and SNP marker validation for oat stem rust resistance gene Pg6 in a diverse collection of Avena accessions. Theoretical and Applied Genetics, 2022, 135, 1307-1318.	1.8	2
2	Toward the development of Ac/Ds transposon-mediated gene tagging system for functional genomics in oat (<i>Avena sativa</i> L.). Functional and Integrative Genomics, 2022, 22, 669-681.	1.4	2
3	The mosaic oat genome gives insights into a uniquely healthy cereal crop. Nature, 2022, 606, 113-119.	13.7	70
4	Genome analysis in <i>Avena sativa</i> reveals hidden breeding barriers and opportunities for oat improvement. Communications Biology, 2022, 5, 474.	2.0	23
5	Genome Assembly of the Canadian two-row Malting Barley cultivar AAC Synergy. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	6
6	Population genomics of Mediterranean oat (<i>A. sativa</i>) reveals high genetic diversity and three loci for heading date. Theoretical and Applied Genetics, 2021, 134, 2063-2077.	1.8	10
7	An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. Molecular Plant, 2021, 14, 874-887.	3.9	56
8	The Genetic Architecture of Milling Quality in Spring Oat Lines of the Collaborative Oat Research Enterprise. Foods, 2021, 10, 2479.	1.9	7
9	Mapping of the stem rust resistance gene Pg13 in cultivated oat. Theoretical and Applied Genetics, 2020, 133, 259-270.	1.8	11
10	A targeted genotyping-by-sequencing tool (Rapture) for genomics-assisted breeding in oat. Theoretical and Applied Genetics, 2020, 133, 653-664.	1.8	10
11	Genetic diversity and genome-wide association analysis in Chinese hulless oat germplasm. Theoretical and Applied Genetics, 2020, 133, 3365-3380.	1.8	12
12	Localization of the Stem Rust Resistance Gene <i>Pg2</i> to Linkage Group Mrg20 in Cultivated Oat (<i>Avena sativa</i>). Phytopathology, 2020, 110, 1721-1726.	1.1	1
13	Implementing within-cross genomic prediction to reduce oat breeding costs. Plant Genome, 2020, 13, e20004.	1.6	11
14	Mapping of the Oat Crown Rust Resistance Gene Pc39 Relative to Single Nucleotide Polymorphism Markers. Plant Disease, 2020, 104, 1507-1513.	0.7	9
15	A genetic linkage map in southern European spring oat identifies multiple quantitative trait loci for adaptation and rust resistance. Plant Breeding, 2019, 138, 82-94.	1.0	17
16	Comparative linkage mapping of diploid, tetraploid, and hexaploid <i>Avena</i> species suggests extensive chromosome rearrangement in ancestral diploids. Scientific Reports, 2019, 9, 12298.	1.6	26
17	Multivariate Genome-Wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (<i>Avena sativa</i> L.). G3: Genes, Genomes, Genetics, 2019, 9, 2963-2975.	0.8	44
18	Genomic insights from the first chromosome-scale assemblies of oat (<i>Avena</i> spp.) diploid species. BMC Biology, 2019, 17, 92.	1.7	58

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19	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	50
20	Haplotype-based genotyping-by-sequencing in oat genome research. Plant Biotechnology Journal, 2018, 16, 1452-1463.	4.1	86
21	Phylogenetic relationships in the genus <i>Avena</i> based on the nuclear Pgk1 gene. PLoS ONE, 2018, 13, e0200047.	1.1	11
22	Genetic mapping and a new PCR-based marker linked to a dwarfing gene in oat (<i>Avena sativa</i> L.). Genome, 2018, 61, 497-503.	0.9	3
23	Genotyping-by-sequencing empowered genetic diversity analysis of Jordanian oat wild relative <i>Avena sterilis</i> . Genetic Resources and Crop Evolution, 2018, 65, 2069-2082.	0.8	5
24	Genetic variation and associations involving <i>Fusarium</i> head blight and deoxynivalenol accumulation in cultivated oat (<i>Avena sativa</i> L.). Plant Breeding, 2017, 136, 620-636.	1.0	20
25	Genome-Wide Association Mapping of Crown Rust Resistance in Oat Elite Germplasm. Plant Genome, 2017, 10, plantgenome2016.10.0107.	1.6	29
26	Population Genomics Related to Adaptation in Elite Oat Germplasm. Plant Genome, 2016, 9, plantgenome2015.10.0103.	1.6	55
27	High-density marker profiling confirms ancestral genomes of <i>Avena</i> species and identifies D-genome chromosomes of hexaploid oat. Theoretical and Applied Genetics, 2016, 129, 2133-2149.	1.8	56
28	A Consensus Map in Cultivated Hexaploid Oat Reveals Conserved Grass Synteny with Substantial Subgenome Rearrangement. Plant Genome, 2016, 9, plantgenome2015.10.0102.	1.6	85
29	Haplotag: Software for Haplotype-Based Genotyping-by-Sequencing Analysis. G3: Genes, Genomes, Genetics, 2016, 6, 857-863.	0.8	49
30	Genome size variation in the genus <i>Avena</i> . Genome, 2016, 59, 209-220.	0.9	55
31	Centromeric position and genomic allocation of a repetitive sequence isolated from chromosome 18D of hexaploid oat, <i>Avena sativa</i> L.. Genetic Resources and Crop Evolution, 2015, 62, 1-4.	0.8	15
32	Using Genotyping-By-Sequencing (GBS) for Genomic Discovery in Cultivated Oat. PLoS ONE, 2014, 9, e102448.	1.1	147
33	Improvement of Oat as a Winter Forage Crop in the Southern United States. Crop Science, 2014, 54, 1336-1346.	0.8	10
34	A SNP Genotyping Array for Hexaploid Oat. Plant Genome, 2014, 7, plantgenome2014.03.0010.	1.6	63
35	Comparative analysis of genetic diversity in Canadian barley assessed by SSR, DarT, and pedigree data. Genome, 2013, 56, 351-358.	0.9	13
36	Suitable dose of ^{60}Co γ -ray for mutation in <i>Roegneria</i> seeds. Journal of Radioanalytical and Nuclear Chemistry, 2013, 295, 1129-1134.	0.7	5

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37	SNP Discovery and Chromosome Anchoring Provide the First Physically-Anchored Hexaploid Oat Map and Reveal Synteny with Model Species. PLoS ONE, 2013, 8, e58068.	1.1	73
38	Genomic, Marker-Assisted, and Pedigree-BLUP Selection Methods for Î²-Glucan Concentration in Elite Oat. Crop Science, 2013, 53, 1894-1906.	0.8	84
39	Tagging and mapping candidate loci for vernalization and flower initiation in hexaploid oat. Molecular Breeding, 2012, 30, 1295-1312.	1.0	23
40	Characterization of chromosome-specific genomic DNA from hexaploid oat. Genome, 2012, 55, 265-268.	0.9	5
41	Quantitative Trait Loci Affecting Oil Content, Oil Composition, and Other Agronomically Important Traits in Oat. Plant Genome, 2012, 5, .	1.6	24
42	Phosphoproteome profile of <i>Fusarium graminearum</i> grown in vitro under nonlimiting conditions. Proteomics, 2012, 12, 1002-1005.	1.3	25
43	Phylogeny and maternal donor of <i>Kengyilia</i> species (Poaceae: Triticeae) based on three cpDNA (matK, Tj ETQq1 1 0,784314 rrgBT /Ove	0.6	14
44	Population structure and linkage disequilibrium in oat (<i>Avena sativa</i> L.): implications for genome-wide association studies. Theoretical and Applied Genetics, 2011, 122, 623-632.	1.8	79
45	Model SNP development for complex genomes based on hexaploid oat using high-throughput 454 sequencing technology. BMC Genomics, 2011, 12, 77.	1.2	84
46	A Set of New Simple Sequence Repeat and Avenin DNA Markers Suitable for Mapping and Fingerprinting Studies in Oat (<i>Avena</i> spp.). Crop Science, 2010, 50, 1207-1218.	0.8	21
47	SPAGHETTI: Simulation Software to Test Genetic Mapping Programs. Journal of Heredity, 2010, 101, 257-259.	1.0	4
48	New DArT markers for oat provide enhanced map coverage and global germplasm characterization. BMC Genomics, 2009, 10, 39.	1.2	135
49	Population structure and linkage disequilibrium in barley assessed by DArT markers. Theoretical and Applied Genetics, 2009, 119, 43-52.	1.8	58
50	Genetic diversity among oat varieties of worldwide origin and associations of AFLP markers with quantitative traits. Theoretical and Applied Genetics, 2008, 117, 1041-1053.	1.8	79
51	Associations Among Oat Traits and Their Responses to the Environment. Journal of Crop Improvement, 2007, 20, 1-29.	0.9	28
52	Loci affecting flowering time in oat under short-day conditions. Genome, 2006, 49, 1528-1538.	0.9	25
53	Oat. , 2006, , 211-242.		9
54	An Integrated Biplot Analysis System for Displaying, Interpreting, and Exploring Genotype × Environment Interaction. Crop Science, 2005, 45, 1004-1016.	0.8	213

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55	A biplot approach for investigating QTL-by-environment patterns. <i>Molecular Breeding</i> , 2005, 15, 31-43.	1.0	20
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.	1.0	8
57	A Curated Internet Database of Oat Pedigrees. <i>Crop Science</i> , 2005, 45, 2269-2272.	0.8	21
58	QTL Identification, Mega-Environment Classification, and Strategy Development for Marker-Based Selection Using Biplots. <i>Journal of Crop Improvement</i> , 2005, 14, 299-324.	0.9	7
59	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.	1.0	40
60	A molecular linkage map with associated QTLs from a hulless Å— covered spring oat population. <i>Theoretical and Applied Genetics</i> , 2004, 108, 1285-1298.	1.8	69
61	A molecular marker map in 'Kanota' Å— 'Ogle' hexaploid oat (<i>Avena</i> spp.) enhanced by additional markers and a robust framework. <i>Genome</i> , 2003, 46, 28-47.	0.9	107
62	Groat yield of naked and covered oat. <i>Canadian Journal of Plant Science</i> , 2001, 81, 727-729.	0.3	9
63	Marker-Based Selection of QTL Affecting Grain and Malt Quality in Two-Row Barley. <i>Crop Science</i> , 2000, 40, 1426-1433.	0.8	42
64	Verifications of a Quantitative Trait Locus Affecting Agronomic Traits in Two-Row Barley. <i>Crop Science</i> , 1999, 39, 248-252.	0.8	27
65	Regions of the Genome that Affect Agronomic Performance in Two-Row Barley. <i>Crop Science</i> , 1996, 36, 1053-1062.	0.8	191
66	Random amplified polymorphic DNA and pedigree relationships in spring barley. <i>Theoretical and Applied Genetics</i> , 1993, 85, 976-984.	1.8	223
67	KIN: Software for Computing Kinship Coefficients. <i>Journal of Heredity</i> , 1993, 84, 238-238.	1.0	52