

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 | Random amplified polymorphic DNA and pedigree relationships in spring barley. <i>Theoretical and Applied Genetics</i> , 1993, 85, 976-984. | 1.8 | 223 |
| 2 | An Integrated Biplot Analysis System for Displaying, Interpreting, and Exploring Genotype × Environment Interaction. <i>Crop Science</i> , 2005, 45, 1004-1016. | 0.8 | 213 |
| 3 | Regions of the Genome that Affect Agronomic Performance in Two-Row Barley. <i>Crop Science</i> , 1996, 36, 1053-1062. | 0.8 | 191 |
| 4 | Using Genotyping-By-Sequencing (GBS) for Genomic Discovery in Cultivated Oat. <i>PLoS ONE</i> , 2014, 9, e102448. | 1.1 | 147 |
| 5 | New DArT markers for oat provide enhanced map coverage and global germplasm characterization. <i>BMC Genomics</i> , 2009, 10, 39. | 1.2 | 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. | 0.9 | 107 |
| 7 | Haplotype-based genotyping-by-sequencing in oat genome research. <i>Plant Biotechnology Journal</i> , 2018, 16, 1452-1463. | 4.1 | 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. | 1.6 | 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. | 1.2 | 84 |
| 10 | Genomic, Marker-Assisted, and Pedigree-BLUP Selection Methods for Î²-Glucan Concentration in Elite Oat. <i>Crop Science</i> , 2013, 53, 1894-1906. | 0.8 | 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. | 1.8 | 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. | 1.8 | 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. | 1.1 | 73 |
| 14 | The mosaic oat genome gives insights into a uniquely healthy cereal crop. <i>Nature</i> , 2022, 606, 113-119. | 13.7 | 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. | 1.8 | 69 |
| 16 | A SNP Genotyping Array for Hexaploid Oat. <i>Plant Genome</i> , 2014, 7, plantgenome2014.03.0010. | 1.6 | 63 |
| 17 | Population structure and linkage disequilibrium in barley assessed by DArT markers. <i>Theoretical and Applied Genetics</i> , 2009, 119, 43-52. | 1.8 | 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. | 1.7 | 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. | 1.8 | 56 |
| 20 | An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. <i>Molecular Plant</i> , 2021, 14, 874-887. | 3.9 | 56 |
| 21 | Population Genomics Related to Adaptation in Elite Oat Germplasm. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0103. | 1.6 | 55 |
| 22 | Genome size variation in the genus <i>Avena</i> . <i>Genome</i> , 2016, 59, 209-220. | 0.9 | 55 |
| 23 | KIN: Software for Computing Kinship Coefficients. <i>Journal of Heredity</i> , 1993, 84, 238-238. | 1.0 | 52 |
| 24 | OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2019, 2019, . | 1.4 | 50 |
| 25 | Haplotag: Software for Haplotype-Based Genotyping-by-Sequencing Analysis. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 857-863. | 0.8 | 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. | 0.8 | 44 |
| 27 | Marker-Based Selection of QTL Affecting Grain and Malt Quality in Two-Row Barley. <i>Crop Science</i> , 2000, 40, 1426-1433. | 0.8 | 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. | 1.0 | 40 |
| 29 | Genome-Wide Association Mapping of Crown Rust Resistance in Oat Elite Germplasm. <i>Plant Genome</i> , 2017, 10, plantgenome2016.10.0107. | 1.6 | 29 |
| 30 | Associations Among Oat Traits and Their Responses to the Environment. <i>Journal of Crop Improvement</i> , 2007, 20, 1-29. | 0.9 | 28 |
| 31 | Verifications of a Quantitative Trait Locus Affecting Agronomic Traits in Two-Row Barley. <i>Crop Science</i> , 1999, 39, 248-252. | 0.8 | 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. | 1.6 | 26 |
| 33 | Loci affecting flowering time in oat under short-day conditions. <i>Genome</i> , 2006, 49, 1528-1538. | 0.9 | 25 |
| 34 | Phosphoproteome profile of <i>Fusarium graminearum</i> grown in vitro under nonlimiting conditions. <i>Proteomics</i> , 2012, 12, 1002-1005. | 1.3 | 25 |
| 35 | Quantitative Trait Loci Affecting Oil Content, Oil Composition, and Other Agronomically Important Traits in Oat. <i>Plant Genome</i> , 2012, 5, . | 1.6 | 24 |
| 36 | Tagging and mapping candidate loci for vernalization and flower initiation in hexaploid oat. <i>Molecular Breeding</i> , 2012, 30, 1295-1312. | 1.0 | 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. | 2.0 | 23 |
| 38 | A Curated Internet Database of Oat Pedigrees. <i>Crop Science</i> , 2005, 45, 2269-2272. | 0.8 | 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. | 0.8 | 21 |
| 40 | A biplot approach for investigating QTL-by-environment patterns. <i>Molecular Breeding</i> , 2005, 15, 31-43. | 1.0 | 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. | 1.0 | 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. | 1.0 | 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. | 0.8 | 15 |
| 44 | Phylogeny and maternal donor of <i>Kengyilia</i> species (Poaceae: Triticeae) based on three cpDNA (matK, <i>rbcL</i> , <i>trnT-trnL</i>) and <i>psaI</i> genes. <i>Journal of Plant Evolution</i> , 2014, 14, 100-108. | 0.8 | 14 |
| 45 | Comparative analysis of genetic diversity in Canadian barley assessed by SSR, DarT, and pedigree data. <i>Genome</i> , 2013, 56, 351-358. | 0.9 | 13 |
| 46 | Genetic diversity and genome-wide association analysis in Chinese hulless oat germplasm. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3365-3380. | 1.8 | 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. | 1.1 | 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. | 1.8 | 11 |
| 49 | Implementing within-cross genomic prediction to reduce oat breeding costs. <i>Plant Genome</i> , 2020, 13, e20004. | 1.6 | 11 |
| 50 | Improvement of Oat as a Winter Forage Crop in the Southern United States. <i>Crop Science</i> , 2014, 54, 1336-1346. | 0.8 | 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. | 1.8 | 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. | 1.8 | 10 |
| 53 | Groat yield of naked and covered oat. <i>Canadian Journal of Plant Science</i> , 2001, 81, 727-729. | 0.3 | 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. | 0.7 | 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. | 1.0 | 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. | 0.9 | 7 |
| 58 | The Genetic Architecture of Milling Quality in Spring Oat Lines of the Collaborative Oat Research Enterprise. <i>Foods</i> , 2021, 10, 2479. | 1.9 | 7 |
| 59 | Genome Assembly of the Canadian two-row Malting Barley cultivar AAC Synergy. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, . | 0.8 | 6 |
| 60 | Characterization of chromosome-specific genomic DNA from hexaploid oat. <i>Genome</i> , 2012, 55, 265-268. | 0.9 | 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. | 0.7 | 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. | 0.8 | 5 |
| 63 | SPAGHETTI: Simulation Software to Test Genetic Mapping Programs. <i>Journal of Heredity</i> , 2010, 101, 257-259. | 1.0 | 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. | 0.9 | 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. | 1.8 | 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. | 1.4 | 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. | 1.1 | 1 |