

Nicholas A Tinker

List of Publications by Year in descending order

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67
papers

2,937
citations

186265
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175258
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70
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docs citations

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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. | 3.6 | 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. | 3.5 | 2 |
| 3 | The mosaic oat genome gives insights into a uniquely healthy cereal crop. Nature, 2022, 606, 113-119. | 27.8 | 70 |
| 4 | Genome analysis in <i>Avena sativa</i> reveals hidden breeding barriers and opportunities for oat improvement. Communications Biology, 2022, 5, 474. | 4.4 | 23 |
| 5 | Genome Assembly of the Canadian two-row Malting Barley cultivar AAC Synergy. G3: Genes, Genomes, Genetics, 2021, 11, . | 1.8 | 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. | 3.6 | 10 |
| 7 | An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. Molecular Plant, 2021, 14, 874-887. | 8.3 | 56 |
| 8 | The Genetic Architecture of Milling Quality in Spring Oat Lines of the Collaborative Oat Research Enterprise. Foods, 2021, 10, 2479. | 4.3 | 7 |
| 9 | Mapping of the stem rust resistance gene Pg13 in cultivated oat. Theoretical and Applied Genetics, 2020, 133, 259-270. | 3.6 | 11 |
| 10 | A targeted genotyping-by-sequencing tool (Rapture) for genomics-assisted breeding in oat. Theoretical and Applied Genetics, 2020, 133, 653-664. | 3.6 | 10 |
| 11 | Genetic diversity and genome-wide association analysis in Chinese hulless oat germplasm. Theoretical and Applied Genetics, 2020, 133, 3365-3380. | 3.6 | 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. | 2.2 | 1 |
| 13 | Implementing within-cross genomic prediction to reduce oat breeding costs. Plant Genome, 2020, 13, e20004. | 2.8 | 11 |
| 14 | Mapping of the Oat Crown Rust Resistance Gene Pc39 Relative to Single Nucleotide Polymorphism Markers. Plant Disease, 2020, 104, 1507-1513. | 1.4 | 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. | 1.9 | 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. | 3.3 | 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. | 1.8 | 44 |
| 18 | Genomic insights from the first chromosome-scale assemblies of oat (<i>Avena</i> spp.) diploid species. BMC Biology, 2019, 17, 92. | 3.8 | 58 |

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|----|--|-----|-----------|
| 19 | OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2019, 2019, . | 3.0 | 50 |
| 20 | Haplotype-based genotyping-by-sequencing in oat genome research. Plant Biotechnology Journal, 2018, 16, 1452-1463. | 8.3 | 86 |
| 21 | Phylogenetic relationships in the genus <i>Avena</i> based on the nuclear Pgk1 gene. PLoS ONE, 2018, 13, e0200047. | 2.5 | 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. | 2.0 | 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. | 1.6 | 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. | 1.9 | 20 |
| 25 | Genome-Wide Association Mapping of Crown Rust Resistance in Oat Elite Germplasm. Plant Genome, 2017, 10, plantgenome2016.10.0107. | 2.8 | 29 |
| 26 | Population Genomics Related to Adaptation in Elite Oat Germplasm. Plant Genome, 2016, 9, plantgenome2015.10.0103. | 2.8 | 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. | 3.6 | 56 |
| 28 | A Consensus Map in Cultivated Hexaploid Oat Reveals Conserved Grass Synteny with Substantial Subgenome Rearrangement. Plant Genome, 2016, 9, plantgenome2015.10.0102. | 2.8 | 85 |
| 29 | Haplotag: Software for Haplotype-Based Genotyping-by-Sequencing Analysis. G3: Genes, Genomes, Genetics, 2016, 6, 857-863. | 1.8 | 49 |
| 30 | Genome size variation in the genus <i>Avena</i> . Genome, 2016, 59, 209-220. | 2.0 | 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. | 1.6 | 15 |
| 32 | Using Genotyping-By-Sequencing (GBS) for Genomic Discovery in Cultivated Oat. PLoS ONE, 2014, 9, e102448. | 2.5 | 147 |
| 33 | Improvement of Oat as a Winter Forage Crop in the Southern United States. Crop Science, 2014, 54, 1336-1346. | 1.8 | 10 |
| 34 | A SNP Genotyping Array for Hexaploid Oat. Plant Genome, 2014, 7, plantgenome2014.03.0010. | 2.8 | 63 |
| 35 | Comparative analysis of genetic diversity in Canadian barley assessed by SSR, DarT, and pedigree data. Genome, 2013, 56, 351-358. | 2.0 | 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. | 1.5 | 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. | 2.5 | 73 |
| 38 | Genomic, Marker-Assisted, and Pedigree-BLUP Selection Methods for Î²-Glucan Concentration in Elite Oat. Crop Science, 2013, 53, 1894-1906. | 1.8 | 84 |
| 39 | Tagging and mapping candidate loci for vernalization and flower initiation in hexaploid oat. Molecular Breeding, 2012, 30, 1295-1312. | 2.1 | 23 |
| 40 | Characterization of chromosome-specific genomic DNA from hexaploid oat. Genome, 2012, 55, 265-268. | 2.0 | 5 |
| 41 | Quantitative Trait Loci Affecting Oil Content, Oil Composition, and Other Agronomically Important Traits in Oat. Plant Genome, 2012, 5, . | 2.8 | 24 |
| 42 | Phosphoproteome profile of <i>Fusarium graminearum</i> grown in vitro under nonlimiting conditions. Proteomics, 2012, 12, 1002-1005. | 2.2 | 25 |
| 43 | Phylogeny and maternal donor of <i>Kengyilia</i> species (Poaceae: Triticeae) based on three cpDNA (matK, Tj ETQq1 1 0.784314 r _{BT} /Ove | 1.3 | 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. | 3.6 | 79 |
| 45 | Model SNP development for complex genomes based on hexaploid oat using high-throughput 454 sequencing technology. BMC Genomics, 2011, 12, 77. | 2.8 | 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. | 1.8 | 21 |
| 47 | SPAGHETTI: Simulation Software to Test Genetic Mapping Programs. Journal of Heredity, 2010, 101, 257-259. | 2.4 | 4 |
| 48 | New DArT markers for oat provide enhanced map coverage and global germplasm characterization. BMC Genomics, 2009, 10, 39. | 2.8 | 135 |
| 49 | Population structure and linkage disequilibrium in barley assessed by DArT markers. Theoretical and Applied Genetics, 2009, 119, 43-52. | 3.6 | 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. | 3.6 | 79 |
| 51 | Associations Among Oat Traits and Their Responses to the Environment. Journal of Crop Improvement, 2007, 20, 1-29. | 1.7 | 28 |
| 52 | Loci affecting flowering time in oat under short-day conditions. Genome, 2006, 49, 1528-1538. | 2.0 | 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. | 1.8 | 213 |

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|----|--|-----|-----------|
| 55 | A biplot approach for investigating QTL-by-environment patterns. <i>Molecular Breeding</i> , 2005, 15, 31-43. | 2.1 | 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. | 2.1 | 8 |
| 57 | A Curated Internet Database of Oat Pedigrees. <i>Crop Science</i> , 2005, 45, 2269-2272. | 1.8 | 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. | 1.7 | 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. | 2.1 | 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. | 3.6 | 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. | 2.0 | 107 |
| 62 | Groat yield of naked and covered oat. <i>Canadian Journal of Plant Science</i> , 2001, 81, 727-729. | 0.9 | 9 |
| 63 | 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 |
| 64 | Verifications of a Quantitative Trait Locus Affecting Agronomic Traits in Two-Row Barley. <i>Crop Science</i> , 1999, 39, 248-252. | 1.8 | 27 |
| 65 | Regions of the Genome that Affect Agronomic Performance in Two-Row Barley. <i>Crop Science</i> , 1996, 36, 1053-1062. | 1.8 | 191 |
| 66 | Random amplified polymorphic DNA and pedigree relationships in spring barley. <i>Theoretical and Applied Genetics</i> , 1993, 85, 976-984. | 3.6 | 223 |
| 67 | KIN: Software for Computing Kinship Coefficients. <i>Journal of Heredity</i> , 1993, 84, 238-238. | 2.4 | 52 |