# Gerald A Tuskan

List of Publications by Year
in descending order



| 233 | 28,455 | 10986 71 | 5988 160 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 249 | 249 | 249 | 26480 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | The Genome of Black Cottonwood, Populus trichocarpa (Torr. & Gray). Science, 2006, 313, 1596-1604. | 12.6 | 3,945 |
| 2 | Lignin Valorization: Improving Lignin Processing in the Biorefinery. Science, 2014, 344, 1246843. | 12.6 | 2,994 |
| 3 | Genome sequencing and analysis of the model grass Brachypodium distachyon. Nature, 2010, 463, 763-768. | 27.8 | 1,685 |
| 4 | The genome of Laccaria bicolor provides insights into mycorrhizal symbiosis. Nature, 2008, 452, 88-92. | 27.8 | 1,003 |
| 5 | Reference genome sequence of the model plant Setaria. Nature Biotechnology, 2012, 30, 555-561. | 17.5 | 864 |
| 6 | The genome of Eucalyptus grandis. Nature, 2014, 510, 356-362. | 27.8 | 725 |
| 7 | Genome of an arbuscular mycorrhizal fungus provides insight into the oldest plant symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20117-20122. | 7.1 | 717 |
| 8 | Obligate biotrophy features unraveled by the genomic analysis of rust fungi. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9166-9171. | 7.1 | 640 |
| 9 | Poplar as a feedstock for biofuels: A review of compositional characteristics. Biofuels, Bioproducts and Biorefining, 2010, 4, 209-226. | 3.7 | 558 |
| 10 | Distinct Microbial Communities within the Endosphere and Rhizosphere of Populus deltoides Roots across Contrasting Soil Types. Applied and Environmental Microbiology, 2011, 77, 5934-5944. | 3.1 | 524 |
| 11 | Lignin content in natural Populus variants affects sugar release. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6300-6305. | 7.1 | 515 |
| 12 | The pineapple genome and the evolution of CAM photosynthesis. Nature Genetics, 2015, 47, 1435-1442. | 21.4 | 472 |
| 13 | The Physcomitrella patens chromosomeâ€scale assembly reveals moss genome structure and evolution. Plant Journal, 2018, 93, 515-533. | 5.7 | 406 |
| 14 | FLOWERING LOCUS T duplication coordinates reproductive and vegetative growth in perennial poplar. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10756-10761. | 7.1 | 370 |
| 15 | Population genomics of Populus trichocarpa identifies signatures of selection and adaptive trait associations. Nature Genetics, 2014, 46, 1089-1096. | 21.4 | 330 |
| 16 | A Multifactor Analysis of Fungal and Bacterial Community Structure in the Root Microbiome of Mature Populus deltoides Trees. PLoS ONE, 2013, 8, e76382. | 2.5 | 315 |
| 17 | The transcriptome of the arbuscular mycorrhizal fungus Glomus intraradices (DAOM 197198) reveals functional tradeoffs in an obligate symbiont. New Phytologist, 2012, 193, 755-769. | 7.3 | 305 |
| 18 | Genomic insights into salt adaptation in a desert poplar. Nature Communications, 2013, 4, 2797. | 12.8 | 286 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Plant host and soil origin influence fungal and bacterial assemblages in the roots of woody plants. Molecular Ecology, 2014, 23, 3356-3370. | 3.9 | 285 |
| 20 | Regulation of Lignin Biosynthesis and Its Role in Growth-Defense Tradeoffs. Frontiers in Plant Science, 2018, 9, 1427. | 3.6 | 231 |
| 21 | Genome-wide analysis of Aux/IAA and ARF gene families in Populus trichocarpa. BMC Plant Biology, 2007, 7, 59. | 3.6 | 218 |
| 22 | A roadmap for research on crassulacean acid metabolism (<scp>CAM</scp>) to enhance sustainable food and bioenergy production in a hotter, drier world. New Phytologist, 2015, 207, 491-504. | 7.3 | 211 |
| 23 | Engineering crassulacean acid metabolism to improve water-use efficiency. Trends in Plant Science, 2014, 19, 327-338. | 8.8 | 206 |
| 24 | Antisense Down-Regulation of 4CL Expression Alters Lignification, Tree Growth, and Saccharification Potential of Field-Grown Poplar Â Â. Plant Physiology, 2010, 154, 874-886. | 4.8 | 195 |
| 25 | Involvement of auxin pathways in modulating root architecture during beneficial plantâ€“microorganism interactions. Plant, Cell and Environment, 2013, 36, 909-919. | 5.7 | 192 |
| 26 | Divergence of the Dof Gene Families in Poplar, Arabidopsis, and Rice Suggests Multiple Modes of Gene Evolution after Duplication. Plant Physiology, 2006, 142, 820-830. | 4.8 | 184 |
| 27 | Specialized Microbiome of a Halophyte and its Role in Helping Non-Host Plants to Withstand Salinity. Scientific Reports, 2016, 6, 32467. | 3.3 | 181 |
| 28 | Genome structure and emerging evidence of an incipient sex chromosome in Populus. Genome Research, 2008, 18, 422-430. | 5.5 | 177 |
| 29 | Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree Populus trichocarpa. New Phytologist, 2012, 196, 713-725. | 7.3 | 173 |
| 30 | Genomeâ€wide association implicates numerous genes underlying ecological trait variation in natural populations of Populus trichocarpa. New Phytologist, 2014, 203, 535-553. | 7.3 | 171 |
| 31 | The KalanchoÃ« genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. Nature Communications, 2017, 8, 1899. | 12.8 | 159 |
| 32 | Genomeâ€wide association mapping for wood characteristics in <scp>P</scp>opulus identifies an array of candidate single nucleotide polymorphisms. New Phytologist, 2013, 200, 710-726. | 7.3 | 158 |
| 33 | Transcript, protein and metabolite temporal dynamics in the CAM plant Agave. Nature Plants, 2016, 2, 16178. | 9.3 | 158 |
| 34 | Phytosequestration: Carbon Biosequestration by Plants and the Prospects of Genetic Engineering. BioScience, 2010, 60, 685-696. | 4.9 | 149 |
| 35 | The willow genome and divergent evolution from poplar after the common genome duplication. Cell Research, 2014, 24, 1274-1277. | 12.0 | 148 |
| 36 | Characterization of microsatellites revealed by genomic sequencing ofPopulus trichocarpa. Canadian Journal of Forest Research, 2004, 34, 85-93. | 1.7 | 145 |

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|---|---|---|---|
| 37 | Plant Host-Associated Mechanisms for Microbial Selection. Frontiers in Plant Science, 2019, 10, 862. | 3.6 | 139 |
| 38 | Large-scale heterospecific segregation distortion in Populus revealed by a dense genetic map. Theoretical and Applied Genetics, 2004, 109, 451-463. | 3.6 | 135 |
| 39 | Variation of S/G Ratio and Lignin Content in a Populus Family Influences the Release of Xylose by Dilute Acid Hydrolysis. Applied Biochemistry and Biotechnology, 2006, 130, 427-435. | 2.9 | 135 |
| 40 | Accelerating Climate Resilient Plant Breeding by Applying Next-Generation Artificial Intelligence. Trends in Biotechnology, 2019, 37, 1217-1235. | 9.3 | 134 |
| 41 | The F-Box Gene Family Is Expanded in Herbaceous Annual Plants Relative to Woody Perennial Plants Â. Plant Physiology, 2008, 148, 1189-1200. | 4.8 | 125 |
| 42 | Plant-Derived Terpenes: A Feedstock for Specialty Biofuels. Trends in Biotechnology, 2017, 35, 227-240. | 9.3 | 124 |
| 43 | A Dual Role of Strigolactones in Phosphate Acquisition and Utilization in Plants. International Journal of Molecular Sciences, 2013, 14, 7681-7701. | 4.1 | 117 |
| 44 | Breeding progress and preparedness for massâ€scale deployment of perennial lignocellulosic biomass crops switchgrass, miscanthus, willow and poplar. GCB Bioenergy, 2019, 11, 118-151. | 5.6 | 116 |
| 45 | Limitations of molecular-marker-aided selection in forest tree breeding. Canadian Journal of Forest Research, 1992, 22, 1050-1061. | 1.7 | 113 |
| 46 | Two Poplar-Associated Bacterial Isolates Induce Additive Favorable Responses in a Constructed Plant-Microbiome System. Frontiers in Plant Science, 2016, 7, 497. | 3.6 | 113 |
| 47 | <scp>Genomeâ€wide association studies</scp> and expressionâ€based quantitative trait loci analyses reveal roles of <scp>HCT</scp>2 in caffeoylquinic acid biosynthesis and its regulation by defenseâ€responsive transcription factors in Populus. New Phytologist, 2018, 220, 502-516. | 7.3 | 112 |
| 48 | Identification of Quantitative Trait Loci Influencing Wood Property Traits in Loblolly Pine (Pinus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 2.9 | 112 |
| 49 | Recent Advances in the Transcriptional Regulation of Secondary Cell Wall Biosynthesis in the Woody Plants. Frontiers in Plant Science, 2018, 9, 1535. | 3.6 | 110 |
| 50 | Poplar Genomics is Getting Popular: The Impact of the Poplar Genome Project on Tree Research. Plant Biology, 2004, 6, 2-4. | 3.8 | 109 |
| 51 | High-resolution genetic mapping of allelic variants associated with cell wall chemistry in Populus. BMC Genomics, 2015, 16, 24. | 2.8 | 106 |
| 52 | An Inâ€Depth Understanding of Biomass Recalcitrance Using Natural Poplar Variants as the Feedstock. ChemSusChem, 2017, 10, 139-150. | 6.8 | 106 |
| 53 | Discovery and annotation of small proteins using genomics, proteomics, and computational approaches. Genome Research, 2011, 21, 634-641. | 5.5 | 105 |
| 54 | Pseudomonas fluorescens Induces Strain-Dependent and Strain-Independent Host Plant Responses in Defense Networks, Primary Metabolism, Photosynthesis, and Fitness. Molecular Plant-Microbe Interactions, 2012, 25, 765-778. | 2.6 | 100 |

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| 55 | <scp>P</scp>opulus trichocarpa cell wall chemistry and ultrastructure trait variation, genetic control and genetic correlations. New Phytologist, 2013, 197, 777-790. | 7.3 | 100 |
| 56 | Significance of Lignin S/G Ratio in Biomass Recalcitrance of Populus trichocarpa Variants for Bioethanol Production. ACS Sustainable Chemistry and Engineering, 2018, 6, 2162-2168. | 6.7 | 100 |
| 57 | Genetic analysis of Physcomitrella patens identifies ABSCISIC ACID NON-RESPONSIVE (ANR), a regulator of ABA responses unique to basal land plants and required for desiccation tolerance. Plant Cell, 2016, 28, tpc.00091.2016. | 6.6 | 98 |
| 58 | Post-fire aspen seedling recruitment across the Yellowstone (USA) Landscape. Landscape Ecology, 2003, 18, 127-140. | 4.2 | 97 |
| 59 | Drought resistance of two hybrid Populus clones grown in a large-scale plantation. Tree Physiology, 1998, 18, 653-658. | 3.1 | 96 |
| 60 | Advances and perspectives on the use of CRISPR/Cas9 systems in plant genomics research. Current Opinion in Plant Biology, 2016, 30, 70-77. | 7.1 | 94 |
| 61 | Toward low-cost biological and hybrid biological/catalytic conversion of cellulosic biomass to fuels. Energy and Environmental Science, 2022, 15, 938-990. | 30.8 | 93 |
| 62 | A 34K <scp>SNP</scp> genotyping array for Populus trichocarpa: Design, application to the study of natural populations and transferability to other Populus species. Molecular Ecology Resources, 2013, 13, 306-323. | 4.8 | 92 |
| 63 | Abiotic Stresses Shift Belowground Populus -Associated Bacteria Toward a Core Stress Microbiome. MSystems, 2018, 3, . | 3.8 | 89 |
| 64 | Highly Efficient Isolation of Populus Mesophyll Protoplasts and Its Application in Transient Expression Assays. PLoS ONE, 2012, 7, e44908. | 2.5 | 89 |
| 65 | ESTABLISHMENT, PERSISTENCE, AND GROWTH OF ASPEN (POPULUS TREMULOIDES) SEEDLINGS IN YELLOWSTONE NATIONAL PARK. Ecology, 2005, 86, 404-418. | 3.2 | 88 |
| 66 | Poplar breeding and testing strategies in the north-central U.S.: Demonstration of potential yield and consideration of future research needs. Forestry Chronicle, 2001, 77, 245-253. | 0.6 | 86 |
| 67 | A study of poplar organosolv lignin after melt rheology treatment as carbon fiber precursors. Green Chemistry, 2016, 18, 5015-5024. | 9.0 | 85 |
| 68 | Multitrait genomeâ€wide association analysis of Populus trichocarpa identifies key polymorphisms controlling morphological and physiological traits. New Phytologist, 2019, 223, 293-309. | 7.3 | 85 |
| 69 | Insights of biomass recalcitrance in natural Populus trichocarpa variants for biomass conversion. Green Chemistry, 2017, 19, 5467-5478. | 9.0 | 82 |
| 70 | Genetic relatedness and female spatial organization in a solitary carnivore, the raccoon,Procyon lotor. Molecular Ecology, 2002, 11, 1115-1124. | 3.9 | 80 |
| 71 | A willow sex chromosome reveals convergent evolution of complex palindromic repeats. Genome Biology, 2020, 21, 38. | 8.8 | 74 |
| 72 | Genome-wide analysis of lectin receptor-like kinases in Populus. BMC Genomics, 2016, 17, 699. | 2.8 | 72 |

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|---|---|---|---|
| 73 | A physical map of the highly heterozygous Populus genome: integration with the genome sequence and genetic map and analysis of haplotype variation. Plant Journal, 2007, 50, 1063-1078. | 5.7 | 70 |
| 74 | Populus trichocarpa and Populus deltoides Exhibit Different Metabolomic Responses to Colonization by the Symbiotic Fungus Laccaria bicolor. Molecular Plant-Microbe Interactions, 2014, 27, 546-556. | 2.6 | 69 |
| 75 | Within tree variability of lignin composition in Populus. Wood Science and Technology, 2008, 42, 649-661. | 3.2 | 68 |
| 76 | Analysis of 4,664 high-quality sequence-finished poplar full-length cDNA clones and their utility for the discovery of genes responding to insect feeding. BMC Genomics, 2008, 9, 57. | 2.8 | 68 |
| 77 | Newly identified helper bacteria stimulate ectomycorrhizal formation in Populus. Frontiers in Plant Science, 2014, 5, 579. | 3.6 | 68 |
| 78 | A host plant genome (Zizania latifolia) after a centuryâ€long endophyte infection. Plant Journal, 2015, 83, 600-609. | 5.7 | 67 |
| 79 | Genetic and physical mapping of Melampsora rust resistance genes in Populus and characterization of linkage disequilibrium and flanking genomic sequence. New Phytologist, 2004, 164, 95-105. | 7.3 | 66 |
| 80 | Short-rotation woody crop systems, atmospheric carbon dioxide and carbon management: A U.S. case study. Forestry Chronicle, 2001, 77, 259-264. | 0.6 | 65 |
| 81 | Knockdown of a laccase in Populus deltoides confers altered cell wall chemistry and increased sugar release. Plant Biotechnology Journal, 2016, 14, 2010-2020. | 8.3 | 64 |
| 82 | Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in Agave. BMC Genomics, 2018, 19, 588. | 2.8 | 64 |
| 83 | Chemical, ultrastructural and supramolecular analysis of tension wood in Populus tremula x alba as a model substrate for reduced recalcitrance. Energy and Environmental Science, 2011, 4, 4962. | 30.8 | 61 |
| 84 | Revisiting the sequencing of the first tree genome: Populus trichocarpa. Tree Physiology, 2013, 33, 357-364. | 3.1 | 61 |
| 85 | Metabolic profiling reveals altered sugar and secondary metabolism in response to UGPase overexpression in Populus. BMC Plant Biology, 2014, 14, 265. | 3.6 | 61 |
| 86 | New technologies accelerate the exploration of non-coding RNAs in horticultural plants. Horticulture Research, 2017, 4, 17031. | 6.3 | 61 |
| 87 | Association mapping, transcriptomics, and transient expression identify candidate genes mediating plantâ€“pathogen interactions in a tree. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11573-11578. | 7.1 | 61 |
| 88 | Characterization of a large sex determination region in Salix purpurea L. (Salicaceae). Molecular Genetics and Genomics, 2018, 293, 1437-1452. | 2.1 | 61 |
| 89 | Structural changes of lignins in natural Populus variants during different pretreatments. Bioresource Technology, 2020, 295, 122240. | 9.6 | 61 |
| 90 | Two High-Throughput Techniques for Determining Wood Properties as Part of a Molecular Genetics Analysis of Hybrid Poplar and Loblolly Pine. Applied Biochemistry and Biotechnology, 1999, 77, 55-66. | 2.9 | 60 |

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| 91 | Metabolic functions of Pseudomonas fluorescens strains from Populus deltoides depend on rhizosphere or endosphere isolation compartment. Frontiers in Microbiology, 2015, 6, 1118. | 3.5 | 60 |
| 92 | <scp>S</scp>phagnum physiology in the context of changing climate: emergent influences of genomics, modelling and hostâ€“microbiome interactions on understanding ecosystem function. Plant, Cell and Environment, 2015, 38, 1737-1751. | 5.7 | 60 |
| 93 | Climateâ€resilient agroforestry: physiological responses to climate change and engineering of crassulacean acid metabolism (<scp>CAM</scp>) as a mitigation strategy. Plant, Cell and Environment, 2015, 38, 1833-1849. | 5.7 | 59 |
| 94 | A 5-Enolpyruvylshikimate 3-Phosphate Synthase Functions as a Transcriptional Repressor in Populus. Plant Cell, 2018, 30, 1645-1660. | 6.6 | 56 |
| 95 | Network-based integration of systems genetics data reveals pathways associated with lignocellulosic biomass accumulation and processing. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1195-1200. | 7.1 | 55 |
| 96 | Annotation and comparative analysis of the glycoside hydrolase genes in Brachypodium distachyon. BMC Genomics, 2010, 11, 600. | 2.8 | 53 |
| 97 | Challenges of the utilization of wood polymers: how can they be overcome?. Applied Microbiology and Biotechnology, 2011, 91, 1525-1536. | 3.6 | 52 |
| 98 | Fungal Endophytes ofPopulus trichocarpaAlter Host Phenotype, Gene Expression, and Rhizobiome Composition. Molecular Plant-Microbe Interactions, 2019, 32, 853-864. | 2.6 | 52 |
| 99 | Phenotypic variation and quantitative trait locus identification for osmotic potential in an interspecific hybrid inbred F2 poplar pedigree grown in contrasting environments. Tree Physiology, 2006, 26, 595-604. | 3.1 | 50 |
| 100 | Genome-wide identification of lineage-specific genes in Arabidopsis, Oryza and Populus. Genomics, 2009, 93, 473-480. | 2.9 | 50 |
| 101 | The obscure events contributing to the evolution of an incipient sex chromosome in Populus: a retrospective working hypothesis. Tree Genetics and Genomes, 2012, 8, 559-571. | 1.6 | 50 |
| 102 | Hardwood Tree Genomics: Unlocking Woody Plant Biology. Frontiers in Plant Science, 2018, 9, 1799. | 3.6 | 50 |
| 103 | Comparative analysis of the transcriptomes of Populus trichocarpa and Arabidopsis thalianasuggests extensive evolution of gene expression regulation in angiosperms. New Phytologist, 2008, 180, 408-420. | 7.3 | 49 |
| 104 | Synthetic biology as it relates to CAM photosynthesis: challenges and opportunities. Journal of Experimental Botany, 2014, 65, 3381-3393. | 4.8 | 49 |
| 105 | Phylogenetic Occurrence of the Phenylpropanoid Pathway and Lignin Biosynthesis in Plants. Frontiers in Plant Science, 2021, 12, 704697. | 3.6 | 49 |
| 106 | Identification of quantitative trait loci affecting ectomycorrhizal symbiosis in an interspecific F1 poplar cross and differential expression of genes in ectomycorrhizas of the two parents: Populus deltoides and Populus trichocarpa. Tree Genetics and Genomes, 2011, 7, 617-627. | 1.6 | 48 |
| 107 | Highly variable SSR markers in Douglas-fir: Mendelian inheritance and map locations. Theoretical and Applied Genetics, 2004, 108, 873-880. | 3.6 | 47 |
| 108 | Multiple levers for overcoming the recalcitrance of lignocellulosic biomass. Biotechnology for Biofuels, 2019, 12, 15. | 6.2 | 47 |

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| 109 | Clonal and seasonal differences in leaf osmotic potential and organic solutes of five hybrid poplar clones grown under field conditions. Tree Physiology, 1998, 18, 645-652. | 3.1 | 46 |
| 110 | MicroSyn: A user friendly tool for detection of microsynteny in a gene family. BMC Bioinformatics, 2011, 12, 79. | 2.6 | 46 |
| 111 | Genomic aspects of research involving polyploid plants. Plant Cell, Tissue and Organ Culture, 2011, 104, 387-397. | 2.3 | 45 |
| 112 | The nature of the progression of drought stress drives differential metabolomic responses in Populus deltoides. Annals of Botany, 2019, 124, 617-626. | 2.9 | 45 |
| 113 | Transgenic Poplar Designed for Biofuels. Trends in Plant Science, 2020, 25, 881-896. | 8.8 | 45 |
| 114 | Identification of candidate genes in Arabidopsis and Populus cell wall biosynthesis using text-mining, co-expression network analysis and comparative genomics. Plant Science, 2011, 181, 675-687. | 3.6 | 44 |
| 115 | Defining the Boundaries and Characterizing the Landscape of Functional Genome Expression in Vascular Tissues of Populus using Shotgun Proteomics. Journal of Proteome Research, 2012, 11, 449-460. | 3.7 | 44 |
| 116 | The Development of Two Flanking SCAR Markers Linked to a Sex Determination Locus in Salix viminalis L. , 2003, 94, 185-189. | | 42 |
| 117 | Poplar Genomics: State of the Science. Critical Reviews in Plant Sciences, 2009, 28, 285-308. | 5.7 | 42 |
| 118 | Mediation of plantâ€“mycorrhizal interaction by a lectin receptor-like kinase. Nature Plants, 2019, 5, 676-680. | 9.3 | 42 |
| 119 | Characterization of Transposable Elements in the Ectomycorrhizal Fungus Laccaria bicolor. PLoS ONE, 2012, 7, e40197. | 2.5 | 38 |
| 120 | Qualitative and quantitative resistances to leaf rust finely mapped within two nucleotideâ€binding site leucineâ€rich repeat (NBSâ€LRR)â€rich genomic regions of chromosome 19 in poplar. New Phytologist, 2011, 192, 151-163. | 7.3 | 37 |
| 121 | 3D Chemical Image using TOFâ€SIMS Revealing the Biopolymer Component Spatial and Lateral Distributions in Biomass. Angewandte Chemie - International Edition, 2012, 51, 12005-12008. | 13.8 | 36 |
| 122 | Identification of quantitative trait loci and candidate genes for cadmium tolerance in Populus. Tree Physiology, 2012, 32, 626-638. | 3.1 | 36 |
| 123 | Populus trichocarpa encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. Scientific Reports, 2017, 7, 382. | 3.3 | 36 |
| 124 | Clonal differences in biomass characteristics, coppice ability, and biomass prediction equations among four Populus clones grown in eastern North Dakota. Canadian Journal of Forest Research, 1992, 22, 348-354. | 1.7 | 34 |
| 125 | Microsatellite primer resource for Populus developed from the mapped sequence scaffolds of the Nisquallyâ€1 genome. New Phytologist, 2009, 181, 498-503. | 7.3 | 34 |
| 126 | Transcriptional and Post-transcriptional Regulation of Lignin Biosynthesis Pathway Genes in Populus. Frontiers in Plant Science, 2020, 11, 652. | 3.6 | 34 |

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|---|---|---|---|
| 127 | Prime Editing Technology and Its Prospects for Future Applications in Plant Biology Research. Biodesign Research, 2020, 2020, . | 1.9 | 34 |
| 128 | CRISPR/Cas9-mediated targeted mutagenesis for functional genomics research of crassulacean acid metabolism plants. Journal of Experimental Botany, 2019, 70, 6621-6629. | 4.8 | 33 |
| 129 | A genetic linkage map for the ectomycorrhizal fungus Laccaria bicolor and its alignment to the wholeâ€genome sequence assemblies. New Phytologist, 2008, 180, 316-328. | 7.3 | 32 |
| 130 | Down-Regulation of KORRIGAN-Like Endo-Î²-1,4-Glucanase Genes Impacts Carbon Partitioning, Mycorrhizal Colonization and Biomass Production in Populus. Frontiers in Plant Science, 2016, 7, 1455. | 3.6 | 32 |
| 131 | Pleiotropic and Epistatic Network-Based Discovery: Integrated Networks for Target Gene Discovery. Frontiers in Energy Research, 2018, 6, . | 2.3 | 32 |
| 132 | Can exascale computing and explainable artificial intelligence applied to plant biology deliver on the United Nations sustainable development goals?. Current Opinion in Biotechnology, 2020, 61, 217-225. | 6.6 | 32 |
| 133 | A New Calmodulin-Binding Protein Expresses in the Context of Secondary Cell Wall Biosynthesis and Impacts Biomass Properties in Populus. Frontiers in Plant Science, 2018, 9, 1669. | 3.6 | 31 |
| 134 | A microarrayâ€based genotyping and genetic mapping approach for highly heterozygous outcrossing species enables localization of a large fraction of the unassembled Populus trichocarpa genome sequence. Plant Journal, 2009, 58, 1054-1067. | 5.7 | 30 |
| 135 | Cytogenetic Analysis of <i>Populus trichocarpa</i> â€“ Ribosomal DNA, Telomere Repeat Sequence, and Marker-selected BACs. Cytogenetic and Genome Research, 2009, 125, 74-80. | 1.1 | 30 |
| 136 | Comparative analysis of GT14/GT14-like gene family in Arabidopsis, Oryza, Populus, Sorghum and Vitis. Plant Science, 2011, 181, 688-695. | 3.6 | 29 |
| 137 | Natural genetic variability reduces recalcitrance in poplar. Biotechnology for Biofuels, 2016, 9, 106. | 6.2 | 29 |
| 138 | Micropropagation of Populus trichocarpa â€˜Nisqually-1â€™: the genotype deriving the Populus reference genome. Plant Cell, Tissue and Organ Culture, 2009, 99, 251-257. | 2.3 | 28 |
| 139 | High Throughput Screening Technologies in Biomass Characterization. Frontiers in Energy Research, 2018, 6, . | 2.3 | 28 |
| 140 | PdWND3A, a wood-associated NAC domain-containing protein, affects lignin biosynthesis and composition in Populus. BMC Plant Biology, 2019, 19, 486. | 3.6 | 28 |
| 141 | Morphophysiological traits as markers for the early selection of conifer genetic families. Canadian Journal of Forest Research, 1992, 22, 1001-1008. | 1.7 | 27 |
| 142 | Defining the genetic components of callus formation: A GWAS approach. PLoS ONE, 2018, 13, e0202519. | 2.5 | 27 |
| 143 | Overexpression of a serine hydroxymethyltransferase increases biomass production and reduces recalcitrance in the bioenergy crop Populus. Sustainable Energy and Fuels, 2019, 3, 195-207. | 4.9 | 27 |
| 144 | Technoeconomic and life-cycle analysis of single-step catalytic conversion of wet ethanol into fungible fuel blendstocks. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12576-12583. | 7.1 | 27 |

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| 145 | Putting the Pieces Together: High-performance LC-MS/MS Provides Network-, Pathway-, and Protein-level Perspectives in Populus. Molecular and Cellular Proteomics, 2013, 12, 106-119. | 3.8 | 26 |
| 146 | Characterization of DWARF14 Genes in Populus. Scientific Reports, 2016, 6, 21593. | 3.3 | 26 |
| 147 | Overexpression of a Domain of Unknown Function 231-containing protein increases O-xylan acetylation and cellulose biosynthesis in Populus. Biotechnology for Biofuels, 2017, 10, 311. | 6.2 | 26 |
| 148 | Mycorrhizal symbionts of Populus to be sequenced by the United States Department of Energy?s Joint Genome Institute. Mycorrhiza, 2004, 14, 63-64. | 2.8 | 25 |
| 149 | Bioinformatics-Based Identification of Candidate Genes from QTLs Associated with Cell Wall Traits in Populus. Bioenergy Research, 2010, 3, 172-182. | 3.9 | 25 |
| 150 | Initial characterization of shade avoidance response suggests functional diversity between Populus phytochrome B genes. New Phytologist, 2012, 196, 726-737. | 7.3 | 25 |
| 151 | Functional Genomics of Drought Tolerance in Bioenergy Crops. Critical Reviews in Plant Sciences, 2014, 33, 205-224. | 5.7 | 25 |
| 152 | Comparative sequence analysis between orthologous regions of theArabidopsisandPopulusgenomes reveals substantial synteny and microcollinearity. Canadian Journal of Forest Research, 2003, 33, 2245-2251. | 1.7 | 24 |
| 153 | Strigolactone-Regulated Proteins Revealed by iTRAQ-Based Quantitative Proteomics in Arabidopsis. Journal of Proteome Research, 2014, 13, 1359-1372. | 3.7 | 24 |
| 154 | Overexpression of an Agave Phosphoenolpyruvate Carboxylase Improves Plant Growth and Stress Tolerance. Cells, 2021, 10, 582. | 4.1 | 24 |
| 155 | Genetic variation in postfire aspen seedlings in Yellowstone National Park. Molecular Ecology, 1999, 8, 1769-1780. | 3.9 | 23 |
| 156 | Efficiency of gene silencing in Arabidopsis: direct inverted repeats vs. transitive RNAi vectors. Plant Biotechnology Journal, 2007, 5, 615-626. | 8.3 | 23 |
| 157 | Conservation and Diversification of Circadian Rhythmicity Between a Model Crassulacean Acid Metabolism Plant KalanchoÃ« fedtschenkoi and a Model C3 Photosynthesis Plant Arabidopsis thaliana. Frontiers in Plant Science, 2018, 9, 1757. | 3.6 | 23 |
| 158 | Characterization of MORE AXILLARY GROWTH Genes in Populus. PLoS ONE, 2014, 9, e102757. | 2.5 | 23 |
| 159 | Characterization of cellulose structure of Populus plants modified in candidate cellulose biosynthesis genes. Biomass and Bioenergy, 2016, 94, 146-154. | 5.7 | 22 |
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