

Gerald A Tuskan

List of Publications by Year in descending order

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233
papers

28,455
citations

10986

71
h-index

5988

160
g-index

249
all docs

249
docs citations

249
times ranked

26480
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Toward low-cost biological and hybrid biological/catalytic conversion of cellulosic biomass to fuels. <i>Energy and Environmental Science</i> , 2022, 15, 938-990. | 30.8 | 93 |
| 2 | Diversity and conservation of plant small secreted proteins associated with arbuscular mycorrhizal symbiosis. <i>Horticulture Research</i> , 2022, 9, . | 6.3 | 1 |
| 3 | An Intein-Mediated Split Cas9 System for Base Editing in Plants. <i>ACS Synthetic Biology</i> , 2022, 11, 2513-2517. | 3.8 | 9 |
| 4 | Economic impact of yield and composition variation in bioenergy crops: <i>Populus trichocarpa</i> . <i>Biofuels, Bioproducts and Biorefining</i> , 2021, 15, 176-188. | 3.7 | 13 |
| 5 | Cover Image, Volume 15, Issue 1. <i>Biofuels, Bioproducts and Biorefining</i> , 2021, 15, i. | 3.7 | 0 |
| 6 | Overexpression of an Agave Phosphoenolpyruvate Carboxylase Improves Plant Growth and Stress Tolerance. <i>Cells</i> , 2021, 10, 582. | 4.1 | 24 |
| 7 | Accurate determination of genotypic variance of cell wall characteristics of a <i>Populus trichocarpa</i> pedigree using high-throughput pyrolysis-molecular beam mass spectrometry. <i>Biotechnology for Biofuels</i> , 2021, 14, 59. | 6.2 | 6 |
| 8 | Transcriptome and Degradome Profiling Reveals a Role of miR530 in the Circadian Regulation of Gene Expression in <i>Kalanchoë marnieriana</i> . <i>Cells</i> , 2021, 10, 1526. | 4.1 | 5 |
| 9 | Advances and perspectives in discovery and functional analysis of small secreted proteins in plants. <i>Horticulture Research</i> , 2021, 8, 130. | 6.3 | 20 |
| 10 | Inference of Gene Regulatory Network Uncovers the Linkage between Circadian Clock and Crassulacean Acid Metabolism in <i>Kalanchoë fedtschenkoi</i> . <i>Cells</i> , 2021, 10, 2217. | 4.1 | 2 |
| 11 | Phylogenetic Occurrence of the Phenylpropanoid Pathway and Lignin Biosynthesis in Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 704697. | 3.6 | 49 |
| 12 | Towards engineering ectomycorrhization into switchgrass bioenergy crops via a lectin receptor-like kinase. <i>Plant Biotechnology Journal</i> , 2021, 19, 2454-2468. | 8.3 | 14 |
| 13 | The Ancient Salicoid Genome Duplication Event: A Platform for Reconstruction of De Novo Gene Evolution in <i>Populus trichocarpa</i> . <i>Genome Biology and Evolution</i> , 2021, 13, . | 2.5 | 9 |
| 14 | Expanding the application of a UV-visible reporter for transient gene expression and stable transformation in plants. <i>Horticulture Research</i> , 2021, 8, 234. | 6.3 | 18 |
| 15 | Heterospecific Neighbor Plants Impact Root Microbiome Diversity and Molecular Function of Root Fungi. <i>Frontiers in Microbiology</i> , 2021, 12, 680267. | 3.5 | 3 |
| 16 | Biological Parts for Plant Biodesign to Enhance Land-Based Carbon Dioxide Removal. <i>Biodesign Research</i> , 2021, 2021, . | 1.9 | 5 |
| 17 | Structural changes of lignins in natural <i>Populus</i> variants during different pretreatments. <i>Bioresource Technology</i> , 2020, 295, 122240. | 9.6 | 61 |
| 18 | Overexpression of a Prefoldin β subunit gene reduces biomass recalcitrance in the bioenergy crop <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 859-871. | 8.3 | 17 |

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|----|--|-----|-----------|
| 19 | Identification of functional single nucleotide polymorphism of <i>Populus trichocarpa</i> PtrEPSPâ€”F and determination of its transcriptional effect. <i>Plant Direct</i> , 2020, 4, e00178. | 1.9 | 4 |
| 20 | Technoeconomic and life-cycle analysis of single-step catalytic conversion of wet ethanol into fungible fuel blendstocks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12576-12583. | 7.1 | 27 |
| 21 | Genome-Wide Association Study of Wood Anatomical and Morphological Traits in <i>Populus trichocarpa</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 545748. | 3.6 | 21 |
| 22 | Sequencing and Analysis of the Sex Determination Region of <i>Populus trichocarpa</i> . <i>Genes</i> , 2020, 11, 843. | 2.4 | 19 |
| 23 | <i>Arabidopsis</i> Câ€”terminal binding protein <i>ANGUSTIFOLIA</i> modulates transcriptional coâ€”regulation of <i>MYB46</i> and <i>WRKY33</i> . <i>New Phytologist</i> , 2020, 228, 1627-1639. | 7.3 | 17 |
| 24 | Transcriptional and Post-transcriptional Regulation of Lignin Biosynthesis Pathway Genes in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 652. | 3.6 | 34 |
| 25 | Transgenic Poplar Designed for Biofuels. <i>Trends in Plant Science</i> , 2020, 25, 881-896. | 8.8 | 45 |
| 26 | Light-responsive expression atlas reveals the effects of light quality and intensity in <i>Kalanchoë fedtschenkoi</i> , a plant with crassulacean acid metabolism. <i>GigaScience</i> , 2020, 9, . | 6.4 | 11 |
| 27 | Can exascale computing and explainable artificial intelligence applied to plant biology deliver on the United Nations sustainable development goals?. <i>Current Opinion in Biotechnology</i> , 2020, 61, 217-225. | 6.6 | 32 |
| 28 | A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biology</i> , 2020, 21, 38. | 8.8 | 74 |
| 29 | Biosystems Design to Accelerate C ₃ -to-CAM Progression. <i>Biodesign Research</i> , 2020, 2020, . | 1.9 | 16 |
| 30 | Plant Biosystems Design Research Roadmap 1.0. <i>Biodesign Research</i> , 2020, 2020, . | 1.9 | 16 |
| 31 | Prime Editing Technology and Its Prospects for Future Applications in Plant Biology Research. <i>Biodesign Research</i> , 2020, 2020, . | 1.9 | 34 |
| 32 | Mediation of plantâ€”mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , 2019, 5, 676-680. | 9.3 | 42 |
| 33 | A Suggestion of Converting Protein Intrinsic Disorder to Structural Entropy Using Shannonâ€”s Information Theory. <i>Entropy</i> , 2019, 21, 591. | 2.2 | 2 |
| 34 | Data Integration in Poplar: â€”Omics Layers and Integration Strategies. <i>Frontiers in Genetics</i> , 2019, 10, 874. | 2.3 | 15 |
| 35 | Comparative genomics can provide new insights into the evolutionary mechanisms and gene function in CAM plants. <i>Journal of Experimental Botany</i> , 2019, 70, 6539-6547. | 4.8 | 21 |
| 36 | Finding New Cell Wall Regulatory Genes in <i>Populus trichocarpa</i> Using Multiple Lines of Evidence. <i>Frontiers in Plant Science</i> , 2019, 10, 1249. | 3.6 | 13 |

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|----|---|-----|-----------|
| 37 | CRISPR/Cas9-mediated targeted mutagenesis for functional genomics research of crassulacean acid metabolism plants. <i>Journal of Experimental Botany</i> , 2019, 70, 6621-6629. | 4.8 | 33 |
| 38 | Overexpression of a serine hydroxymethyltransferase increases biomass production and reduces recalcitrance in the bioenergy crop <i>Populus</i> . <i>Sustainable Energy and Fuels</i> , 2019, 3, 195-207. | 4.9 | 27 |
| 39 | The unexpected malleability of lignin. <i>Nature Plants</i> , 2019, 5, 128-128. | 9.3 | 6 |
| 40 | Fungal Endophytes of <i>Populus trichocarpa</i> Alter Host Phenotype, Gene Expression, and Rhizobiome Composition. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 853-864. | 2.6 | 52 |
| 41 | Genome-wide association studies of bark texture in <i>Populus trichocarpa</i> . <i>Tree Genetics and Genomes</i> , 2019, 15, 1. | 1.6 | 13 |
| 42 | Multiple levers for overcoming the recalcitrance of lignocellulosic biomass. <i>Biotechnology for Biofuels</i> , 2019, 12, 15. | 6.2 | 47 |
| 43 | Plant Host-Associated Mechanisms for Microbial Selection. <i>Frontiers in Plant Science</i> , 2019, 10, 862. | 3.6 | 139 |
| 44 | Wavelet-Based Genomic Signal Processing for Centromere Identification and Hypothesis Generation. <i>Frontiers in Genetics</i> , 2019, 10, 487. | 2.3 | 11 |
| 45 | Accelerating Climate Resilient Plant Breeding by Applying Next-Generation Artificial Intelligence. <i>Trends in Biotechnology</i> , 2019, 37, 1217-1235. | 9.3 | 134 |
| 46 | Multi-Phenotype Association Decomposition: Unraveling Complex Gene-Phenotype Relationships. <i>Frontiers in Genetics</i> , 2019, 10, 417. | 2.3 | 20 |
| 47 | Comparative Genomics Analysis Provides New Insight Into Molecular Basis of Stomatal Movement in <i>Kalanchoe fedtschenkoi</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 292. | 3.6 | 8 |
| 48 | Investigating the correlation of biomass recalcitrance with pyrolysis oil using poplar as the feedstock. <i>Bioresource Technology</i> , 2019, 289, 121589. | 9.6 | 18 |
| 49 | Multitrait genome-wide association analysis of <i>Populus trichocarpa</i> identifies key polymorphisms controlling morphological and physiological traits. <i>New Phytologist</i> , 2019, 223, 293-309. | 7.3 | 85 |
| 50 | Identification of <i>Populus</i> Small RNAs Responsive to Mutualistic Interactions With Mycorrhizal Fungi, <i>Laccaria bicolor</i> and <i>Rhizophagus irregularis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 515. | 3.5 | 17 |
| 51 | The nature of the progression of drought stress drives differential metabolomic responses in <i>Populus deltoides</i> . <i>Annals of Botany</i> , 2019, 124, 617-626. | 2.9 | 45 |
| 52 | Engineering Tree Seasonal Cycles of Growth Through Chromatin Modification. <i>Frontiers in Plant Science</i> , 2019, 10, 412. | 3.6 | 17 |
| 53 | Population-level approaches reveal novel aspects of lignin biosynthesis, content, composition and structure. <i>Current Opinion in Biotechnology</i> , 2019, 56, 250-257. | 6.6 | 20 |
| 54 | PdWND3A, a wood-associated NAC domain-containing protein, affects lignin biosynthesis and composition in <i>Populus</i> . <i>BMC Plant Biology</i> , 2019, 19, 486. | 3.6 | 28 |

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|----|---|-----|-----------|
| 55 | Breeding progress and preparedness for mass-scale deployment of perennial lignocellulosic biomass crops switchgrass, miscanthus, willow and poplar. <i>GCB Bioenergy</i> , 2019, 11, 118-151. | 5.6 | 116 |
| 56 | Abiotic Stresses Shift Belowground <i>Populus</i> -Associated Bacteria Toward a Core Stress Microbiome. <i>MSystems</i> , 2018, 3, . | 3.8 | 89 |
| 57 | The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533. | 5.7 | 406 |
| 58 | Significance of Lignin S/G Ratio in Biomass Recalcitrance of <i>Populus trichocarpa</i> Variants for Bioethanol Production. <i>ACS Sustainable Chemistry and Engineering</i> , 2018, 6, 2162-2168. | 6.7 | 100 |
| 59 | Conservation and Diversification of Circadian Rhythmicity Between a Model Crassulacean Acid Metabolism Plant <i>Kalanchoe fedtschenkoi</i> and a Model C3 Photosynthesis Plant <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1757. | 3.6 | 23 |
| 60 | High Throughput Screening Technologies in Biomass Characterization. <i>Frontiers in Energy Research</i> , 2018, 6, . | 2.3 | 28 |
| 61 | Recent Advances in the Transcriptional Regulation of Secondary Cell Wall Biosynthesis in the Woody Plants. <i>Frontiers in Plant Science</i> , 2018, 9, 1535. | 3.6 | 110 |
| 62 | Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799. | 3.6 | 50 |
| 63 | A New Calmodulin-Binding Protein Expresses in the Context of Secondary Cell Wall Biosynthesis and Impacts Biomass Properties in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1669. | 3.6 | 31 |
| 64 | PtWOX11 acts as master regulator conducting the expression of key transcription factors to induce de novo shoot organogenesis in poplar. <i>Plant Molecular Biology</i> , 2018, 98, 389-406. | 3.9 | 21 |
| 65 | Association mapping, transcriptomics, and transient expression identify candidate genes mediating plant-pathogen interactions in a tree. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11573-11578. | 7.1 | 61 |
| 66 | Defining the genetic components of callus formation: A GWAS approach. <i>PLoS ONE</i> , 2018, 13, e0202519. | 2.5 | 27 |
| 67 | Regulation of Lignin Biosynthesis and Its Role in Growth-Defense Tradeoffs. <i>Frontiers in Plant Science</i> , 2018, 9, 1427. | 3.6 | 231 |
| 68 | Understanding the influences of different pretreatments on recalcitrance of <i>Populus</i> natural variants. <i>Bioresource Technology</i> , 2018, 265, 75-81. | 9.6 | 20 |
| 69 | Classification of Complete Proteomes of Different Organisms and Protein Sets Based on Their Protein Distributions in Terms of Some Key Attributes of Proteins. <i>International Journal of Genomics</i> , 2018, 2018, 1-12. | 1.6 | 3 |
| 70 | Perspectives on the basic and applied aspects of crassulacean acid metabolism (CAM) research. <i>Plant Science</i> , 2018, 274, 394-401. | 3.6 | 18 |
| 71 | A Variable Polyglutamine Repeat Affects Subcellular Localization and Regulatory Activity of a <i>Populus</i> ANGUSTIFOLIA Protein. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2631-2641. | 1.8 | 9 |
| 72 | Pleiotropic and Epistatic Network-Based Discovery: Integrated Networks for Target Gene Discovery. <i>Frontiers in Energy Research</i> , 2018, 6, . | 2.3 | 32 |

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|----|--|------|-----------|
| 73 | <sc>Genome-wide association studies</sc> and expression-based quantitative trait loci analyses reveal roles of <sc>HCT</sc> 2 in caffeoylquinic acid biosynthesis and its regulation by defense-responsive transcription factors in <i>Populus</i>. <i>New Phytologist</i> , 2018, 220, 502-516. | 7.3 | 112 |
| 74 | Characterization of a large sex determination region in <i>Salix purpurea</i> L. (Salicaceae). <i>Molecular Genetics and Genomics</i> , 2018, 293, 1437-1452. | 2.1 | 61 |
| 75 | Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in <i>Agave</i> . <i>BMC Genomics</i> , 2018, 19, 588. | 2.8 | 64 |
| 76 | A 5-Enolpyruvylshikimate 3-Phosphate Synthase Functions as a Transcriptional Repressor in <i>Populus</i>. <i>Plant Cell</i> , 2018, 30, 1645-1660. | 6.6 | 56 |
| 77 | Quantitative proteome profile of water deficit stress responses in eastern cottonwood (<i>Populus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 17 | 2.5 | 17 |
| 78 | Network-based integration of systems genetics data reveals pathways associated with lignocellulosic biomass accumulation and processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1195-1200. | 7.1 | 55 |
| 79 | Overexpression of a Domain of Unknown Function 266-containing protein results in high cellulose content, reduced recalcitrance, and enhanced plant growth in the bioenergy crop <i>Populus</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 74. | 6.2 | 22 |
| 80 | Effects of Biomass Accessibility and Klason Lignin Contents during Consolidated Bioprocessing in <i>Populus trichocarpa</i>. <i>ACS Sustainable Chemistry and Engineering</i> , 2017, 5, 5075-5081. | 6.7 | 20 |
| 81 | <i>Populus trichocarpa</i> encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. <i>Scientific Reports</i> , 2017, 7, 382. | 3.3 | 36 |
| 82 | Insights of biomass recalcitrance in natural <i>Populus trichocarpa</i> variants for biomass conversion. <i>Green Chemistry</i> , 2017, 19, 5467-5478. | 9.0 | 82 |
| 83 | The <i>Kalanchoë</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899. | 12.8 | 159 |
| 84 | New technologies accelerate the exploration of non-coding RNAs in horticultural plants. <i>Horticulture Research</i> , 2017, 4, 17031. | 6.3 | 61 |
| 85 | An In-Depth Understanding of Biomass Recalcitrance Using Natural Poplar Variants as the Feedstock. <i>ChemSusChem</i> , 2017, 10, 139-150. | 6.8 | 106 |
| 86 | Plant-Derived Terpenes: A Feedstock for Specialty Biofuels. <i>Trends in Biotechnology</i> , 2017, 35, 227-240. | 9.3 | 124 |
| 87 | Overexpression of a Domain of Unknown Function 231-containing protein increases O-xylan acetylation and cellulose biosynthesis in <i>Populus</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 311. | 6.2 | 26 |
| 88 | Agronomic performance of <i>Populus deltoides</i> trees engineered for biofuel production. <i>Biotechnology for Biofuels</i> , 2017, 10, 253. | 6.2 | 22 |
| 89 | Quantitative trait locus mapping of <i>Populus</i> bark features and stem diameter. <i>BMC Plant Biology</i> , 2017, 17, 224. | 3.6 | 14 |
| 90 | Two Poplar-Associated Bacterial Isolates Induce Additive Favorable Responses in a Constructed Plant-Microbiome System. <i>Frontiers in Plant Science</i> , 2016, 7, 497. | 3.6 | 113 |

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|-----|--|-----|-----------|
| 91 | Down-Regulation of KORRIGAN-Like Endo- β -1,4-Glucanase Genes Impacts Carbon Partitioning, Mycorrhizal Colonization and Biomass Production in Populus. <i>Frontiers in Plant Science</i> , 2016, 7, 1455. | 3.6 | 32 |
| 92 | Characterization of DWARF14 Genes in Populus. <i>Scientific Reports</i> , 2016, 6, 21593. | 3.3 | 26 |
| 93 | Knockdown of a laccase in <i>Populus deltoides</i> confers altered cell wall chemistry and increased sugar release. <i>Plant Biotechnology Journal</i> , 2016, 14, 2010-2020. | 8.3 | 64 |
| 94 | Characterization of cellulose structure of Populus plants modified in candidate cellulose biosynthesis genes. <i>Biomass and Bioenergy</i> , 2016, 94, 146-154. | 5.7 | 22 |
| 95 | Transcript, protein and metabolite temporal dynamics in the CAM plant Agave. <i>Nature Plants</i> , 2016, 2, 16178. | 9.3 | 158 |
| 96 | Genome-wide analysis of lectin receptor-like kinases in Populus. <i>BMC Genomics</i> , 2016, 17, 699. | 2.8 | 72 |
| 97 | Specialized Microbiome of a Halophyte and its Role in Helping Non-Host Plants to Withstand Salinity. <i>Scientific Reports</i> , 2016, 6, 32467. | 3.3 | 181 |
| 98 | An innovative platform for quick and flexible joining of assorted DNA fragments. <i>Scientific Reports</i> , 2016, 6, 19278. | 3.3 | 20 |
| 99 | Natural genetic variability reduces recalcitrance in poplar. <i>Biotechnology for Biofuels</i> , 2016, 9, 106. | 6.2 | 29 |
| 100 | Genetic analysis of <i>Physcomitrella patens</i> identifies ABSCISIC ACID NON-RESPONSIVE (ANR), a regulator of ABA responses unique to basal land plants and required for desiccation tolerance. <i>Plant Cell</i> , 2016, 28, tpc.00091.2016. | 6.6 | 98 |
| 101 | A study of poplar organosolv lignin after melt rheology treatment as carbon fiber precursors. <i>Green Chemistry</i> , 2016, 18, 5015-5024. | 9.0 | 85 |
| 102 | Simultaneous knockdown of six non-family genes using a single synthetic RNAi fragment in <i>Arabidopsis thaliana</i> . <i>Plant Methods</i> , 2016, 12, 16. | 4.3 | 12 |
| 103 | Advances and perspectives on the use of CRISPR/Cas9 systems in plant genomics research. <i>Current Opinion in Plant Biology</i> , 2016, 30, 70-77. | 7.1 | 94 |
| 104 | Scaling nitrogen and carbon interactions: what are the consequences of biological buffering?. <i>Ecology and Evolution</i> , 2015, 5, 2839-2850. | 1.9 | 4 |
| 105 | A roadmap for research on crassulacean acid metabolism (CAM) to enhance sustainable food and bioenergy production in a hotter, drier world. <i>New Phytologist</i> , 2015, 207, 491-504. | 7.3 | 211 |
| 106 | A host plant genome (<i>Zizania latifolia</i>) after a century-long endophyte infection. <i>Plant Journal</i> , 2015, 83, 600-609. | 5.7 | 67 |
| 107 | Metabolic functions of <i>Pseudomonas fluorescens</i> strains from <i>Populus deltoides</i> depend on rhizosphere or endosphere isolation compartment. <i>Frontiers in Microbiology</i> , 2015, 6, 1118. | 3.5 | 60 |
| 108 | High-resolution genetic mapping of allelic variants associated with cell wall chemistry in Populus. <i>BMC Genomics</i> , 2015, 16, 24. | 2.8 | 106 |

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|-----|---|------|-----------|
| 109 | The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442. | 21.4 | 472 |
| 110 | Integrating mRNA and Protein Sequencing Enables the Detection and Quantitative Profiling of Natural Protein Sequence Variants of <i>Populus trichocarpa</i> . <i>Journal of Proteome Research</i> , 2015, 14, 5318-5326. | 3.7 | 6 |
| 111 | Climate-resilient agroforestry: physiological responses to climate change and engineering of crassulacean acid metabolism (CAM) as a mitigation strategy. <i>Plant, Cell and Environment</i> , 2015, 38, 1833-1849. | 5.7 | 59 |
| 112 | <i>Sphagnum</i> physiology in the context of changing climate: emergent influences of genomics, modelling and host-microbiome interactions on understanding ecosystem function. <i>Plant, Cell and Environment</i> , 2015, 38, 1737-1751. | 5.7 | 60 |
| 113 | The willow genome and divergent evolution from poplar after the common genome duplication. <i>Cell Research</i> , 2014, 24, 1274-1277. | 12.0 | 148 |
| 114 | Newly identified helper bacteria stimulate ectomycorrhizal formation in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 579. | 3.6 | 68 |
| 115 | Metabolic profiling reveals altered sugar and secondary metabolism in response to UGPase overexpression in <i>Populus</i> . <i>BMC Plant Biology</i> , 2014, 14, 265. | 3.6 | 61 |
| 116 | Engineering crassulacean acid metabolism to improve water-use efficiency. <i>Trends in Plant Science</i> , 2014, 19, 327-338. | 8.8 | 206 |
| 117 | Synthetic biology as it relates to CAM photosynthesis: challenges and opportunities. <i>Journal of Experimental Botany</i> , 2014, 65, 3381-3393. | 4.8 | 49 |
| 118 | Lignin Valorization: Improving Lignin Processing in the Biorefinery. <i>Science</i> , 2014, 344, 1246843. | 12.6 | 2,994 |
| 119 | Functional Genomics of Drought Tolerance in Bioenergy Crops. <i>Critical Reviews in Plant Sciences</i> , 2014, 33, 205-224. | 5.7 | 25 |
| 120 | The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362. | 27.8 | 725 |
| 121 | Strigolactone-Regulated Proteins Revealed by iTRAQ-Based Quantitative Proteomics in <i>Arabidopsis</i> . <i>Journal of Proteome Research</i> , 2014, 13, 1359-1372. | 3.7 | 24 |
| 122 | Genome-wide association implicates numerous genes underlying ecological trait variation in natural populations of <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2014, 203, 535-553. | 7.3 | 171 |
| 123 | Population genomics of <i>Populus trichocarpa</i> identifies signatures of selection and adaptive trait associations. <i>Nature Genetics</i> , 2014, 46, 1089-1096. | 21.4 | 330 |
| 124 | Plant host and soil origin influence fungal and bacterial assemblages in the roots of woody plants. <i>Molecular Ecology</i> , 2014, 23, 3356-3370. | 3.9 | 285 |
| 125 | <i>Populus trichocarpa</i> and <i>Populus deltoides</i> Exhibit Different Metabolomic Responses to Colonization by the Symbiotic Fungus <i>Laccaria bicolor</i> . <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 546-556. | 2.6 | 69 |
| 126 | Characterization of MORE AXILLARY GROWTH Genes in <i>Populus</i> . <i>PLoS ONE</i> , 2014, 9, e102757. | 2.5 | 23 |

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|-----|---|------|-----------|
| 127 | Genome-wide association mapping for wood characteristics in <i>Populus</i> identifies an array of candidate single nucleotide polymorphisms. <i>New Phytologist</i> , 2013, 200, 710-726. | 7.3 | 158 |
| 128 | A 34K SNP genotyping array for <i>Populus trichocarpa</i> : Design, application to the study of natural populations and transferability to other <i>Populus</i> species. <i>Molecular Ecology Resources</i> , 2013, 13, 306-323. | 4.8 | 92 |
| 129 | Genomic insights into salt adaptation in a desert poplar. <i>Nature Communications</i> , 2013, 4, 2797. | 12.8 | 286 |
| 130 | Genome of an arbuscular mycorrhizal fungus provides insight into the oldest plant symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20117-20122. | 7.1 | 717 |
| 131 | A Dual Role of Strigolactones in Phosphate Acquisition and Utilization in Plants. <i>International Journal of Molecular Sciences</i> , 2013, 14, 7681-7701. | 4.1 | 117 |
| 132 | Extending the Arabidopsis flowering paradigm to a mass flowering phenomenon in the tropics. <i>Molecular Ecology</i> , 2013, 22, 4603-4605. | 3.9 | 1 |
| 133 | <i>Populus trichocarpa</i> cell wall chemistry and ultrastructure trait variation, genetic control and genetic correlations. <i>New Phytologist</i> , 2013, 197, 777-790. | 7.3 | 100 |
| 134 | Involvement of auxin pathways in modulating root architecture during beneficial plant-microorganism interactions. <i>Plant, Cell and Environment</i> , 2013, 36, 909-919. | 5.7 | 192 |
| 135 | Moving Away from the Reference Genome: Evaluating a Peptide Sequencing Tagging Approach for Single Amino Acid Polymorphism Identifications in the Genus <i>Populus</i> . <i>Journal of Proteome Research</i> , 2013, 12, 3642-3651. | 3.7 | 9 |
| 136 | Putting the Pieces Together: High-performance LC-MS/MS Provides Network-, Pathway-, and Protein-level Perspectives in <i>Populus</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 106-119. | 3.8 | 26 |
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