

# Gerald A Tuskan

## List of Publications by Year in descending order

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233  
papers

28,455  
citations

10956

71  
h-index

5965

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.	15.6	93
2	Diversity and conservation of plant small secreted proteins associated with arbuscular mycorrhizal symbiosis. <i>Horticulture Research</i> , 2022, 9, .	2.9	1
3	An Intein-Mediated Split Cas9 System for Base Editing in Plants. <i>ACS Synthetic Biology</i> , 2022, 11, 2513-2517.	1.9	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.	1.9	13
5	Cover Image, Volume 15, Issue 1. <i>Biofuels, Bioproducts and Biorefining</i> , 2021, 15, i.	1.9	0
6	Overexpression of an Agave Phosphoenolpyruvate Carboxylase Improves Plant Growth and Stress Tolerance. <i>Cells</i> , 2021, 10, 582.	1.8	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.	1.8	5
9	Advances and perspectives in discovery and functional analysis of small secreted proteins in plants. <i>Horticulture Research</i> , 2021, 8, 130.	2.9	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.	1.8	2
11	Phylogenetic Occurrence of the Phenylpropanoid Pathway and Lignin Biosynthesis in Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 704697.	1.7	49
12	Towards engineering ectomycorrhization into switchgrass bioenergy crops via a lectin receptor-like kinase. <i>Plant Biotechnology Journal</i> , 2021, 19, 2454-2468.	4.1	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, .	1.1	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.	2.9	18
15	Heterospecific Neighbor Plants Impact Root Microbiome Diversity and Molecular Function of Root Fungi. <i>Frontiers in Microbiology</i> , 2021, 12, 680267.	1.5	3
16	Biological Parts for Plant Biodesign to Enhance Land-Based Carbon Dioxide Removal. <i>Biodesign Research</i> , 2021, 2021, .	0.8	5
17	Structural changes of lignins in natural <i>Populus</i> variants during different pretreatments. <i>Bioresource Technology</i> , 2020, 295, 122240.	4.8	61
18	Overexpression of a Prefoldin $\beta$ subunit gene reduces biomass recalcitrance in the bioenergy crop <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 859-871.	4.1	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.	0.8	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.	3.3	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.	1.7	21
22	Sequencing and Analysis of the Sex Determination Region of <i>Populus trichocarpa</i> . <i>Genes</i> , 2020, 11, 843.	1.0	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.	3.5	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.	1.7	34
25	Transgenic Poplar Designed for Biofuels. <i>Trends in Plant Science</i> , 2020, 25, 881-896.	4.3	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, .	3.3	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.	3.3	32
28	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biology</i> , 2020, 21, 38.	3.8	74
29	Biosystems Design to Accelerate C <sub>3</sub> -to-CAM Progression. <i>Biodesign Research</i> , 2020, 2020, .	0.8	16
30	Plant Biosystems Design Research Roadmap 1.0. <i>Biodesign Research</i> , 2020, 2020, .	0.8	16
31	Prime Editing Technology and Its Prospects for Future Applications in Plant Biology Research. <i>Biodesign Research</i> , 2020, 2020, .	0.8	34
32	Mediation of plantâ€”mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , 2019, 5, 676-680.	4.7	42
33	A Suggestion of Converting Protein Intrinsic Disorder to Structural Entropy Using Shannonâ€”s Information Theory. <i>Entropy</i> , 2019, 21, 591.	1.1	2
34	Data Integration in Poplar: â€”Omics Layers and Integration Strategies. <i>Frontiers in Genetics</i> , 2019, 10, 874.	1.1	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.	2.4	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.	1.7	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.	2.4	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.	2.5	27
39	The unexpected malleability of lignin. <i>Nature Plants</i> , 2019, 5, 128-128.	4.7	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.	1.4	52
41	Genome-wide association studies of bark texture in <i>Populus trichocarpa</i> . <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	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.	1.7	139
44	Wavelet-Based Genomic Signal Processing for Centromere Identification and Hypothesis Generation. <i>Frontiers in Genetics</i> , 2019, 10, 487.	1.1	11
45	Accelerating Climate Resilient Plant Breeding by Applying Next-Generation Artificial Intelligence. <i>Trends in Biotechnology</i> , 2019, 37, 1217-1235.	4.9	134
46	Multi-Phenotype Association Decomposition: Unraveling Complex Gene-Phenotype Relationships. <i>Frontiers in Genetics</i> , 2019, 10, 417.	1.1	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.	1.7	8
48	Investigating the correlation of biomass recalcitrance with pyrolysis oil using poplar as the feedstock. <i>Bioresource Technology</i> , 2019, 289, 121589.	4.8	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.	3.5	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.	1.5	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.	1.4	45
52	Engineering Tree Seasonal Cycles of Growth Through Chromatin Modification. <i>Frontiers in Plant Science</i> , 2019, 10, 412.	1.7	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.	3.3	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.	1.6	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.	2.5	116
56	Abiotic Stresses Shift Belowground <i>Populus</i> -Associated Bacteria Toward a Core Stress Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	89
57	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	2.8	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.	3.2	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.	1.7	23
60	High Throughput Screening Technologies in Biomass Characterization. <i>Frontiers in Energy Research</i> , 2018, 6, .	1.2	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.	1.7	110
62	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	1.7	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.	1.7	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.	2.0	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.	3.3	61
66	Defining the genetic components of callus formation: A GWAS approach. <i>PLoS ONE</i> , 2018, 13, e0202519.	1.1	27
67	Regulation of Lignin Biosynthesis and Its Role in Growth-Defense Tradeoffs. <i>Frontiers in Plant Science</i> , 2018, 9, 1427.	1.7	231
68	Understanding the influences of different pretreatments on recalcitrance of <i>Populus</i> natural variants. <i>Bioresource Technology</i> , 2018, 265, 75-81.	4.8	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.	0.8	3
70	Perspectives on the basic and applied aspects of crassulacean acid metabolism (CAM) research. <i>Plant Science</i> , 2018, 274, 394-401.	1.7	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.	0.8	9
72	Pleiotropic and Epistatic Network-Based Discovery: Integrated Networks for Target Gene Discovery. <i>Frontiers in Energy Research</i> , 2018, 6, .	1.2	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.	3.5	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.	1.0	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.	1.2	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.	3.1	56
77	Quantitative proteome profile of water deficit stress responses in eastern cottonwood ( <i>Populus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 17	1.1	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.	3.3	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.	3.2	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.	1.6	36
82	Insights of biomass recalcitrance in natural <i>Populus trichocarpa</i> variants for biomass conversion. <i>Green Chemistry</i> , 2017, 19, 5467-5478.	4.6	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.	5.8	159
84	New technologies accelerate the exploration of non-coding RNAs in horticultural plants. <i>Horticulture Research</i> , 2017, 4, 17031.	2.9	61
85	An In-Depth Understanding of Biomass Recalcitrance Using Natural Poplar Variants as the Feedstock. <i>ChemSusChem</i> , 2017, 10, 139-150.	3.6	106
86	Plant-Derived Terpenes: A Feedstock for Specialty Biofuels. <i>Trends in Biotechnology</i> , 2017, 35, 227-240.	4.9	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.	1.6	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.	1.7	113

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91	Down-Regulation of KORRIGAN-Like Endo- $\beta$ -1,4-Glucanase Genes Impacts Carbon Partitioning, Mycorrhizal Colonization and Biomass Production in Populus. <i>Frontiers in Plant Science</i> , 2016, 7, 1455.	1.7	32
92	Characterization of DWARF14 Genes in Populus. <i>Scientific Reports</i> , 2016, 6, 21593.	1.6	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.	4.1	64
94	Characterization of cellulose structure of Populus plants modified in candidate cellulose biosynthesis genes. <i>Biomass and Bioenergy</i> , 2016, 94, 146-154.	2.9	22
95	Transcript, protein and metabolite temporal dynamics in the CAM plant Agave. <i>Nature Plants</i> , 2016, 2, 16178.	4.7	158
96	Genome-wide analysis of lectin receptor-like kinases in Populus. <i>BMC Genomics</i> , 2016, 17, 699.	1.2	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.	1.6	181
98	An innovative platform for quick and flexible joining of assorted DNA fragments. <i>Scientific Reports</i> , 2016, 6, 19278.	1.6	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.	3.1	98
101	A study of poplar organosolv lignin after melt rheology treatment as carbon fiber precursors. <i>Green Chemistry</i> , 2016, 18, 5015-5024.	4.6	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.	1.9	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.	3.5	94
104	Scaling nitrogen and carbon interactions: what are the consequences of biological buffering?. <i>Ecology and Evolution</i> , 2015, 5, 2839-2850.	0.8	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.	3.5	211
106	A host plant genome ( <i>Zizania latifolia</i> ) after a century-long endophyte infection. <i>Plant Journal</i> , 2015, 83, 600-609.	2.8	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.	1.5	60
108	High-resolution genetic mapping of allelic variants associated with cell wall chemistry in Populus. <i>BMC Genomics</i> , 2015, 16, 24.	1.2	106

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109	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	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.	1.8	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.	2.8	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.	2.8	60
113	The willow genome and divergent evolution from poplar after the common genome duplication. <i>Cell Research</i> , 2014, 24, 1274-1277.	5.7	148
114	Newly identified helper bacteria stimulate ectomycorrhizal formation in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 579.	1.7	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.	1.6	61
116	Engineering crassulacean acid metabolism to improve water-use efficiency. <i>Trends in Plant Science</i> , 2014, 19, 327-338.	4.3	206
117	Synthetic biology as it relates to CAM photosynthesis: challenges and opportunities. <i>Journal of Experimental Botany</i> , 2014, 65, 3381-3393.	2.4	49
118	Lignin Valorization: Improving Lignin Processing in the Biorefinery. <i>Science</i> , 2014, 344, 1246843.	6.0	2,994
119	Functional Genomics of Drought Tolerance in Bioenergy Crops. <i>Critical Reviews in Plant Sciences</i> , 2014, 33, 205-224.	2.7	25
120	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	13.7	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.	1.8	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.	3.5	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.	9.4	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.	2.0	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.	1.4	69
126	Characterization of MORE AXILLARY GROWTH Genes in <i>Populus</i> . <i>PLoS ONE</i> , 2014, 9, e102757.	1.1	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.	3.5	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.	2.2	92
129	Genomic insights into salt adaptation in a desert poplar. <i>Nature Communications</i> , 2013, 4, 2797.	5.8	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.	3.3	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.	1.8	117
132	Extending the Arabidopsis flowering paradigm to a mass flowering phenomenon in the tropics. <i>Molecular Ecology</i> , 2013, 22, 4603-4605.	2.0	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.	3.5	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.	2.8	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.	1.8	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.	2.5	26
137	Revisiting the sequencing of the first tree genome: <i>Populus trichocarpa</i> . <i>Tree Physiology</i> , 2013, 33, 357-364.	1.4	61
138	Evolutionary analyses of non-family genes in plants. <i>Plant Journal</i> , 2013, 73, 788-797.	2.8	7
139	A Multifactor Analysis of Fungal and Bacterial Community Structure in the Root Microbiome of Mature <i>Populus deltoides</i> Trees. <i>PLoS ONE</i> , 2013, 8, e76382.	1.1	315
140	Genome Anchored QTLs for Biomass Productivity in Hybrid <i>Populus</i> Grown under Contrasting Environments. <i>PLoS ONE</i> , 2013, 8, e54468.	1.1	20
141	From systems biology to photosynthesis and whole-plant physiology. <i>Plant Signaling and Behavior</i> , 2012, 7, 260-262.	1.2	13
142	Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2012, 196, 713-725.	3.5	173
143	Initial characterization of shade avoidance response suggests functional diversity between <i>Populus</i> phytochrome B genes. <i>New Phytologist</i> , 2012, 196, 726-737.	3.5	25
144	3D Chemical Image using TOF-SIMS Revealing the Biopolymer Component Spatial and Lateral Distributions in Biomass. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 12005-12008.	7.2	36

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