

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	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	6.0	3,945
2	Lignin Valorization: Improving Lignin Processing in the Biorefinery. <i>Science</i> , 2014, 344, 1246843.	6.0	2,994
3	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	13.7	1,685
4	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	13.7	1,003
5	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	9.4	864
6	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	13.7	725
7	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
8	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	3.3	640
9	Poplar as a feedstock for biofuels: A review of compositional characteristics. <i>Biofuels, Bioproducts and Biorefining</i> , 2010, 4, 209-226.	1.9	558
10	Distinct Microbial Communities within the Endosphere and Rhizosphere of <i>Populus deltoides</i> Roots across Contrasting Soil Types. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5934-5944.	1.4	524
11	Lignin content in natural <i>Populus</i> variants affects sugar release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6300-6305.	3.3	515
12	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
13	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
14	<i>FLOWERING LOCUS T</i> duplication coordinates reproductive and vegetative growth in perennial poplar. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10756-10761.	3.3	370
15	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
16	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
17	The transcriptome of the arbuscular mycorrhizal fungus <i>Glomus intraradices</i> (DAOM 197198) reveals functional tradeoffs in an obligate symbiont. <i>New Phytologist</i> , 2012, 193, 755-769.	3.5	305
18	Genomic insights into salt adaptation in a desert poplar. <i>Nature Communications</i> , 2013, 4, 2797.	5.8	286

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19	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
20	Regulation of Lignin Biosynthesis and Its Role in Growth-Defense Tradeoffs. <i>Frontiers in Plant Science</i> , 2018, 9, 1427.	1.7	231
21	Genome-wide analysis of Aux/IAA and ARF gene families in <i>Populus trichocarpa</i> . <i>BMC Plant Biology</i> , 2007, 7, 59.	1.6	218
22	A roadmap for research on crassulacean acid metabolism (<sc>CAM</sc>) to enhance sustainable food and bioenergy production in a hotter, drier world. <i>New Phytologist</i> , 2015, 207, 491-504.	3.5	211
23	Engineering crassulacean acid metabolism to improve water-use efficiency. <i>Trends in Plant Science</i> , 2014, 19, 327-338.	4.3	206
24	Antisense Down-Regulation of <i>4CL</i> Expression Alters Lignification, Tree Growth, and Saccharification Potential of Field-Grown Poplar Å Å. <i>Plant Physiology</i> , 2010, 154, 874-886.	2.3	195
25	Involvement of auxin pathways in modulating root architecture during beneficial plant-Åmicroorganism interactions. <i>Plant, Cell and Environment</i> , 2013, 36, 909-919.	2.8	192
26	Divergence of the Dof Gene Families in Poplar, Arabidopsis, and Rice Suggests Multiple Modes of Gene Evolution after Duplication. <i>Plant Physiology</i> , 2006, 142, 820-830.	2.3	184
27	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
28	Genome structure and emerging evidence of an incipient sex chromosome in <i>Populus</i>. <i>Genome Research</i> , 2008, 18, 422-430.	2.4	177
29	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
30	Genome-Åwide 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
31	The <i>Kalancho</i> Å genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899.	5.8	159
32	Genome-Åwide association mapping for wood characteristics in <i><sc>P</sc>opulus</i> identifies an array of candidate single nucleotide polymorphisms. <i>New Phytologist</i> , 2013, 200, 710-726.	3.5	158
33	Transcript, protein and metabolite temporal dynamics in the CAM plant <i>Agave</i> . <i>Nature Plants</i> , 2016, 2, 16178.	4.7	158
34	Phytosequestration: Carbon Biosequestration by Plants and the Prospects of Genetic Engineering. <i>BioScience</i> , 2010, 60, 685-696.	2.2	149
35	The willow genome and divergent evolution from poplar after the common genome duplication. <i>Cell Research</i> , 2014, 24, 1274-1277.	5.7	148
36	Characterization of microsatellites revealed by genomic sequencing of <i>Populus trichocarpa</i> . <i>Canadian Journal of Forest Research</i> , 2004, 34, 85-93.	0.8	145

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37	Plant Host-Associated Mechanisms for Microbial Selection. <i>Frontiers in Plant Science</i> , 2019, 10, 862.	1.7	139
38	Large-scale heterospecific segregation distortion in <i>Populus</i> revealed by a dense genetic map. <i>Theoretical and Applied Genetics</i> , 2004, 109, 451-463.	1.8	135
39	Variation of S/G Ratio and Lignin Content in a <i>Populus</i> Family Influences the Release of Xylose by Dilute Acid Hydrolysis. <i>Applied Biochemistry and Biotechnology</i> , 2006, 130, 427-435.	1.4	135
40	Accelerating Climate Resilient Plant Breeding by Applying Next-Generation Artificial Intelligence. <i>Trends in Biotechnology</i> , 2019, 37, 1217-1235.	4.9	134
41	The F-Box Gene Family Is Expanded in Herbaceous Annual Plants Relative to Woody Perennial Plants. <i>Plant Physiology</i> , 2008, 148, 1189-1200.	2.3	125
42	Plant-Derived Terpenes: A Feedstock for Specialty Biofuels. <i>Trends in Biotechnology</i> , 2017, 35, 227-240.	4.9	124
43	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
44	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
45	Limitations of molecular-marker-aided selection in forest tree breeding. <i>Canadian Journal of Forest Research</i> , 1992, 22, 1050-1061.	0.8	113
46	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
47	Genome-wide association studies and expression-based quantitative trait loci analyses reveal roles of HCT2 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
48	Identification of Quantitative Trait Loci Influencing Wood Property Traits in Loblolly Pine (<i>Pinus taeda</i>). <i>Journal of Heredity</i> , 2010, 101, 112-121.	1.2	112
49	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
50	Poplar Genomics is Getting Popular: The Impact of the Poplar Genome Project on Tree Research. <i>Plant Biology</i> , 2004, 6, 2-4.	1.8	109
51	High-resolution genetic mapping of allelic variants associated with cell wall chemistry in <i>Populus</i> . <i>BMC Genomics</i> , 2015, 16, 24.	1.2	106
52	An In-Depth Understanding of Biomass Recalcitrance Using Natural Poplar Variants as the Feedstock. <i>ChemSusChem</i> , 2017, 10, 139-150.	3.6	106
53	Discovery and annotation of small proteins using genomics, proteomics, and computational approaches. <i>Genome Research</i> , 2011, 21, 634-641.	2.4	105
54	<i>Pseudomonas fluorescens</i> Induces Strain-Dependent and Strain-Independent Host Plant Responses in Defense Networks, Primary Metabolism, Photosynthesis, and Fitness. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 765-778.	1.4	100

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55	<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
56	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
57	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
58	Post-fire aspen seedling recruitment across the Yellowstone (USA) Landscape. <i>Landscape Ecology</i> , 2003, 18, 127-140.	1.9	97
59	Drought resistance of two hybrid <i>Populus</i> clones grown in a large-scale plantation. <i>Tree Physiology</i> , 1998, 18, 653-658.	1.4	96
60	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
61	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
62	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
63	Abiotic Stresses Shift Belowground <i>Populus</i> -Associated Bacteria Toward a Core Stress Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	89
64	Highly Efficient Isolation of <i>Populus</i> Mesophyll Protoplasts and Its Application in Transient Expression Assays. <i>PLoS ONE</i> , 2012, 7, e44908.	1.1	89
65	ESTABLISHMENT, PERSISTENCE, AND GROWTH OF ASPEN (<i>POPULUS TREMULOIDES</i>) SEEDLINGS IN YELLOWSTONE NATIONAL PARK. <i>Ecology</i> , 2005, 86, 404-418.	1.5	88
66	Poplar breeding and testing strategies in the north-central U.S.: Demonstration of potential yield and consideration of future research needs. <i>Forestry Chronicle</i> , 2001, 77, 245-253.	0.5	86
67	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
68	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
69	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
70	Genetic relatedness and female spatial organization in a solitary carnivore, the raccoon, <i>Procyon lotor</i> . <i>Molecular Ecology</i> , 2002, 11, 1115-1124.	2.0	80
71	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biology</i> , 2020, 21, 38.	3.8	74
72	Genome-wide analysis of lectin receptor-like kinases in <i>Populus</i> . <i>BMC Genomics</i> , 2016, 17, 699.	1.2	72

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73	A physical map of the highly heterozygous <i>Populus</i> genome: integration with the genome sequence and genetic map and analysis of haplotype variation. <i>Plant Journal</i> , 2007, 50, 1063-1078.	2.8	70
74	<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
75	Within tree variability of lignin composition in <i>Populus</i> . <i>Wood Science and Technology</i> , 2008, 42, 649-661.	1.4	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. <i>BMC Genomics</i> , 2008, 9, 57.	1.2	68
77	Newly identified helper bacteria stimulate ectomycorrhizal formation in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 579.	1.7	68
78	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
79	Genetic and physical mapping of <i>Melampsora</i> rust resistance genes in <i>Populus</i> and characterization of linkage disequilibrium and flanking genomic sequence. <i>New Phytologist</i> , 2004, 164, 95-105.	3.5	66
80	Short-rotation woody crop systems, atmospheric carbon dioxide and carbon management: A U.S. case study. <i>Forestry Chronicle</i> , 2001, 77, 259-264.	0.5	65
81	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
82	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
83	Chemical, ultrastructural and supramolecular analysis of tension wood in <i>Populus tremula x alba</i> as a model substrate for reduced recalcitrance. <i>Energy and Environmental Science</i> , 2011, 4, 4962.	15.6	61
84	Revisiting the sequencing of the first tree genome: <i>Populus trichocarpa</i> . <i>Tree Physiology</i> , 2013, 33, 357-364.	1.4	61
85	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
86	New technologies accelerate the exploration of non-coding RNAs in horticultural plants. <i>Horticulture Research</i> , 2017, 4, 17031.	2.9	61
87	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
88	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
89	Structural changes of lignins in natural <i>Populus</i> variants during different pretreatments. <i>Bioresource Technology</i> , 2020, 295, 122240.	4.8	61
90	Two High-Throughput Techniques for Determining Wood Properties as Part of a Molecular Genetics Analysis of Hybrid Poplar and Loblolly Pine. <i>Applied Biochemistry and Biotechnology</i> , 1999, 77, 55-66.	1.4	60

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91	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
92	<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
93	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
94	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
95	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
96	Annotation and comparative analysis of the glycoside hydrolase genes in <i>Brachypodium distachyon</i> . <i>BMC Genomics</i> , 2010, 11, 600.	1.2	53
97	Challenges of the utilization of wood polymers: how can they be overcome?. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 1525-1536.	1.7	52
98	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
99	Phenotypic variation and quantitative trait locus identification for osmotic potential in an interspecific hybrid inbred F2 poplar pedigree grown in contrasting environments. <i>Tree Physiology</i> , 2006, 26, 595-604.	1.4	50
100	Genome-wide identification of lineage-specific genes in <i>Arabidopsis</i> , <i>Oryza</i> and <i>Populus</i> . <i>Genomics</i> , 2009, 93, 473-480.	1.3	50
101	The obscure events contributing to the evolution of an incipient sex chromosome in <i>Populus</i> : a retrospective working hypothesis. <i>Tree Genetics and Genomes</i> , 2012, 8, 559-571.	0.6	50
102	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	1.7	50
103	Comparative analysis of the transcriptomes of <i>Populus trichocarpa</i> and <i>Arabidopsis thaliana</i> suggests extensive evolution of gene expression regulation in angiosperms. <i>New Phytologist</i> , 2008, 180, 408-420.	3.5	49
104	Synthetic biology as it relates to CAM photosynthesis: challenges and opportunities. <i>Journal of Experimental Botany</i> , 2014, 65, 3381-3393.	2.4	49
105	Phylogenetic Occurrence of the Phenylpropanoid Pathway and Lignin Biosynthesis in Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 704697.	1.7	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: <i>Populus deltoides</i> and <i>Populus trichocarpa</i> . <i>Tree Genetics and Genomes</i> , 2011, 7, 617-627.	0.6	48
107	Highly variable SSR markers in Douglas-fir: Mendelian inheritance and map locations. <i>Theoretical and Applied Genetics</i> , 2004, 108, 873-880.	1.8	47
108	Multiple levers for overcoming the recalcitrance of lignocellulosic biomass. <i>Biotechnology for Biofuels</i> , 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. <i>Tree Physiology</i> , 1998, 18, 645-652.	1.4	46
110	MicroSyn: A user friendly tool for detection of microsynteny in a gene family. <i>BMC Bioinformatics</i> , 2011, 12, 79.	1.2	46
111	Genomic aspects of research involving polyploid plants. <i>Plant Cell, Tissue and Organ Culture</i> , 2011, 104, 387-397.	1.2	45
112	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
113	Transgenic Poplar Designed for Biofuels. <i>Trends in Plant Science</i> , 2020, 25, 881-896.	4.3	45
114	Identification of candidate genes in <i>Arabidopsis</i> and <i>Populus</i> cell wall biosynthesis using text-mining, co-expression network analysis and comparative genomics. <i>Plant Science</i> , 2011, 181, 675-687.	1.7	44
115	Defining the Boundaries and Characterizing the Landscape of Functional Genome Expression in Vascular Tissues of <i>Populus</i> using Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 449-460.	1.8	44
116	The Development of Two Flanking SCAR Markers Linked to a Sex Determination Locus in <i>Salix viminalis</i> L., 2003, 94, 185-189.		42
117	Poplar Genomics: State of the Science. <i>Critical Reviews in Plant Sciences</i> , 2009, 28, 285-308.	2.7	42
118	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , 2019, 5, 676-680.	4.7	42
119	Characterization of Transposable Elements in the Ectomycorrhizal Fungus <i>Laccaria bicolor</i> . <i>PLoS ONE</i> , 2012, 7, e40197.	1.1	38
120	Qualitative and quantitative resistances to leaf rust finely mapped within two nucleotide-binding site leucine-rich repeat (NBS-LRR)-rich genomic regions of chromosome 19 in poplar. <i>New Phytologist</i> , 2011, 192, 151-163.	3.5	37
121	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
122	Identification of quantitative trait loci and candidate genes for cadmium tolerance in <i>Populus</i> . <i>Tree Physiology</i> , 2012, 32, 626-638.	1.4	36
123	<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
124	Clonal differences in biomass characteristics, coppice ability, and biomass prediction equations among four <i>Populus</i> clones grown in eastern North Dakota. <i>Canadian Journal of Forest Research</i> , 1992, 22, 348-354.	0.8	34
125	Microsatellite primer resource for <i>Populus</i> developed from the mapped sequence scaffolds of the Nisqually genome. <i>New Phytologist</i> , 2009, 181, 498-503.	3.5	34
126	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

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127	Prime Editing Technology and Its Prospects for Future Applications in Plant Biology Research. <i>BioDesign Research</i> , 2020, 2020, .	0.8	34
128	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
129	A genetic linkage map for the ectomycorrhizal fungus <i>Laccaria bicolor</i> and its alignment to the whole-genome sequence assemblies. <i>New Phytologist</i> , 2008, 180, 316-328.	3.5	32
130	Down-Regulation of KORRIGAN-Like Endo-1,4-Glucanase Genes Impacts Carbon Partitioning, Mycorrhizal Colonization and Biomass Production in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1455.	1.7	32
131	Pleiotropic and Epistatic Network-Based Discovery: Integrated Networks for Target Gene Discovery. <i>Frontiers in Energy Research</i> , 2018, 6, .	1.2	32
132	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
133	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
134	A microarray-based genotyping and genetic mapping approach for highly heterozygous outcrossing species enables localization of a large fraction of the unassembled <i>Populus trichocarpa</i> genome sequence. <i>Plant Journal</i> , 2009, 58, 1054-1067.	2.8	30
135	Cytogenetic Analysis of <i>Populus trichocarpa</i> : Ribosomal DNA, Telomere Repeat Sequence, and Marker-selected BACs. <i>Cytogenetic and Genome Research</i> , 2009, 125, 74-80.	0.6	30
136	Comparative analysis of GT14/GT14-like gene family in <i>Arabidopsis</i> , <i>Oryza</i> , <i>Populus</i> , <i>Sorghum</i> and <i>Vitis</i> . <i>Plant Science</i> , 2011, 181, 688-695.	1.7	29
137	Natural genetic variability reduces recalcitrance in poplar. <i>Biotechnology for Biofuels</i> , 2016, 9, 106.	6.2	29
138	Micropropagation of <i>Populus trichocarpa</i> "Nisqually-1": the genotype deriving the <i>Populus</i> reference genome. <i>Plant Cell, Tissue and Organ Culture</i> , 2009, 99, 251-257.	1.2	28
139	High Throughput Screening Technologies in Biomass Characterization. <i>Frontiers in Energy Research</i> , 2018, 6, .	1.2	28
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