

Lee E Gunter

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

8,241
citations

172207

29
h-index

182168

51
g-index

53
all docs

53
docs citations

53
times ranked

9480
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	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
3	<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
4	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
5	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
6	Antisense Down-Regulation of <i>4CL</i> Expression Alters Lignification, Tree Growth, and Saccharification Potential of Field-Grown Poplar. <i>Plant Physiology</i> , 2010, 154, 874-886.	2.3	195
7	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
8	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
9	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
10	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
11	Phenotypic variation in growth and biomass distribution for two advanced-generation pedigrees of hybrid poplar. <i>Canadian Journal of Forest Research</i> , 2005, 35, 1779-1789.	0.8	134
12	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
13	Diversity among Populations of Switchgrass Based on RAPD Markers. <i>Crop Science</i> , 1996, 36, 1017-1022.	0.8	115
14	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
15	Genome-wide association studies and expression-based quantitative trait loci analyses reveal roles of <i>HCT2</i> 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
16	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
17	Discovery and annotation of small proteins using genomics, proteomics, and computational approaches. <i>Genome Research</i> , 2011, 21, 634-641.	2.4	105
18	Connecting genes, coexpression modules, and molecular signatures to environmental stress phenotypes in plants. <i>BMC Systems Biology</i> , 2008, 2, 16.	3.0	102

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19	A 34K <i>SNP</i> 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
20	Abiotic Stresses Shift Belowground <i>Populus</i> -Associated Bacteria Toward a Core Stress Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	89
21	Comparative physiology and transcriptional networks underlying the heat shock response in <i>Populus trichocarpa</i> , <i>Arabidopsis thaliana</i> and <i>Glycine max</i> . <i>Plant, Cell and Environment</i> , 2011, 34, 1488-1506.	2.8	71
22	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
23	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
24	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
25	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
26	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
27	The Development of Two Flanking SCAR Markers Linked to a Sex Determination Locus in <i>Salix viminalis</i> L. , 2003, 94, 185-189.		42
28	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , 2019, 5, 676-680.	4.7	42
29	Microsatellite primer resource for <i>Populus</i> developed from the mapped sequence scaffolds of the <i>Nisqually</i> genome. <i>New Phytologist</i> , 2009, 181, 498-503.	3.5	34
30	Phylogenetic relationships of the Juglandaceae. <i>Plant Systematics and Evolution</i> , 1994, 192, 11-29.	0.3	32
31	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
32	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
33	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
34	Defining the genetic components of callus formation: A GWAS approach. <i>PLoS ONE</i> , 2018, 13, e0202519.	1.1	27
35	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
36	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

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37	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
38	Comparative sequence analysis between orthologous regions of the <i>Arabidopsis</i> and <i>Populus</i> genomes reveals substantial synteny and microcollinearity. <i>Canadian Journal of Forest Research</i> , 2003, 33, 2245-2251.	0.8	24
39	Genetic variation in postfire aspen seedlings in Yellowstone National Park. <i>Molecular Ecology</i> , 1999, 8, 1769-1780.	2.0	23
40	Phytobiome and Transcriptional Adaptation of <i>Populus deltoides</i> to Acute Progressive Drought and Cyclic Drought. <i>Phytobiomes Journal</i> , 2018, 2, 249-260.	1.4	23
41	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
42	Agronomic performance of <i>Populus deltoides</i> trees engineered for biofuel production. <i>Biotechnology for Biofuels</i> , 2017, 10, 253.	6.2	22
43	Differential Detection of Genetic Loci Underlying Stem and Root Lignin Content in <i>Populus</i> . <i>PLoS ONE</i> , 2010, 5, e14021.	1.1	20
44	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
45	Genetic variation and spatial structure in sugar maple (<i>Acer saccharum</i> Marsh.) and implications for predicted global-scale environmental change. <i>Global Change Biology</i> , 2000, 6, 335-344.	4.2	19
46	Quantitative proteome profile of water deficit stress responses in eastern cottonwood (<i>Populus</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 3	1.1	17
47	Overexpression of a <i>Prefoldin Î²</i> subunit gene reduces biomass recalcitrance in the bioenergy crop <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 859-871.	4.1	17
48	Development of AFLP and RAPD markers linked to a locus associated with twisted growth in corkscrew willow (<i>Salix matsudana</i> 'Tortuosa'). <i>Tree Physiology</i> , 2007, 27, 1575-1583.	1.4	11
49	Correlating laser-induced breakdown spectroscopy with neutron activation analysis to determine the elemental concentration in the ionome of the <i>Populus trichocarpa</i> leaf. <i>Spectrochimica Acta, Part B: Atomic Spectroscopy</i> , 2017, 138, 46-53.	1.5	11
50	Analysis of sex-linked, sequence-characterized amplified region markers in <i>Salix eriocephala</i> . <i>Canadian Journal of Forest Research</i> , 2003, 33, 1785-1790.	0.8	7
51	Scaling nitrogen and carbon interactions: what are the consequences of biological buffering?. <i>Ecology and Evolution</i> , 2015, 5, 2839-2850.	0.8	4
52	Assessment of genetic similarity among 'Alamo' switchgrass seed lots using RAPD markers. <i>Seed Science and Technology</i> , 2003, 31, 681-689.	0.6	3