

Jill L Wegrzyn

List of Publications by Citations

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Version: 2024-04-25

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

104
papers

4,219
citations

36
h-index

63
g-index

117
ext. papers

5,421
ext. citations

5.3
avg, IF

5.1
L-index

#	Paper	IF	Citations
104	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> , 2014 , 15, R59	18.3	347
103	Patterns of population structure and environmental associations to aridity across the range of loblolly pine (<i>Pinus taeda</i> L., Pinaceae). <i>Genetics</i> , 2010 , 185, 969-82	4	283
102	Sequencing and assembly of the 22-gb loblolly pine genome. <i>Genetics</i> , 2014 , 196, 875-90	4	211
101	Proteases for processing proneuropeptides into peptide neurotransmitters and hormones. <i>Annual Review of Pharmacology and Toxicology</i> , 2008 , 48, 393-423	17.9	188
100	Back to nature: ecological genomics of loblolly pine (<i>Pinus taeda</i> , Pinaceae). <i>Molecular Ecology</i> , 2010 , 19, 3789-805	5.7	170
99	Association genetics of coastal Douglas fir (<i>Pseudotsuga menziesii</i> var. <i>menziesii</i> , Pinaceae). I. Cold-hardiness related traits. <i>Genetics</i> , 2009 , 182, 1289-302	4	168
98	Unique features of the loblolly pine (<i>Pinus taeda</i> L.) megagenome revealed through sequence annotation. <i>Genetics</i> , 2014 , 196, 891-909	4	146
97	15 years of GDR: New data and functionality in the Genome Database for Rosaceae. <i>Nucleic Acids Research</i> , 2019 , 47, D1137-D1145	20.1	129
96	The walnut (<i>Juglans regia</i>) genome sequence reveals diversity in genes coding for the biosynthesis of non-structural polyphenols. <i>Plant Journal</i> , 2016 , 87, 507-32	6.9	127
95	Sequence of the Sugar Pine Megagenome. <i>Genetics</i> , 2016 , 204, 1613-1626	4	119
94	The <i>Pinus taeda</i> genome is characterized by diverse and highly diverged repetitive sequences. <i>BMC Genomics</i> , 2010 , 11, 420	4.5	115
93	Disentangling the roles of history and local selection in shaping clinal variation of allele frequencies and gene expression in Norway spruce (<i>Picea abies</i>). <i>Genetics</i> , 2012 , 191, 865-81	4	112
92	Association genetics of traits controlling lignin and cellulose biosynthesis in black cottonwood (<i>Populus trichocarpa</i> , Salicaceae) secondary xylem. <i>New Phytologist</i> , 2010 , 188, 515-32	9.8	109
91	Association mapping of quantitative disease resistance in a natural population of loblolly pine (<i>Pinus taeda</i> L.). <i>Genetics</i> , 2010 , 186, 677-86	4	79
90	Multilocus patterns of nucleotide diversity and divergence reveal positive selection at candidate genes related to cold hardiness in coastal Douglas Fir (<i>Pseudotsuga menziesii</i> var. <i>menziesii</i>). <i>Genetics</i> , 2009 , 183, 289-98	4	79
89	TreeGenes: A forest tree genome database. <i>International Journal of Plant Genomics</i> , 2008 , 2008, 412875		76
88	Lineage, fate, and fate potential of NG2-glia. <i>Brain Research</i> , 2016 , 1638, 116-128	3.7	73

87	Association genetics of chemical wood properties in black poplar (<i>Populus nigra</i>). <i>New Phytologist</i> , 2013 , 197, 162-176	9.8	61
86	Association genetics of the loblolly pine (<i>Pinus taeda</i> , Pinaceae) metabolome. <i>New Phytologist</i> , 2012 , 193, 890-902	9.8	59
85	Development and implementation of a highly-multiplexed SNP array for genetic mapping in maritime pine and comparative mapping with loblolly pine. <i>BMC Genomics</i> , 2011 , 12, 368	4.5	57
84	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 3157-3167	3.2	55
83	Association genetics of carbon isotope discrimination, height and foliar nitrogen in a natural population of <i>Pinus taeda</i> L. <i>Heredity</i> , 2011 , 107, 105-14	3.6	55
82	Genomic Relationship Matrix for Correcting Pedigree Errors in Breeding Populations: Impact on Genetic Parameters and Genomic Selection Accuracy. <i>Crop Science</i> , 2014 , 54, 1115-1123	2.4	50
81	SNP markers trace familial linkages in a cloned population of <i>Pinus taeda</i> prospects for genomic selection. <i>Tree Genetics and Genomes</i> , 2012 , 8, 1307-1318	2.1	47
80	Association genetics of oleoresin flow in loblolly pine: discovering genes and predicting phenotype for improved resistance to bark beetles and bioenergy potential. <i>New Phytologist</i> , 2013 , 199, 89-100	9.8	45
79	An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. <i>GigaScience</i> , 2017 , 6, 1-4	7.6	44
78	Cysteine Cathepsins in the secretory vesicle produce active peptides: Cathepsin L generates peptide neurotransmitters and cathepsin B produces beta-amyloid of Alzheimer's disease. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012 , 1824, 89-104	4	44
77	Proteomics of neuroendocrine secretory vesicles reveal distinct functional systems for biosynthesis and exocytosis of peptide hormones and neurotransmitters. <i>Journal of Proteome Research</i> , 2007 , 6, 1652-65	5.6	42
76	Insights into the loblolly pine genome: characterization of BAC and fosmid sequences. <i>PLoS ONE</i> , 2013 , 8, e72439	3.7	41
75	Contrasting patterns of nucleotide diversity for four conifers of Alpine European forests. <i>Evolutionary Applications</i> , 2012 , 5, 762-75	4.8	40
74	Comparative mapping in <i>Pinus</i> : sugar pine (<i>Pinus lambertiana</i> Dougl.) and loblolly pine (<i>Pinus taeda</i> L.). <i>Tree Genetics and Genomes</i> , 2011 , 7, 457-468	2.1	40
73	Proteomics of dense core secretory vesicles reveal distinct protein categories for secretion of neuroeffectors for cell-cell communication. <i>Journal of Proteome Research</i> , 2010 , 9, 5002-24	5.6	40
72	Water availability drives signatures of local adaptation in whitebark pine (<i>Pinus albicaulis</i> Engelm.) across fine spatial scales of the Lake Tahoe Basin, USA. <i>Molecular Ecology</i> , 2017 , 26, 3168-3185	5.7	37
71	Transcriptomic imprints of adaptation to fresh water: parallel evolution of osmoregulatory gene expression in the Alewife. <i>Molecular Ecology</i> , 2017 , 26, 831-848	5.7	37
70	Genetic structure and association mapping of adaptive and selective traits in the east Texas loblolly pine (<i>Pinus taeda</i> L.) breeding populations. <i>Tree Genetics and Genomes</i> , 2013 , 9, 1161-1178	2.1	36

69	Bioinformatic analyses of mammalian 5'UTR sequence properties of mRNAs predicts alternative translation initiation sites. <i>BMC Bioinformatics</i> , 2008 , 9, 232	3.6	36
68	Discovering candidate genes that regulate resin canal number in <i>Pinus taeda</i> stems by integrating genetic analysis across environments, ages, and populations. <i>New Phytologist</i> , 2015 , 205, 627-41	9.8	35
67	Combined de novo and genome guided assembly and annotation of the <i>Pinus patula</i> juvenile shoot transcriptome. <i>BMC Genomics</i> , 2015 , 16, 1057	4.5	34
66	The evolutionary genetics of the genes underlying phenotypic associations for loblolly pine (<i>Pinus taeda</i> , Pinaceae). <i>Genetics</i> , 2013 , 195, 1353-72	4	33
65	EnTAP: Bringing faster and smarter functional annotation to non-model eukaryotic transcriptomes. <i>Molecular Ecology Resources</i> , 2020 , 20, 591-604	8.4	32
64	Assessing the Gene Content of the Megagenome: Sugar Pine (<i>Pinus lambertiana</i>). <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3787-3802	3.2	30
63	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	28
62	Multilocus analyses reveal little evidence for lineage-wide adaptive evolution within major clades of soft pines (<i>Pinus</i> subgenus <i>Strobus</i>). <i>Molecular Ecology</i> , 2013 , 22, 5635-50	5.7	27
61	Open access to tree genomes: the path to a better forest. <i>Genome Biology</i> , 2013 , 14, 120	18.3	26
60	PineSAP--sequence alignment and SNP identification pipeline. <i>Bioinformatics</i> , 2009 , 25, 2609-10	7.2	26
59	Targeted Capture Sequencing in Whitebark Pine Reveals Range-Wide Demographic and Adaptive Patterns Despite Challenges of a Large, Repetitive Genome. <i>Frontiers in Plant Science</i> , 2016 , 7, 484	6.2	25
58	Growing and cultivating the forest genomics database, TreeGenes. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018, 1-11	5	24
57	A Reference Genome Sequence for Giant Sequoia. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 3907-3919	3.2	22
56	Comparative Transcriptomics Among Four White Pine Species. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 1461-1474	3.2	20
55	Neuropeptidomic components generated by proteomic functions in secretory vesicles for cell-cell communication. <i>AAPS Journal</i> , 2010 , 12, 635-45	3.7	20
54	Expression profiling in <i>Pinus radiata</i> infected with <i>Fusarium circinatum</i> . <i>Tree Genetics and Genomes</i> , 2017 , 13, 1	2.1	19
53	Defence transcriptome assembly and pathogenesis related gene family analysis in <i>Pinus tecunumanii</i> (low elevation). <i>BMC Genomics</i> , 2018 , 19, 632	4.5	19
52	Combination of multipoint maximum likelihood (MML) and regression mapping algorithms to construct a high-density genetic linkage map for loblolly pine (<i>Pinus taeda</i> L.). <i>Tree Genetics and Genomes</i> , 2013 , 9, 1529-1535	2.1	19

51	Transcription through the eye of a needle: daily and annual cyclic gene expression variation in Douglas-fir needles. <i>BMC Genomics</i> , 2017 , 18, 558	4.5	18
50	JAK/STAT3 regulated global gene expression dynamics during late-stage reprogramming process. <i>BMC Genomics</i> , 2018 , 19, 183	4.5	17
49	Mapping Fusiform Rust Resistance Genes within a Complex Mating Design of Loblolly Pine. <i>Forests</i> , 2014 , 5, 347-362	2.8	17
48	Uniform standards for genome databases in forest and fruit trees. <i>Tree Genetics and Genomes</i> , 2012 , 8, 549-557	2.1	17
47	Demonstration of GTG as an alternative initiation codon for the serpin endopin 2B-2. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 327, 837-44	3.4	16
46	Cyberinfrastructure to Improve Forest Health and Productivity: The Role of Tree Databases in Connecting Genomes, Phenomes, and the Environment. <i>Frontiers in Plant Science</i> , 2019 , 10, 813	6.2	15
45	Patterns of neutral and adaptive genetic diversity across the natural range of sugar pine (<i>Pinus lambertiana</i> Dougl.). <i>Tree Genetics and Genomes</i> , 2016 , 12, 1	2.1	15
44	Association of loblolly pine xylem development gene expression with single-nucleotide polymorphisms. <i>Tree Physiology</i> , 2013 , 33, 763-74	4.2	14
43	New extension software modules to enhance searching and display of transcriptome data in Tripal databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	13
42	YeATS - a tool suite for analyzing RNA-seq derived transcriptome identifies a highly transcribed putative extensin in heartwood/sapwood transition zone in black walnut. <i>F1000Research</i> , 2015 , 4, 155	3.6	13
41	Co-option of wing-patterning genes underlies the evolution of the treehopper helmet. <i>Nature Ecology and Evolution</i> , 2020 , 4, 250-260	12.3	13
40	Poor maternal nutrition during gestation alters the expression of genes involved in muscle development and metabolism in lambs. <i>Journal of Animal Science</i> , 2016 , 94, 3093-9	0.7	13
39	Linking phenotype, genotype and environment to unravel genetic components underlying cold hardiness in coastal Douglas-fir (<i>Pseudotsuga menziesii</i> var. <i>menziesii</i>). <i>Tree Genetics and Genomes</i> , 2018 , 14, 1	2.1	12
38	Transcriptome Analysis Reveals Differential Gene Expression and a Possible Role of Gibberellins in a Shade-Tolerant Mutant of Perennial Ryegrass. <i>Frontiers in Plant Science</i> , 2017 , 8, 868	6.2	12
37	Drought stress in <i>Pinus taeda</i> L. induces coordinated transcript accumulation of genes involved in the homogentisate pathway. <i>Tree Genetics and Genomes</i> , 2017 , 13, 1	2.1	11
36	Dual RNA-Seq Analysis of the Pine- Interaction in Resistant () and Susceptible () Hosts. <i>Microorganisms</i> , 2019 , 7,	4.9	11
35	Tripal v3: an ontology-based toolkit for construction of FAIR biological community databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	11
34	Cyberinfrastructure and resources to enable an integrative approach to studying forest trees. <i>Evolutionary Applications</i> , 2020 , 13, 228-241	4.8	11

33	gFACs: Gene Filtering, Analysis, and Conversion to Unify Genome Annotations Across Alignment and Gene Prediction Frameworks. <i>Genomics, Proteomics and Bioinformatics</i> , 2019 , 17, 305-310	6.5	10
32	The protein architecture of human secretory vesicles reveals differential regulation of signaling molecule secretion by protein kinases. <i>PLoS ONE</i> , 2012 , 7, e41134	3.7	9
31	Generation, functional annotation and comparative analysis of black spruce (<i>Picea mariana</i>) ESTs: an important conifer genomic resource. <i>BMC Genomics</i> , 2013 , 14, 702	4.5	9
30	Green plant genomes: What we know in an era of rapidly expanding opportunities.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	9
29	Transcriptomic profile of leaf tissue from the leguminous tree, <i>Millettia pinnata</i> . <i>Tree Genetics and Genomes</i> , 2016 , 12, 1	2.1	9
28	YeATS - a tool suite for analyzing RNA-seq derived transcriptome identifies a highly transcribed putative extensin in heartwood/sapwood transition zone in black walnut. <i>F1000Research</i> , 2015 , 4, 155	3.6	8
27	Toward genomic selection in : Integrating resources to support array design in a complex conifer genome. <i>Applications in Plant Sciences</i> , 2021 , 9, e11439	2.3	8
26	CartograTree: connecting tree genomes, phenotypes and environment. <i>Molecular Ecology Resources</i> , 2013 , 13, 528-37	8.4	7
25	An extension of the Plant Ontology project supporting wood anatomy and development research. <i>IAWA Journal</i> , 2012 , 33, 113-117	2.3	7
24	Comparative genomics of six <i>Juglans</i> species reveals disease-associated gene family contractions. <i>Plant Journal</i> , 2020 , 102, 410-423	6.9	7
23	Tripal MapViewer: A tool for interactive visualization and comparison of genetic maps. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	5
22	The <i>Cycas</i> genome and the early evolution of seed plants.. <i>Nature Plants</i> , 2022 ,	11.5	5
21	Quantitative trait loci influencing forking defects in an outbred pedigree of loblolly pine. <i>BMC Genetics</i> , 2016 , 17, 138	2.6	4
20	Standards recommendations for the Earth BioGenome Project.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	4
19	Assembled and annotated 26.5 Gbp coast redwood genome: a resource for estimating evolutionary adaptive potential and investigating hexaploid origin.. <i>G3: Genes, Genomes, Genetics</i> , 2022 , 12,	3.2	4
18	The giant sequoia genome and proliferation of disease resistance genes		4
17	EnTAP: Bringing Faster and Smarter Functional Annotation to Non-Model Eukaryotic Transcriptomes		3
16	A genome-wide SNP genotyping resource for tropical pine tree species. <i>Molecular Ecology Resources</i> , 2021 ,	8.4	3

15	ChloroMitoCU: Codon patterns across organelle genomes for functional genomics and evolutionary applications. <i>DNA Research</i> , 2017 , 24, 327-332	4.5	2
14	Transcription through the eye of a needle: daily and annual cycles of gene expression variation in Douglas-fir needles		2
13	Transcriptome of weeping pinyon pine, <i>Pinus pincea</i> , shows differences across heterogeneous habitats. <i>Trees - Structure and Function</i> , 2021 , 35, 1351-1365	2.6	2
12	Tripal, a community update after 10 years of supporting open source, standards-based genetic, genomic and breeding databases. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
11	High gene space divergence contrasts with frozen vegetative architecture in the moss family Funariaceae. <i>Molecular Phylogenetics and Evolution</i> , 2021 , 154, 106965	4.1	2
10	Virus evolution affected early COVID-19 spread		1
9	Tripal and Galaxy: supporting reproducible scientific workflows for community biological databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2020 , 2020,	5	1
8	Strategies of tolerance reflected in two North American maple genomes.. <i>Plant Journal</i> , 2021 ,	6.9	1
7	Extensive Variation in Drought-Induced Gene Expression Changes Between Loblolly Pine Genotypes. <i>Frontiers in Genetics</i> , 2021 , 12, 661440	4.5	0
6	Gene Frequency Shift in Relict <i>Abies pinsapo</i> Forests Associated with Drought-Induced Mortality: Preliminary Evidence of Local-Scale Divergent Selection. <i>Forests</i> , 2021 , 12, 1220	2.8	0
5	De novo assembly of a fruit transcriptome set identifies AmMYB10 as a key regulator of anthocyanin biosynthesis in <i>Aronia melanocarpa</i> .. <i>BMC Plant Biology</i> , 2022 , 22, 143	5.3	0
4	Neuropeptides: Chemical Activity Profiling and Proteomic Approaches1		
3	Evolutionary Histories of Gene Families in Angiosperm Trees. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016 , 121-137	0.2	
2	Comparative analysis of differential gene expression indicates divergence in ontogenetic strategies of leaves in two conifer genera.. <i>Ecology and Evolution</i> , 2022 , 12, e8611	2.8	
1	Bioinformatic approach for the discovery of cis-eQTL signals during fruit ripening of a woody species as grape (<i>Vitis vinifera</i> L.).. <i>Scientific Reports</i> , 2022 , 12, 7481	4.9	