Jill L Wegrzyn

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/441757/publications.pdf

Version: 2024-02-01

101 papers	6,125 citations	70961 41 h-index	82410 72 g-index
117 all docs	117 docs citations	117 times ranked	6210 citing authors

#	Article	IF	Citations
1	A genomeâ€wide SNP genotyping resource for tropical pine tree species. Molecular Ecology Resources, 2022, 22, 695-710.	2.2	10
2	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	33
3	Green plant genomes: What we know in an era of rapidly expanding opportunities. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	65
4	Assembled and annotated 26.5 Gbp coast redwood genome: a resource for estimating evolutionary adaptive potential and investigating hexaploid origin. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	28
5	Comparative analysis of differential gene expression indicates divergence in ontogenetic strategies of leaves in two conifer genera. Ecology and Evolution, 2022, 12, e8611.	0.8	3
6	Strategies of tolerance reflected in two North American maple genomes. Plant Journal, 2022, 109, 1591-1613.	2.8	5
7	De novo assembly of a fruit transcriptome set identifies AmMYB10 as a key regulator of anthocyanin biosynthesis in Aronia melanocarpa. BMC Plant Biology, 2022, 22, 143.	1.6	3
8	NLR diversity and candidate fusiform rust resistance genes in loblolly pine. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	6
9	The Cycas genome and the early evolution of seed plants. Nature Plants, 2022, 8, 389-401.	4.7	80
10	Bioinformatic approach for the discovery of cis-eQTL signals during fruit ripening of a woody species as grape (Vitis vinifera L.). Scientific Reports, 2022, 12, 7481.	1.6	0
11	High gene space divergence contrasts with frozen vegetative architecture in the moss family Funariaceae. Molecular Phylogenetics and Evolution, 2021, 154, 106965.	1.2	5
12	Transcriptome of weeping pinyon pine, Pinus pinceana, shows differences across heterogeneous habitats. Trees - Structure and Function, 2021, 35, 1351-1365.	0.9	4
13	Extensive Variation in Drought-Induced Gene Expression Changes Between Loblolly Pine Genotypes. Frontiers in Genetics, 2021, 12, 661440.	1.1	3
14	Toward genomic selection in Pinus taeda: Integrating resources to support array design in a complex conifer genome. Applications in Plant Sciences, 2021, 9, e11439.	0.8	19
15	Tripal, a community update after 10Âyears of supporting open source, standards-based genetic, genomic and breeding databases. Briefings in Bioinformatics, 2021, 22, .	3.2	6
16	Gene Frequency Shift in Relict Abies pinsapo Forests Associated with Drought-Induced Mortality: Preliminary Evidence of Local-Scale Divergent Selection. Forests, 2021, 12, 1220.	0.9	4
17	<scp>EnTAP</scp>: Bringing faster and smarter functional annotation to nonâ€model eukaryotic transcriptomes. Molecular Ecology Resources, 2020, 20, 591-604.	2.2	111
18	Cyberinfrastructure and resources to enable an integrative approach to studying forest trees. Evolutionary Applications, 2020, 13, 228-241.	1.5	12

#	Article	IF	Citations
19	Comparative genomics of six Juglans species reveals diseaseâ€associated gene family contractions. Plant Journal, 2020, 102, 410-423.	2.8	25
20	Co-option of wing-patterning genes underlies the evolution of the treehopper helmet. Nature Ecology and Evolution, 2020, 4, 250-260.	3.4	38
21	Tripal and Galaxy: supporting reproducible scientific workflows for community biological databases. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	1
22	A Reference Genome Sequence for Giant Sequoia. G3: Genes, Genomes, Genetics, 2020, 10, 3907-3919.	0.8	67
23	Tripal v3: an ontology-based toolkit for construction of FAIR biological community databases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	22
24	gFACs: Gene Filtering, Analysis, and Conversion to Unify Genome Annotations Across Alignment and Gene Prediction Frameworks. Genomics, Proteomics and Bioinformatics, 2019, 17, 305-310.	3.0	37
25	Dual RNA-Seq Analysis of the Pine-Fusarium circinatum Interaction in Resistant (Pinus tecunumanii) and Susceptible (Pinus patula) Hosts. Microorganisms, 2019, 7, 315.	1.6	18
26	Cyberinfrastructure to Improve Forest Health and Productivity: The Role of Tree Databases in Connecting Genomes, Phenomes, and the Environment. Frontiers in Plant Science, 2019, 10, 813.	1.7	24
27	15 years of GDR: New data and functionality in the Genome Database for Rosaceae. Nucleic Acids Research, 2019, 47, D1137-D1145.	6.5	285
28	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	5
29	Linking phenotype, genotype and environment to unravel genetic components underlying cold hardiness in coastal Douglas-fir (Pseudotsuga menziesii var. menziesii). Tree Genetics and Genomes, 2018, 14, 1.	0.6	15
30	Comparative Transcriptomics Among Four White Pine Species. G3: Genes, Genomes, Genetics, 2018, 8, 1461-1474.	0.8	35
31	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	52
32	Growing and cultivating the forest genomics database, TreeGenes. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-11.	1.4	40
33	JAK/STAT3 regulated global gene expression dynamics during late-stage reprogramming process. BMC Genomics, 2018, 19, 183.	1.2	22
34	Defence transcriptome assembly and pathogenesis related gene family analysis in Pinus tecunumanii (low elevation). BMC Genomics, 2018, 19, 632.	1.2	32
35	Drought stress in Pinus taeda L. induces coordinated transcript accumulation of genes involved in the homogentisate pathway. Tree Genetics and Genomes, 2017, 13, 1.	0.6	16
36	ChloroMitoCU: Codon patterns across organelle genomes for functional genomics and evolutionary applications. DNA Research, 2017, 24, 327-332.	1.5	2

#	Article	IF	Citations
37	Expression profiling in Pinus radiata infected with Fusarium circinatum. Tree Genetics and Genomes, 2017, 13, 1.	0.6	31
38	Water availability drives signatures of local adaptation in whitebark pine (Pinus albicaulis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7	2.0	51
39	Transcriptomic imprints of adaptation to fresh water: parallel evolution of osmoregulatory gene expression in the Alewife. Molecular Ecology, 2017, 26, 831-848.	2.0	54
40	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. G3: Genes, Genomes, Genetics, 2017, 7, 3157-3167.	0.8	103
41	An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. GigaScience, 2017, 6, 1-4.	3.3	71
42	Transcription through the eye of a needle: daily and annual cyclic gene expression variation in Douglas-fir needles. BMC Genomics, 2017, 18, 558.	1.2	35
43	New extension software modules to enhance searching and display of transcriptome data in Tripal databases. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	15
44	Transcriptome Analysis Reveals Differential Gene Expression and a Possible Role of Gibberellins in a Shade-Tolerant Mutant of Perennial Ryegrass. Frontiers in Plant Science, 2017, 8, 868.	1.7	17
45	Assessing the Gene Content of the Megagenome: Sugar Pine (Pinus lambertiana). G3: Genes, Genomes, Genetics, 2016, 6, 3787-3802.	0.8	51
46	Targeted Capture Sequencing in Whitebark Pine Reveals Range-Wide Demographic and Adaptive Patterns Despite Challenges of a Large, Repetitive Genome. Frontiers in Plant Science, 2016, 7, 484.	1.7	38
47	Evolutionary Histories of Gene Families in Angiosperm Trees. Plant Genetics and Genomics: Crops and Models, 2016, , 121-137.	0.3	0
48	Poor maternal nutrition during gestation alters the expression of genes involved in muscle development and metabolism in lambs1. Journal of Animal Science, 2016, 94, 3093-3099.	0.2	21
49	Transcriptomic profile of leaf tissue from the leguminous tree, Millettia pinnata. Tree Genetics and Genomes, 2016, 12, 1.	0.6	11
50	Sequence of the Sugar Pine Megagenome. Genetics, 2016, 204, 1613-1626.	1.2	169
51	Quantitative trait loci influencing forking defects in an outbred pedigree of loblolly pine. BMC Genetics, 2016, 17, 138.	2.7	5
52	The walnut (Juglans regia) genome sequence reveals diversity in genes coding for the biosynthesis of nonâ€structural polyphenols. Plant Journal, 2016, 87, 507-532.	2.8	233
53	Patterns of neutral and adaptive genetic diversity across the natural range of sugar pine (Pinus) Tj ETQq1 1 0.784314 rgBT /Overlock	0.6	18
54	Lineage, fate, and fate potential of NG2-glia. Brain Research, 2016, 1638, 116-128.	1.1	100

#	Article	IF	Citations
55	Combined de novo and genome guided assembly and annotation of the Pinus patula juvenile shoot transcriptome. BMC Genomics, 2015, 16, 1057.	1.2	44
56	Demonstration of GTG as an endogenous initiation codon for a human mRNA transcript revealed by molecular cloning of the serpin endopin 2B.. Journal of Biological Chemistry, 2015, 290, 19010.	1.6	0
57	Discovering candidate genes that regulate resin canal number in <scp>P</scp>inus taeda stems by integrating genetic analysis across environments, ages, and populations. New Phytologist, 2015, 205, 627-641.	3.5	45
58	YeATS - a tool suite for analyzing RNA-seq derived transcriptome identifies a highly transcribed putative extensin in heartwood/sapwood transition zone in black walnut. F1000Research, 2015, 4, 155.	0.8	10
59	YeATS - a tool suite for analyzing RNA-seq derived transcriptome identifies a highly transcribed putative extensin in heartwood/sapwood transition zone in black walnut. F1000Research, 2015, 4, 155.	0.8	23
60	Genomic Relationship Matrix for Correcting Pedigree Errors in Breeding Populations: Impact on Genetic Parameters and Genomic Selection Accuracy. Crop Science, 2014, 54, 1115-1123.	0.8	77
61	Mapping Fusiform Rust Resistance Genes within a Complex Mating Design of Loblolly Pine. Forests, 2014, 5, 347-362.	0.9	22
62	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. Genetics, 2014, 196, 875-890.	1.2	286
63	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. Genome Biology, 2014, 15, R59.	13.9	424
64	Unique Features of the Loblolly Pine (Pinus taeda L.) Megagenome Revealed Through Sequence Annotation. Genetics, 2014, 196, 891-909.	1.2	207
65	Multilocus analyses reveal little evidence for lineageâ€wide adaptive evolution within major clades of soft pines (<scp>P</scp>inus subgenus <scp>S</scp>trobus). Molecular Ecology, 2013, 22, 5635-5650.	2.0	45
66	Combination of multipoint maximum likelihood (MML) and regression mapping algorithms to construct a high-density genetic linkage map for loblolly pine (Pinus taeda L.). Tree Genetics and Genomes, 2013, 9, 1529-1535.	0.6	23
67	Open access to tree genomes: the path to a better forest. Genome Biology, 2013, 14, 120.	3.8	46
68	Association genetics of chemical wood properties in black poplar (Populus nigra). New Phytologist, 2013, 197, 162-176.	3.5	81
69	CartograTree: connecting tree genomes, phenotypes and environment. Molecular Ecology Resources, 2013, 13, 528-537.	2.2	9
70	Association genetics of oleoresin flow in loblolly pine: discovering genes and predicting phenotype for improved resistance to bark beetles and bioenergy potential. New Phytologist, 2013, 199, 89-100.	3.5	58
71	Genetic structure and association mapping of adaptive and selective traits in the east Texas loblolly pine (Pinus taeda L.) breeding populations. Tree Genetics and Genomes, 2013, 9, 1161-1178.	0.6	40
72	Association of loblolly pine xylem development gene expression with single-nucleotide polymorphisms. Tree Physiology, 2013, 33, 763-774.	1.4	21

#	Article	IF	Citations
73	The Evolutionary Genetics of the Genes Underlying Phenotypic Associations for Loblolly Pine (Pinus taeda, Pinaceae). Genetics, 2013, 195, 1353-1372.	1.2	41
74	Generation, functional annotation and comparative analysis of black spruce (Picea mariana) ESTs: an important conifer genomic resource. BMC Genomics, 2013, 14, 702.	1.2	10
75	Insights into the Loblolly Pine Genome: Characterization of BAC and Fosmid Sequences. PLoS ONE, 2013, 8, e72439.	1.1	46
76	An extension of the Plant Ontology project supporting wood anatomy and development research. IAWA Journal, 2012, 33, 113-117.	2.7	8
77	SNP markers trace familial linkages in a cloned population of Pinus taedaâ€"prospects for genomic selection. Tree Genetics and Genomes, 2012, 8, 1307-1318.	0.6	62
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. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 89-104.	1.1	67
79	The Protein Architecture of Human Secretory Vesicles Reveals Differential Regulation of Signaling Molecule Secretion by Protein Kinases. PLoS ONE, 2012, 7, e41134.	1.1	11
80	Disentangling the Roles of History and Local Selection in Shaping Clinal Variation of Allele Frequencies and Gene Expression in Norway Spruce (Picea abies). Genetics, 2012, 191, 865-881.	1.2	195
81	Uniform standards for genome databases in forest and fruit trees. Tree Genetics and Genomes, 2012, 8, 549-557.	0.6	20
82	Association genetics of the loblolly pine (Pinus taeda, Pinaceae) metabolome. New Phytologist, 2012, 193, 890-902.	3.5	78
83	Contrasting patterns of nucleotide diversity for four conifers of Alpine European forests. Evolutionary Applications, 2012, 5, 762-775.	1.5	49
84	Association genetics of carbon isotope discrimination, height and foliar nitrogen in a natural population of Pinus taeda L. Heredity, 2011, 107, 105-114.	1.2	67
85	Comparative mapping in Pinus: sugar pine (Pinus lambertiana Dougl.) and loblolly pine (Pinus taeda L.). Tree Genetics and Genomes, 2011, 7, 457-468.	0.6	47
86	Development and implementation of a highly-multiplexed SNP array for genetic mapping in maritime pine and comparative mapping with loblolly pine. BMC Genomics, 2011, 12, 368.	1.2	66
87	Neuropeptidomic Components Generated by Proteomic Functions in Secretory Vesicles for Cellâ€"Cell Communication. AAPS Journal, 2010, 12, 635-645.	2.2	23
88	The Pinus taeda genome is characterized by diverse and highly diverged repetitive sequences. BMC Genomics, 2010, 11, 420.	1.2	144
89	Association genetics of traits controlling lignin and cellulose biosynthesis in black cottonwood (Populus trichocarpa, Salicaceae) secondary xylem. New Phytologist, 2010, 188, 515-532.	3.5	134
90	Back to nature: ecological genomics of loblolly pine (Pinus taeda, Pinaceae). Molecular Ecology, 2010, 19, 3789-3805.	2.0	204

#	Article	IF	Citations
91	Association Mapping of Quantitative Disease Resistance in a Natural Population of Loblolly Pine (Pinus taeda L.). Genetics, 2010, 186, 677-686.	1.2	94
92	Proteomics of Dense Core Secretory Vesicles Reveal Distinct Protein Categories for Secretion of Neuroeffectors for Cellâ˜Cell Communication. Journal of Proteome Research, 2010, 9, 5002-5024.	1.8	48
93	Patterns of Population Structure and Environmental Associations to Aridity Across the Range of Loblolly Pine (Pinus taeda L., Pinaceae). Genetics, 2010, 185, 969-982.	1.2	332
94	Multilocus Patterns of Nucleotide Diversity and Divergence Reveal Positive Selection at Candidate Genes Related to Cold Hardiness in Coastal Douglas Fir (Pseudotsuga menziesii var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 617 To	1.2	95
95	Association Genetics of Coastal Douglas Fir (Pseudotsuga menziesii var. menziesii,) Tj ETQq1 1 0.784314 rgBT /Overloc	1.2	193
96	PineSAPâ€"sequence alignment and SNP identification pipeline. Bioinformatics, 2009, 25, 2609-2610.	1.8	30
97	Bioinformatic analyses of mammalian 5'-UTR sequence properties of mRNAs predicts alternative translation initiation sites. BMC Bioinformatics, 2008, 9, 232.	1.2	43
98	Proteases for Processing Proneuropeptides into Peptide Neurotransmitters and Hormones. Annual Review of Pharmacology and Toxicology, 2008, 48, 393-423.	4.2	215
99	TreeGenes: A Forest Tree Genome Database. International Journal of Plant Genomics, 2008, 2008, 1-7.	2.2	89
100	Proteomics of Neuroendocrine Secretory Vesicles Reveal Distinct Functional Systems for Biosynthesis and Exocytosis of Peptide Hormones and Neurotransmitters. Journal of Proteome Research, 2007, 6, 1652-1665.	1.8	44
101	Demonstration of GTG as an alternative initiation codon for the serpin endopin 2B-2. Biochemical and Biophysical Research Communications, 2005, 327, 837-844.	1.0	21