# Jill L Wegrzyn

## List of Publications by Year in Descending Order

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| 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 | Standards recommendations for the Earth BioGenome Project.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119, | 11.5 | 4 |
| 103 | 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, | 11.5 | 9 |
| 102 | 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, | 3.2 | 4 |
| 101 | Comparative analysis of differential gene expression indicates divergence in ontogenetic strategies of leaves in two conifer genera.. *Ecology and Evolution*, **2022**, 12, e8611 | 2.8 | |
| 100 | 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 | 5.3 | 0 |
| 99 | The Cycas genome and the early evolution of seed plants.. *Nature Plants*, **2022**, | 11.5 | 5 |
| 98 | 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 | 4.9 | |
| 97 | Transcriptome of weeping pinyon pine, Pinus pinceana, shows differences across heterogeneous habitats. *Trees - Structure and Function*, **2021**, 35, 1351-1365 | 2.6 | 2 |
| 96 | Extensive Variation in Drought-Induced Gene Expression Changes Between Loblolly Pine Genotypes. *Frontiers in Genetics*, **2021**, 12, 661440 | 4.5 | 0 |
| 95 | Toward genomic selection in : Integrating resources to support array design in a complex conifer genome. *Applications in Plant Sciences*, **2021**, 9, e11439 | 2.3 | 8 |
| 94 | Tripal, a community update after 10 years of supporting open source, standards-based genetic, genomic and breeding databases. *Briefings in Bioinformatics*, **2021**, 22, | 13.4 | 2 |
| 93 | High gene space divergence contrasts with frozen vegetative architecture in the moss family Funariaceae. *Molecular Phylogenetics and Evolution*, **2021**, 154, 106965 | 4.1 | 2 |
| 92 | A genome-wide SNP genotyping resource for tropical pine tree species. *Molecular Ecology Resources*, **2021**, | 8.4 | 3 |
| 91 | Gene Frequency Shift in Relict Abies pinsapo Forests Associated with Drought-Induced Mortality: Preliminary Evidence of Local-Scale Divergent Selection. *Forests*, **2021**, 12, 1220 | 2.8 | 0 |
| 90 | Strategies of tolerance reflected in two North American maple genomes.. *Plant Journal*, **2021**, | 6.9 | 1 |
| 89 | EnTAP: Bringing faster and smarter functional annotation to non-model eukaryotic transcriptomes. *Molecular Ecology Resources*, **2020**, 20, 591-604 | 8.4 | 32 |
| 88 | Cyberinfrastructure and resources to enable an integrative approach to studying forest trees. *Evolutionary Applications*, **2020**, 13, 228-241 | 4.8 | 11 |

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| 87 | Comparative genomics of six Juglans species reveals disease-associated gene family contractions. *Plant Journal*, **2020**, 102, 410-423 | 6.9 | 7 |
| 86 | Co-option of wing-patterning genes underlies the evolution of the treehopper helmet. *Nature Ecology and Evolution*, **2020**, 4, 250-260 | 12.3 | 13 |
| 85 | Tripal and Galaxy: supporting reproducible scientific workflows for community biological databases. *Database: the Journal of Biological Databases and Curation*, **2020**, 2020, | 5 | 1 |
| 84 | A Reference Genome Sequence for Giant Sequoia. *G3: Genes, Genomes, Genetics*, **2020**, 10, 3907-3919 | 3.2 | 22 |
| 83 | gFACs: Gene Filtering, Analysis, and Conversion to Unify Genome Annotations Across Alignment and Gene Prediction Frameworks. *Genomics, Proteomics and Bioinformatics*, **2019**, 17, 305-310 | 6.5 | 10 |
| 82 | Dual RNA-Seq Analysis of the Pine- Interaction in Resistant () and Susceptible () Hosts. *Microorganisms*, **2019**, 7, | 4.9 | 11 |
| 81 | 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 | 6.2 | 15 |
| 80 | Tripal v3: an ontology-based toolkit for construction of FAIR biological community databases. *Database: the Journal of Biological Databases and Curation*, **2019**, 2019, | 5 | 11 |
| 79 | Tripal MapViewer: A tool for interactive visualization and comparison of genetic maps. *Database: the Journal of Biological Databases and Curation*, **2019**, 2019, | 5 | 5 |
| 78 | 15 years of GDR: New data and functionality in the Genome Database for Rosaceae. *Nucleic Acids Research*, **2019**, 47, D1137-D1145 | 20.1 | 129 |
| 77 | 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 | 2.1 | 12 |
| 76 | Comparative Transcriptomics Among Four White Pine Species. *G3: Genes, Genomes, Genetics*, **2018**, 8, 1461-1474 | 3.2 | 20 |
| 75 | JAK/STAT3 regulated global gene expression dynamics during late-stage reprogramming process. *BMC Genomics*, **2018**, 19, 183 | 4.5 | 17 |
| 74 | Defence transcriptome assembly and pathogenesis related gene family analysis in Pinus tecunumanii (low elevation). *BMC Genomics*, **2018**, 19, 632 | 4.5 | 19 |
| 73 | AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. *Database: the Journal of Biological Databases and Curation*, **2018**, 2018, | 5 | 28 |
| 72 | Growing and cultivating the forest genomics database, TreeGenes. *Database: the Journal of Biological Databases and Curation*, **2018**, 2018, 1-11 | 5 | 24 |
| 71 | Drought stress in Pinus taeda L. induces coordinated transcript accumulation of genes involved in the homogentisate pathway. *Tree Genetics and Genomes*, **2017**, 13, 1 | 2.1 | 11 |
| 70 | ChloroMitoCU: Codon patterns across organelle genomes for functional genomics and evolutionary applications. *DNA Research*, **2017**, 24, 327-332 | 4.5 | 2 |

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| 69 | Expression profiling in Pinus radiata infected with Fusarium circinatum. *Tree Genetics and Genomes*, **2017**, 13, 1 | 2.1 | 19 |
| 68 | Water availability drives signatures of local adaptation in whitebark pine (Pinus albicaulis Engelm.) across fine spatial scales of the Lake Tahoe Basin, USA. *Molecular Ecology*, **2017**, 26, 3168-3185 | 5.7 | 37 |
| 67 | Transcriptomic imprints of adaptation to fresh water: parallel evolution of osmoregulatory gene expression in the Alewife. *Molecular Ecology*, **2017**, 26, 831-848 | 5.7 | 37 |
| 66 | The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. *G3: Genes, Genomes, Genetics*, **2017**, 7, 3157-3167 | 3.2 | 55 |
| 65 | An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. *GigaScience*, **2017**, 6, 1-4 | 7.6 | 44 |
| 64 | Transcription through the eye of a needle: daily and annual cyclic gene expression variation in Douglas-fir needles. *BMC Genomics*, **2017**, 18, 558 | 4.5 | 18 |
| 63 | 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, | 5 | 13 |
| 62 | 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 | 6.2 | 12 |
| 61 | Lineage, fate, and fate potential of NG2-glia. *Brain Research*, **2016**, 1638, 116-128 | 3.7 | 73 |
| 60 | Sequence of the Sugar Pine Megagenome. *Genetics*, **2016**, 204, 1613-1626 | 4 | 119 |
| 59 | Quantitative trait loci influencing forking defects in an outbred pedigree of loblolly pine. *BMC Genetics*, **2016**, 17, 138 | 2.6 | 4 |
| 58 | The walnut (Juglans regia) genome sequence reveals diversity in genes coding for the biosynthesis of non-structural polyphenols. *Plant Journal*, **2016**, 87, 507-32 | 6.9 | 127 |
| 57 | Patterns of neutral and adaptive genetic diversity across the natural range of sugar pine (Pinus lambertiana Dougl.). *Tree Genetics and Genomes*, **2016**, 12, 1 | 2.1 | 15 |
| 56 | Assessing the Gene Content of the Megagenome: Sugar Pine (Pinus lambertiana). *G3: Genes, Genomes, Genetics*, **2016**, 6, 3787-3802 | 3.2 | 30 |
| 55 | 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 | 6.2 | 25 |
| 54 | Evolutionary Histories of Gene Families in Angiosperm Trees. *Plant Genetics and Genomics: Crops and Models*, **2016**, 121-137 | 0.2 | |
| 53 | Poor maternal nutrition during gestation alters the expression of genes involved in muscle development and metabolism in lambs. *Journal of Animal Science*, **2016**, 94, 3093-9 | 0.7 | 13 |
| 52 | Transcriptomic profile of leaf tissue from the leguminous tree, Millettia pinnata. *Tree Genetics and Genomes*, **2016**, 12, 1 | 2.1 | 9 |

| 51 | Combined de novo and genome guided assembly and annotation of the Pinus patula juvenile shoot transcriptome. *BMC Genomics*, **2015**, 16, 1057 | 4.5 | 34 |
| 50 | Discovering candidate genes that regulate resin canal number in Pinus taeda stems by integrating genetic analysis across environments, ages, and populations. *New Phytologist*, **2015**, 205, 627-41 | 9.8 | 35 |
| 49 | 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 | 3.6 | 8 |
| 48 | 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 | 3.6 | 13 |
| 47 | Unique features of the loblolly pine (Pinus taeda L.) megagenome revealed through sequence annotation. *Genetics*, **2014**, 196, 891-909 | 4 | 146 |
| 46 | Genomic Relationship Matrix for Correcting Pedigree Errors in Breeding Populations: Impact on Genetic Parameters and Genomic Selection Accuracy. *Crop Science*, **2014**, 54, 1115-1123 | 2.4 | 50 |
| 45 | Mapping Fusiform Rust Resistance Genes within a Complex Mating Design of Loblolly Pine. *Forests*, **2014**, 5, 347-362 | 2.8 | 17 |
| 44 | Sequencing and assembly of the 22-gb loblolly pine genome. *Genetics*, **2014**, 196, 875-90 | 4 | 211 |
| 43 | Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. *Genome Biology*, **2014**, 15, R59 | 18.3 | 347 |
| 42 | Multilocus analyses reveal little evidence for lineage-wide adaptive evolution within major clades of soft pines (Pinus subgenus Strobus). *Molecular Ecology*, **2013**, 22, 5635-50 | 5.7 | 27 |
| 41 | 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 | 2.1 | 19 |
| 40 | Open access to tree genomes: the path to a better forest. *Genome Biology*, **2013**, 14, 120 | 18.3 | 26 |
| 39 | Association genetics of chemical wood properties in black poplar (Populus nigra). *New Phytologist*, **2013**, 197, 162-176 | 9.8 | 61 |
| 38 | CartograTree: connecting tree genomes, phenotypes and environment. *Molecular Ecology Resources*, **2013**, 13, 528-37 | 8.4 | 7 |
| 37 | 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 | 9.8 | 45 |
| 36 | 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 | 2.1 | 36 |
| 35 | Association of loblolly pine xylem development gene expression with single-nucleotide polymorphisms. *Tree Physiology*, **2013**, 33, 763-74 | 4.2 | 14 |
| 34 | The evolutionary genetics of the genes underlying phenotypic associations for loblolly pine (Pinus taeda, Pinaceae). *Genetics*, **2013**, 195, 1353-72 | 4 | 33 |

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| 33 | Generation, functional annotation and comparative analysis of black spruce (Picea mariana) ESTs: an important conifer genomic resource. *BMC Genomics*, **2013**, 14, 702 | 4.5 | 9 |
| 32 | Insights into the loblolly pine genome: characterization of BAC and fosmid sequences. *PLoS ONE*, **2013**, 8, e72439 | 3.7 | 41 |
| 31 | Contrasting patterns of nucleotide diversity for four conifers of Alpine European forests. *Evolutionary Applications*, **2012**, 5, 762-75 | 4.8 | 40 |
| 30 | SNP markers trace familial linkages in a cloned population of Pinus taeda—prospects for genomic selection. *Tree Genetics and Genomes*, **2012**, 8, 1307-1318 | 2.1 | 47 |
| 29 | 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 | 4 | 44 |
| 28 | The protein architecture of human secretory vesicles reveals differential regulation of signaling molecule secretion by protein kinases. *PLoS ONE*, **2012**, 7, e41134 | 3.7 | 9 |
| 27 | 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, 865-81 | 4 | 112 |
| 26 | Uniform standards for genome databases in forest and fruit trees. *Tree Genetics and Genomes*, **2012**, 8, 549-557 | 2.1 | 17 |
| 25 | Association genetics of the loblolly pine (Pinus taeda, Pinaceae) metabolome. *New Phytologist*, **2012**, 193, 890-902 | 9.8 | 59 |
| 24 | An extension of the Plant Ontology project supporting wood anatomy and development research. *IAWA Journal*, **2012**, 33, 113-117 | 2.3 | 7 |
| 23 | Association genetics of carbon isotope discrimination, height and foliar nitrogen in a natural population of Pinus taeda L. *Heredity*, **2011**, 107, 105-14 | 3.6 | 55 |
| 22 | Comparative mapping in Pinus: sugar pine (Pinus lambertiana Dougl.) and loblolly pine (Pinus taeda L.). *Tree Genetics and Genomes*, **2011**, 7, 457-468 | 2.1 | 40 |
| 21 | 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 | 4.5 | 57 |
| 20 | Association genetics of traits controlling lignin and cellulose biosynthesis in black cottonwood (Populus trichocarpa, Salicaceae) secondary xylem. *New Phytologist*, **2010**, 188, 515-32 | 9.8 | 109 |
| 19 | Back to nature: ecological genomics of loblolly pine (Pinus taeda, Pinaceae). *Molecular Ecology*, **2010**, 19, 3789-805 | 5.7 | 170 |
| 18 | Association mapping of quantitative disease resistance in a natural population of loblolly pine (Pinus taeda L.). *Genetics*, **2010**, 186, 677-86 | 4 | 79 |
| 17 | Proteomics of dense core secretory vesicles reveal distinct protein categories for secretion of neuroeffectors for cell-cell communication. *Journal of Proteome Research*, **2010**, 9, 5002-24 | 5.6 | 40 |
| 16 | Patterns of population structure and environmental associations to aridity across the range of loblolly pine (Pinus taeda L., Pinaceae). *Genetics*, **2010**, 185, 969-82 | 4 | 283 |

# List of Publications

| 15 | Neuropeptidomic components generated by proteomic functions in secretory vesicles for cell-cell communication. *AAPS Journal*, **2010**, 12, 635-45 | 3.7 | 20 |
|----|---|---|---|
| 14 | The Pinus taeda genome is characterized by diverse and highly diverged repetitive sequences. *BMC Genomics*, **2010**, 11, 420 | 4.5 | 115 |
| 13 | Multilocus patterns of nucleotide diversity and divergence reveal positive selection at candidate genes related to cold hardiness in coastal Douglas Fir (Pseudotsuga menziesii var. menziesii). *Genetics*, **2009**, 183, 289-98 | 4 | 79 |
| 12 | Association genetics of coastal Douglas fir (Pseudotsuga menziesii var. menziesii, Pinaceae). I. Cold-hardiness related traits. *Genetics*, **2009**, 182, 1289-302 | 4 | 168 |
| 11 | PineSAP--sequence alignment and SNP identification pipeline. *Bioinformatics*, **2009**, 25, 2609-10 | 7.2 | 26 |
| 10 | Bioinformatic analyses of mammalian 5TUTR sequence properties of mRNAs predicts alternative translation initiation sites. *BMC Bioinformatics*, **2008**, 9, 232 | 3.6 | 36 |
| 9 | Proteases for processing proneuropeptides into peptide neurotransmitters and hormones. *Annual Review of Pharmacology and Toxicology*, **2008**, 48, 393-423 | 17.9 | 188 |
| 8 | TreeGenes: A forest tree genome database. *International Journal of Plant Genomics*, **2008**, 2008, 412875 | | 76 |
| 7 | Proteomics of neuroendocrine secretory vesicles reveal distinct functional systems for biosynthesis and exocytosis of peptide hormones and neurotransmitters. *Journal of Proteome Research*, **2007**, 6, 1652-65 | 5.6 | 42 |
| 6 | Demonstration of GTG as an alternative initiation codon for the serpin endopin 2B-2. *Biochemical and Biophysical Research Communications*, **2005**, 327, 837-44 | 3.4 | 16 |
| 5 | Neuropeptides: Chemical Activity Profiling and Proteomic Approaches1 | | |
| 4 | Transcription through the eye of a needle: daily and annual cycles of gene expression variation in Douglas-fir needles | | 2 |
| 3 | The giant sequoia genome and proliferation of disease resistance genes | | 4 |
| 2 | Virus evolution affected early COVID-19 spread | | 1 |
| 1 | EnTAP: Bringing Faster and Smarter Functional Annotation to Non-Model Eukaryotic Transcriptomes | | 3 |