

# Andrew J Eckert

## List of Publications by Year in descending order

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Version: 2024-02-01

64  
papers

4,439  
citations

147801

31  
h-index

114465

63  
g-index

72  
all docs

72  
docs citations

72  
times ranked

4916  
citing authors

#	ARTICLE	IF	CITATIONS
1	A practical guide to environmental association analysis in landscape genomics. <i>Molecular Ecology</i> , 2015, 24, 4348-4370.	3.9	584
2	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, 969-982.	2.9	332
3	Putting the landscape into the genomics of trees: approaches for understanding local adaptation and population responses to changing climate. <i>Tree Genetics and Genomes</i> , 2013, 9, 901-911.	1.6	261
4	Back to nature: ecological genomics of loblolly pine ( <i>Pinus taeda</i> , Pinaceae). <i>Molecular Ecology</i> , 2010, 19, 3789-3805.	3.9	204
5	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, 865-881.	2.9	195
6	Association Genetics of Coastal Douglas Fir ( <i>Pseudotsuga menziesii</i> var. <i>menziesii</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.9	193
7	Sequence of the Sugar Pine Megagenome. <i>Genetics</i> , 2016, 204, 1613-1626.	2.9	169
8	Phylogeny, historical biogeography, and patterns of diversification for <i>Pinus</i> (Pinaceae): Phylogenetic tests of fossil-based hypotheses. <i>Molecular Phylogenetics and Evolution</i> , 2006, 40, 166-182.	2.7	155
9	A molecular phylogeny and classification of Bignoniaceae. <i>American Journal of Botany</i> , 2009, 96, 1731-1743.	1.7	151
10	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, 515-532.	7.3	134
11	Does gene flow destroy phylogenetic signal? The performance of three methods for estimating species phylogenies in the presence of gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 832-842.	2.7	132
12	High-throughput genotyping and mapping of single nucleotide polymorphisms in loblolly pine ( <i>Pinus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.8	119
13	The Molecular Systematics of <i>Rhododendron</i> (Ericaceae): A Phylogeny Based Upon <i>RPB2</i> Gene Sequences. <i>Systematic Botany</i> , 2005, 30, 616-626.	0.5	96
14	Association Mapping of Quantitative Disease Resistance in a Natural Population of Loblolly Pine ( <i>Pinus taeda</i> L.). <i>Genetics</i> , 2010, 186, 677-686.	2.9	94
15	Landscape genomic analysis of candidate genes for climate adaptation in a California endemic oak, <i>Quercus lobata</i> . <i>American Journal of Botany</i> , 2016, 103, 33-46.	1.7	93
16	The geographical and environmental determinants of genetic diversity for four alpine conifers of the European Alps. <i>Molecular Ecology</i> , 2012, 21, 5530-5545.	3.9	92
17	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.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.8	91
18	The genomics of local adaptation in trees: are we out of the woods yet?. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	87

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19	Association genetics of the loblolly pine ( <i>Pinus taeda</i> , Pinaceae) metabolome. <i>New Phytologist</i> , 2012, 193, 890-902.	7.3	78
20	The emerging field of geogenomics: Constraining geological problems with genetic data. <i>Earth-Science Reviews</i> , 2014, 135, 38-47.	9.1	68
21	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, 105-114.	2.6	67
22	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.	2.8	66
23	RADseq approaches and applications for forest tree genetics. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	58
24	Water availability drives signatures of local adaptation in whitebark pine ( <i>Pinus albicaulis</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 51</i>	3.9	51
25	Contrasting patterns of nucleotide diversity for four conifers of Alpine European forests. <i>Evolutionary Applications</i> , 2012, 5, 762-775.	3.1	49
26	The role of hybridization during ecological divergence of southwestern white pine ( <i>Pinus</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 T</i>	3.9	48
27	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.	1.6	47
28	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, 5635-5650.	3.9	45
29	Local adaptation at fine spatial scales: an example from sugar pine ( <i>Pinus lambertiana</i> , Pinaceae). <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	42
30	The Evolutionary Genetics of the Genes Underlying Phenotypic Associations for Loblolly Pine ( <i>Pinus taeda</i> , Pinaceae). <i>Genetics</i> , 2013, 195, 1353-1372.	2.9	41
31	A phylogeographical analysis of the range disjunction for foxtail pine ( <i>Pinus balfouriana</i> ) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 38</i>	3.9	38
32	Colonization of volcanic deserts from productive patches. <i>American Journal of Botany</i> , 2005, 92, 27-36.	1.7	31
33	Single-Locus versus Multilocus Patterns of Local Adaptation to Climate in Eastern White Pine ( <i>Pinus</i> ) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 28</i>	2.5	28
34	DnaSAM: Software to perform neutrality testing for large datasets with complex null models. <i>Molecular Ecology Resources</i> , 2010, 10, 542-545.	4.8	27
35	Natural variation in expression of genes involved in xylem development in loblolly pine ( <i>Pinus taeda</i> ) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 27</i>	1.6	27
36	High rate of adaptive evolution in two widespread European pines. <i>Molecular Ecology</i> , 2017, 26, 6857-6870.	3.9	27

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37	Population biology of sugar pine ( <i>Pinus lambertiana</i> Dougl.) with reference to historical disturbances in the Lake Tahoe Basin: Implications for restoration. <i>Forest Ecology and Management</i> , 2011, 262, 770-779.	3.2	24
38	Spatially variable natural selection and the divergence between parapatric subspecies of lodgepole pine ( <i>Pinus contorta</i> , Pinaceae). <i>American Journal of Botany</i> , 2012, 99, 1323-1334.	1.7	24
39	The genetic architecture of local adaptation I: the genomic landscape of foxtail pine ( <i>Pinus</i> ) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i> 2015, 11, 1.	1.6	22
40	Signatures of natural selection on <i>Pinus cembra</i> and <i>P. mugo</i> along elevational gradients in the Alps. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	22
41	Population assignment reveals low migratory connectivity in a weakly structured songbird. <i>Molecular Ecology</i> , 2019, 28, 2122-2135.	3.9	22
42	Genetic signatures of natural selection in response to air pollution in red spruce ( <i>Pinus rubens</i> , Pinaceae). <i>Molecular Ecology</i> , 2013, 22, 5877-5889.	3.9	21
43	Association of loblolly pine xylem development gene expression with single-nucleotide polymorphisms. <i>Tree Physiology</i> , 2013, 33, 763-774.	3.1	21
44	An empirical evaluation of two-stage species tree inference strategies using a multilocus dataset from North American pines. <i>BMC Evolutionary Biology</i> , 2014, 14, 67.	3.2	21
45	Polygenic adaptation and negative selection across traits, years and environments in a long-lived plant species ( <i>Pinus pinaster</i> Ait., Pinaceae). <i>Molecular Ecology</i> , 2022, 31, 2089-2105.	3.9	21
46	Combining Genotype, Phenotype, and Environment to Infer Potential Candidate Genes. <i>Journal of Heredity</i> , 2017, 108, esw077.	2.4	20
47	Modelling multilocus selection in an individual-based, spatially-explicit landscape genetics framework. <i>Molecular Ecology Resources</i> , 2020, 20, 605-615.	4.8	20
48	Evolutionary genomics of gypsy moth populations sampled along a latitudinal gradient. <i>Molecular Ecology</i> , 2019, 28, 2206-2223.	3.9	19
49	Toward genomic selection in <i>Pinus taeda</i> : Integrating resources to support array design in a complex conifer genome. <i>Applications in Plant Sciences</i> , 2021, 9, e11439.	2.1	19
50	Adaptive evolution in a conifer hybrid zone is driven by a mosaic of recently introgressed and background genetic variants. <i>Communications Biology</i> , 2021, 4, 160.	4.4	17
51	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.	1.6	15
52	Influence of substrate type and microsite availability on the persistence of foxtail pine ( <i>Pinus</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 T</i> 1615-1624.	1.7	13
53	Can gypsy moth stand the heat? A reciprocal transplant experiment with an invasive forest pest across its southern range margin. <i>Biological Invasions</i> , 2019, 21, 1365-1378.	2.4	13
54	Genotyping-by-sequencing and ecological niche modeling illuminate phylogeography, admixture, and Pleistocene range dynamics in quaking aspen ( <i>Populus tremuloides</i> ). <i>Ecology and Evolution</i> , 2020, 10, 4609-4629.	1.9	13

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55	Effects of historical demography and ecological context on spatial patterns of genetic diversity within foxtail pine ( <i>Pinus balfouriana</i> ; Pinaceae) stands located in the Klamath Mountains, California. <i>American Journal of Botany</i> , 2010, 97, 650-659.	1.7	11
56	Seeing the forest for the trees: statistical phylogeography in a changing world. <i>New Phytologist</i> , 2011, 189, 894-897.	7.3	11
57	Defining the landscape of adaptive genetic diversity. <i>Molecular Ecology</i> , 2012, 21, 2836-2838.	3.9	10
58	Morphological Differences in <i>Pinus strobiformis</i> Across Latitudinal and Elevational Gradients. <i>Frontiers in Plant Science</i> , 2020, 11, 559697.	3.6	10
59	Thermal Sensitivity of Gypsy Moth (Lepidoptera: Erebidæ) During Larval and Pupal Development. <i>Environmental Entomology</i> , 2018, 47, 1623-1631.	1.4	9
60	ENVIRONMENTAL AND ECOLOGICAL EFFECTS ON SIZE CLASS DISTRIBUTIONS OF FOXTAIL PINE ( <i>PINUS</i> )	0.4	8
61	Effect of fire and thinning on fine-scale genetic structure and gene flow in fire-suppressed populations of sugar pine ( <i>Pinus lambertiana</i> Dougl.). <i>Forest Ecology and Management</i> , 2019, 447, 115-129.	3.2	4
62	Landscape Biology of Western White Pine: Implications for Conservation of a Widely-Distributed Five-Needle Pine at Its Southern Range Limit. <i>Forests</i> , 2016, 7, 93.	2.1	2
63	Determining the when, where and how of conifer speciation: a challenge arising from the study of the evolutionary history of a relict conifer <i>Pseudotsuga schrenkii</i> . <i>Annals of Botany</i> , 2020, 125, v-vii.	2.9	2
64	Population and conservation genomics of forest trees: seeing the forest for the trees. <i>BMC Proceedings</i> , 2011, 5, .	1.6	1