

# Stephen P Difazio

## List of Publications by Year in descending order

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Version: 2024-02-01

78  
papers

10,548  
citations

76196

40  
h-index

69108

77  
g-index

93  
all docs

93  
docs citations

93  
times ranked

11166  
citing authors

#	ARTICLE	IF	CITATIONS
1	Abundance of Major Cell Wall Components in Natural Variants and Pedigrees of <i>Populus trichocarpa</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 757810.	1.7	3
2	ISSRseq: An extensible method for reduced representation sequencing. <i>Methods in Ecology and Evolution</i> , 2022, 13, 668-681.	2.2	9
3	A General Model to Explain Repeated Turnovers of Sex Determination in the Salicaceae. <i>Molecular Biology and Evolution</i> , 2021, 38, 968-980.	3.5	53
4	Hybrid speciation via inheritance of alternate alleles of parental isolating genes. <i>Molecular Plant</i> , 2021, 14, 208-222.	3.9	68
5	Accurate determination of genotypic variance of cell wall characteristics of a <i>Populus trichocarpa</i> pedigree using high-throughput pyrolysis-molecular beam mass spectrometry. <i>Biotechnology for Biofuels</i> , 2021, 14, 59.	6.2	6
6	Characterization of <i>Salix nigra</i> floral insect community and activity of three native <i>Andrena</i> bees. <i>Ecology and Evolution</i> , 2021, 11, 4688-4700.	0.8	5
7	Integrative genomics reveals paths to sex dimorphism in <i>Salix purpurea</i> L. <i>Horticulture Research</i> , 2021, 8, 170.	2.9	12
8	Sexual dimorphism in the dioecious willow <i>Salix purpurea</i> . <i>American Journal of Botany</i> , 2021, 108, 1374-1387.	0.8	14
9	Sex determination through X-Y heterogamety in <i>Salix nigra</i> . <i>Heredity</i> , 2021, 126, 630-639.	1.2	26
10	Phylogenomics of the genus <i>Populus</i> reveals extensive interspecific gene flow and balancing selection. <i>New Phytologist</i> , 2020, 225, 1370-1382.	3.5	93
11	Genome-Wide Association Study of Wood Anatomical and Morphological Traits in <i>Populus trichocarpa</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 545748.	1.7	21
12	A targeted sequence capture array for phylogenetics and population genomics in the Salicaceae. <i>Applications in Plant Sciences</i> , 2020, 8, e11394.	0.8	9
13	Sequencing and Analysis of the Sex Determination Region of <i>Populus trichocarpa</i> . <i>Genes</i> , 2020, 11, 843.	1.0	19
14	Host plant genetic control of associated fungal and insect species in a <i>Populus</i> hybrid cross. <i>Ecology and Evolution</i> , 2020, 10, 5119-5134.	0.8	4
15	Improved genome assembly provides new insights into genome evolution in a desert poplar ( <i>Populus euphratica</i> ). <i>Molecular Ecology Resources</i> , 2020, 20, 781-794.	2.2	45
16	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biology</i> , 2020, 21, 38.	3.8	74
17	Pathways to sex determination in plants: how many roads lead to Rome?. <i>Current Opinion in Plant Biology</i> , 2020, 54, 61-68.	3.5	54
18	Finding New Cell Wall Regulatory Genes in <i>Populus trichocarpa</i> Using Multiple Lines of Evidence. <i>Frontiers in Plant Science</i> , 2019, 10, 1249.	1.7	13

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19	Wavelet-Based Genomic Signal Processing for Centromere Identification and Hypothesis Generation. <i>Frontiers in Genetics</i> , 2019, 10, 487.	1.1	11
20	Multi-Phenotype Association Decomposition: Unraveling Complex Gene-Phenotype Relationships. <i>Frontiers in Genetics</i> , 2019, 10, 417.	1.1	20
21	Genetic diversity and population structure of native, naturalized, and cultivated <i>Salix purpurea</i> . <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	13
22	Joint linkage and association mapping of complex traits in shrub willow ( <i>Salix purpurea</i> L.). <i>Annals of Botany</i> , 2019, 124, 701-715.	1.4	37
23	Multitrait genome-wide association analysis of <i>Populus trichocarpa</i> identifies key polymorphisms controlling morphological and physiological traits. <i>New Phytologist</i> , 2019, 223, 293-309.	3.5	85
24	Large effect quantitative trait loci for salicinoid phenolic glycosides in <i>Populus</i> : Implications for gene discovery. <i>Ecology and Evolution</i> , 2018, 8, 3726-3737.	0.8	6
25	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	1.7	50
26	Adaptive introgression and maintenance of a trispecies hybrid complex in range-edge populations of <i>Populus</i> . <i>Molecular Ecology</i> , 2018, 27, 4820-4838.	2.0	56
27	Pleiotropic and Epistatic Network-Based Discovery: Integrated Networks for Target Gene Discovery. <i>Frontiers in Energy Research</i> , 2018, 6, .	1.2	32
28	Characterization of a large sex determination region in <i>Salix purpurea</i> L. (Salicaceae). <i>Molecular Genetics and Genomics</i> , 2018, 293, 1437-1452.	1.0	61
29	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
30	Insights of biomass recalcitrance in natural <i>Populus trichocarpa</i> variants for biomass conversion. <i>Green Chemistry</i> , 2017, 19, 5467-5478.	4.6	82
31	Agronomic performance of <i>Populus deltoides</i> trees engineered for biofuel production. <i>Biotechnology for Biofuels</i> , 2017, 10, 253.	6.2	22
32	Geographical barriers and climate influence demographic history in narrowleaf cottonwoods. <i>Heredity</i> , 2015, 114, 387-396.	1.2	27
33	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
34	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
35	Genome-wide association mapping for wood characteristics in <i>Populus</i> identifies an array of candidate single nucleotide polymorphisms. <i>New Phytologist</i> , 2013, 200, 710-726.	3.5	158
36	A 34K SNP 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

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37	Genomic insights into salt adaptation in a desert poplar. <i>Nature Communications</i> , 2013, 4, 2797.	5.8	286
38	Predicting whole genome protein interaction networks from primary sequence data in model and non-model organisms using ENTS. <i>BMC Genomics</i> , 2013, 14, 608.	1.2	28
39	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
40	Contrasting patterns of evolution following whole genome versus tandem duplication events in <i>Populus</i> . <i>Genome Research</i> , 2012, 22, 95-105.	2.4	126
41	Identification of quantitative trait loci and candidate genes for cadmium tolerance in <i>Populus</i> . <i>Tree Physiology</i> , 2012, 32, 626-638.	1.4	36
42	The obscure events contributing to the evolution of an incipient sex chromosome in <i>Populus</i> : a retrospective working hypothesis. <i>Tree Genetics and Genomes</i> , 2012, 8, 559-571.	0.6	50
43	Gene flow and simulation of transgene dispersal from hybrid poplar plantations. <i>New Phytologist</i> , 2012, 193, 903-915.	3.5	49
44	<i>Populus</i> . , 2011, , 1-28.		14
45	Poplar Genome Microarrays. , 2011, , 112-127.		12
46	The <i>Populus</i> Genome Sequence. , 2011, , 85-111.		0
47	Population substructure in continuous and fragmented stands of <i>Populus trichocarpa</i> . <i>Heredity</i> , 2010, 105, 348-357.	1.2	26
48	The <i>Populus</i> Genome and Comparative Genomics. , 2010, , 67-90.		5
49	The <i>Populus</i> Genome Initiative. , 2010, , 243-274.		0
50	Extensive pollen flow in two ecologically contrasting populations of <i>Populus trichocarpa</i> . <i>Molecular Ecology</i> , 2009, 18, 357-373.	2.0	65
51	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
52	Poplar Genomics: State of the Science. <i>Critical Reviews in Plant Sciences</i> , 2009, 28, 285-308.	2.7	42
53	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	13.7	1,003
54	A dense linkage map of hybrid cottonwood ( <i>Populus fremontii</i> × <i>P. angustifolia</i> ) contributes to long-term ecological research and comparison mapping in a model forest tree. <i>Heredity</i> , 2008, 100, 59-70.	1.2	44

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55	Extending Genomics to Natural Communities and Ecosystems. <i>Science</i> , 2008, 320, 492-495.	6.0	189
56	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
57	An efficient method for purification of PCR products for sequencing. <i>BioTechniques</i> , 2008, 44, 921-923.	0.8	17
58	Efficiency of gene silencing in <i>Arabidopsis</i> : direct inverted repeats vs. transitive RNAi vectors. <i>Plant Biotechnology Journal</i> , 2007, 5, 615-626.	4.1	23
59	A physical map of the highly heterozygous <i>Populus</i> genome: integration with the genome sequence and genetic map and analysis of haplotype variation. <i>Plant Journal</i> , 2007, 50, 1063-1078.	2.8	70
60	Genome-wide analysis of Aux/IAA and ARF gene families in <i>Populus trichocarpa</i> . <i>BMC Plant Biology</i> , 2007, 7, 59.	1.6	218
61	Genetic containment of forest plantations. <i>Tree Genetics and Genomes</i> , 2007, 3, 75-100.	0.6	112
62	A framework for community and ecosystem genetics: from genes to ecosystems. <i>Nature Reviews Genetics</i> , 2006, 7, 510-523.	7.7	911
63	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	6.0	3,945
64	The <i>Populus</i> homeobox gene ARBORKNOX1 reveals overlapping mechanisms regulating the shoot apical meristem and the vascular cambium. <i>Plant Molecular Biology</i> , 2006, 61, 917-932.	2.0	141
65	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
66	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
67	Poplar Genomics is Getting Popular: The Impact of the Poplar Genome Project on Tree Research. <i>Plant Biology</i> , 2004, 6, 2-4.	1.8	109
68	Mycorrhizal symbionts of <i>Populus</i> to be sequenced by the United States Department of Energy's Joint Genome Institute. <i>Mycorrhiza</i> , 2004, 14, 63-64.	1.3	25
69	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
70	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
71	Emerging Use of Gene Expression Microarrays in Plant Physiology. <i>Comparative and Functional Genomics</i> , 2003, 4, 216-224.	2.0	17
72	The CP4 transgene provides high levels of tolerance to Roundup® herbicide in field-grown hybrid poplars. <i>Canadian Journal of Forest Research</i> , 2002, 32, 967-976.	0.8	66

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73	Genetically modified poplars in context. Forestry Chronicle, 2001, 77, 271-279.	0.5	45
74	Structure and expression of duplicate AGAMOUS orthologues in poplar. Plant Molecular Biology, 2000, 44, 619-634.	2.0	88
75	Environmental effects of genetically engineered woody biomass crops. Biomass and Bioenergy, 1998, 14, 403-414.	2.9	62
76	Factors limiting seed production of <i>Taxus Brevifolia</i> (Taxaceae) in Western Oregon. American Journal of Botany, 1998, 85, 910-918.	0.8	33
77	Strobilus production and growth of Pacific yew under a range of over story conditions in western Oregon. Canadian Journal of Forest Research, 1997, 27, 986-993.	0.8	6
78	Variation in sex expression of <i>Taxus brevifolia</i> in western Oregon. Canadian Journal of Botany, 1996, 74, 1943-1946.	1.2	9