Witold M Wachowiak

List of Publications by Year
in descending order

53	1,160	394421	434195
papers	citations	19 h-index	31 g-index

55	55	55	980
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Demographic History Has Influenced Nucleotide Diversity in European Pinus sylvestris Populations. Genetics, 2007, 177, 1713-1724.	2.9	154
2	Search for nucleotide diversity patterns of local adaptation in dehydrins and other cold-related candidate genes in Scots pine (Pinus sylvestris L.). Tree Genetics and Genomes, 2009, 5, 117-132.	1.6	105
3	Hybridisation processes in sympatric populations of pines Pinus sylvestris L., P. mugo Turra and P. uliginosa Neumann. Plant Systematics and Evolution, 2008, 271, 29-40.	0.9	55
4	High genetic diversity at the extreme range edge: nucleotide variation at nuclear loci in Scots pine (Pinus sylvestris L.) in Scotland. Heredity, 2011, 106, 775-787.	2.6	54
5	Cryptic speciation in liverworts â€“ a case study in the Aneura pinguis complex. Botanical Journal of the Linnean Society, 2007, 155, 273-282.	1.6	51
6	Geographical patterns of nucleotide diversity and population differentiation in three closely related European pine species in thePinus mugocomplex. Botanical Journal of the Linnean Society, 2013, 172, 225-238.	1.6	48
7	Selection on Nuclear Genes in a Pinus Phylogeny. Molecular Biology and Evolution, 2009, 26, 893-905.	8.9	44
8	Speciation history of three closely related pines Pinus mugo (T.), P.Âuliginosa (N.) and P.Âsylvestris (L.). Molecular Ecology, 2011, 20, 1729-1743.	3.9	42
9	Comparative transcriptomics of a complex of four European pine species. BMC Genomics, 2015, 16, 234.	2.8	40
10	Hybridization in contact zone between temperate European pine species. Tree Genetics and Genomes, 2016, 12, 1.	1.6	31
11	Cryptic hybrids between Pinus uncinata and P. sylvestris. Botanical Journal of the Linnean Society, 0, 163, 473-485.	1.6	30
12	Evidence of natural reciprocal hybridisation between Pinus uliginosa and P. sylvestris in the sympatric population of the species. Flora: Morphology, Distribution, Functional Ecology of Plants, 2005, 200, 563-568.	1.2	29
13	The biogeography and genetic relationships ofJuniperus oxycedrusand related taxa from the Mediterranean and Macaronesian regions. Botanical Journal of the Linnean Society, 2014, 174, 637-653.	1.6	27
14	A critical evaluation of reproductive barriers between closely related species using DNA markers - a case study in Pinus. Plant Systematics and Evolution, 2006, 257, 1-8.	0.9	25
15	Development of a single nucleotide polymorphism array for population genomic studies in four European pine species. Molecular Ecology Resources, 2020, 20, 1697-1705.	4.8	25
16	Contrasting patterns of genetic variation in core and peripheral populations of highly outcrossing and wind pollinated forest tree species. AoB PLANTS, 2016, 8, .	2.3	23
17	Genetic variation in Taxus baccata L.: A case study supporting Polandâ€™s protection and restoration program. Forest Ecology and Management, 2018, 409, 148-160.	3.2	22
18	Lack of evidence on hybrid swarm in the sympatric population of Pinus mugo and P. sylvestris. Flora: Morphology, Distribution, Functional Ecology of Plants, 2006, 201, 307-316.	1.2	21

#	Article	IF	Citations
19	Understanding the evolution of native pinewoods in Scotland will benefit their future management and conservation. Forestry, 2010, 83, 535-545.	2.3	21
20	Substantial heritable variation for susceptibility to Dothistroma septosporum within populations of native British Scots pine (Pinus sylvestris). Plant Pathology, 2016, 65, 987-996.	2.4	21
21	Reciprocal controlled crosses between Pinus sylvestris and P. mugo verified by a species-specific cpDNA marker. Journal of Applied Genetics, 2005, 46, 41-3.	1.9	20
22	Ecology and management history drive spatial genetic structure in Scots pine. Forest Ecology and Management, 2017, 400, 68-76.	3.2	18
23	Reconstructing the plant mitochondrial genome for marker discovery: a case study using Pinus. Molecular Ecology Resources, 2017, 17, 943-954.	4.8	18
24	High genetic similarity between Polish and North European Scots pine (Pinus sylvestris L.) populations at nuclear gene loci. Tree Genetics and Genomes, 2014, 10, 1015-1025.	1.6	17
25	Early phenology and growth trait variation in closely related European pine species. Ecology and Evolution, 2018, 8, 655-666.	1.9	16
26	Species specific cpDNA markers useful for studies on the hybridisation between Pinus mugo and P. sylvestris. Acta Societatis Botanicorum Poloniae, 2014, 69, 273-276.	0.8	16
27	Molecular signatures of divergence and selection in closely related pine taxa. Tree Genetics and Genomes, 2018, 14, 83.	1.6	15
28	Genetic characteristics of Scots pine in Poland and reference populations based on nuclear and chloroplast microsatellite markers. Silva Fennica, 2017, 51, .	1.3	15
29	Substructuring of Scots pine in Europe based on polymorphism at chloroplast microsatellite loci. Flora: Morphology, Distribution, Functional Ecology of Plants, 2016, 220, 142-149.	1.2	14
30	Taming the massive genome of Scots pine with PiSy50k, a new genotyping array for conifer research. Plant Journal, 2022, 109, 1337-1350.	5.7	13
31	Nuclear microsatellite markers reveal the low genetic structure of Pinus mugo Turra (dwarf) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.9	12
32	Among population differentiation at nuclear genes in native Scots pine (Pinus sylvestris L.) in Scotland. Flora: Morphology, Distribution, Functional Ecology of Plants, 2013, 208, 79-86.	1.2	11
33	Current Approaches and Perspectives in Population Genetics of Scots Pine (Pinus sylvestris L.). Forest Science, 2016, 62, 343-354.	1.0	11
34	Population history of European mountain pines Pinus mugo and Pinus uncinata revealed by mitochondrial DNA markers. Journal of Systematics and Evolution, 2020, 58, 474-486.	3.1	11
35	Interspecific gene flow and ecological selection in a pine (Pinus sp.) contact zone. Plant Systematics and Evolution, 2015, 301, 1643-1652.	0.9	8
36	Patterns ofmtDNA variation reveal complex evolutionary history of relict and endangered peat bog pine (Pinus uliginosa). AoB PLANTS, 2019, 11, plz015.	2.3	8

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37	Genetic Consequences of Hybridization in Relict Isolated Trees Pinus sylvestris and the Pinus mugo Complex. Forests, 2020, 11, 1086.	2.1	8
38	Molecular and paleoâ€climatic data uncover the impact of an ancient bottleneck on the demographic history and contemporary genetic structure of endangered Pinus uliginosa. Journal of Systematics and Evolution, 2021, 59, 596-610.	3.1	8
39	Different patterns of genetic structure of relict and isolated populations of endangered peat-bog pine (Pinus uliginosa Neumann). Journal of Applied Genetics, 2009, 50, 329-339.	1.9	7
40	Genetic evaluation of seeds of highly endangered Pinus uliginosa Neumann from WÄ™gliniec reserve for ex-situ conservation program. Acta Societatis Botanicorum Poloniae, 2011, 74, 237-242.	0.8	7
41	Utility of closely related taxa for genetic studies of adaptive variation and speciation: Current state and perspectives in plants with focus on forest tree species. Journal of Systematics and Evolution, 2016, 54, 17-28.	3.1	6
42	Cross-amplification and multiplexing of cpSSRs and nSSRs in two closely related pine species (Pinus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.6	5
43	Admixture and selection patterns across the European distribution of Scots pine, Pinus sylvestris (Pinaceae). Botanical Journal of the Linnean Society, 2022, 200, 416-432.	1.6	5
44	Candidate Genes for the High-Altitude Adaptations of Two Mountain Pine Taxa. International Journal of Molecular Sciences, 2021, 22, 3477.	4.1	4
45	Long-term growth performance and productivity of Scots pine (Pinus sylvestris L.) populations. Acta Societatis Botanicorum Poloniae, 2017, 86, .	0.8	4
46	Identifying and testing markerâ€“trait associations for growth and phenology in three pine species: Implications for genomic prediction. Evolutionary Applications, 2022, 15, 330-348.	3.1	4
47	Hybridization and introgression of native and foreignSorbustree species in unique environments of protected mountainous areas. AoB PLANTS, 2021, 13, plaa070.	2.3	3
48	The genetic assessment of the natural regeneration capacities of black poplar populations in the modern river valley landscapes. Forest Ecology and Management, 2019, 448, 150-159.	3.2	2
49	Heterogeneous patterns of genetic variation at nuclear genes and quantitative traits in a Scots pine provenance trial. Acta Societatis Botanicorum Poloniae, 2019, 88, .	0.8	2
50	Molecular Signatures of Reticulate Evolution within the Complex of European Pine Taxa. Forests, 2021, 12, 489.	2.1	1
51	Low effective population size and high spatial genetic structure of black poplar populations from the Oder valley in Poland. Annals of Forest Science, 2021, 78, 1.	2.0	1
52	Are There Any Traces of Pinus uliginosa in the StoÅ‚owe Mountains Outside the Wielkie Torfowisko Batorowskie and BÅ‚Ä™dne SkaÅ‚y?. Acta Societatis Botanicorum Poloniae, 0, 90, .	0.8	1
53	Evolutionary targets of gene expression divergence in a complex of closely related pine species. Journal of Systematics and Evolution, 2023, 61, 198-212.	3.1	1