

Jaroslav Klářipřítěl

List of Publications by Year in descending order

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68
papers

2,407
citations

270111

25
h-index

263392

45
g-index

74
all docs

74
docs citations

74
times ranked

2386
citing authors

#	ARTICLE	IF	CITATIONS
1	Development and Validation of a 36K SNP Array for Radiata Pine (<i>Pinus radiata</i> D.Don). <i>Forests</i> , 2022, 13, 176.	0.9	8
2	Genomics-Enabled Management of Genetic Resources in Radiata Pine. <i>Forests</i> , 2022, 13, 282.	0.9	4
3	Chasing genetic correlation breakers to stimulate population resilience to climate change. <i>Scientific Reports</i> , 2022, 12, 8238.	1.6	1
4	<i>Quercus</i> species divergence is driven by natural selection on evolutionarily less integrated traits. <i>Heredity</i> , 2021, 126, 366-382.	1.2	5
5	The Use of "Genotyping-by-Sequencing" to Recover Shared Genealogy in Genetically Diverse Eucalyptus Populations. <i>Forests</i> , 2021, 12, 904.	0.9	4
6	Genetic Variation in Drought-Tolerance Traits and Their Relationships to Growth in <i>Pinus radiata</i> D. Don Under Water Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 766803.	1.7	4
7	Indication of Quantitative Multiple Disease Resistance to Foliar Pathogens in <i>Pinus radiata</i> D.Don in New Zealand. <i>Frontiers in Plant Science</i> , 2020, 11, 1044.	1.7	3
8	Effect of trait's expression level on single-step genomic evaluation of resistance to <i>Dothistroma</i> needle blight. <i>BMC Plant Biology</i> , 2020, 20, 205.	1.6	14
9	Linkage disequilibrium vs. pedigree: Genomic selection prediction accuracy in conifer species. <i>PLoS ONE</i> , 2020, 15, e0232201.	1.1	28
10	Genotype-by-environment interaction in coast redwood outside natural distribution - search for environmental cues. <i>BMC Genetics</i> , 2020, 21, 15.	2.7	7
11	Genomic Diversity Evaluation of <i>Populus trichocarpa</i> Germplasm for Rare Variant Genetic Association Studies. <i>Frontiers in Genetics</i> , 2020, 10, 1384.	1.1	11
12	Drought Stress Adaptation in Norway Spruce and Related Genomics Work. <i>Compendium of Plant Genomes</i> , 2020, , 129-153.	0.3	4
13	Marker Selection in Multivariate Genomic Prediction Improves Accuracy of Low Heritability Traits. <i>Frontiers in Genetics</i> , 2020, 11, 499094.	1.1	23
14	Efficiency of genomic prediction across two <i>Eucalyptus nitens</i> seed orchards with different selection histories. <i>Heredity</i> , 2019, 122, 370-379.	1.2	42
15	The phylogenomics of diversification on an island: applying anchored hybrid enrichment to New Zealand <i>Leptospermum scoparium</i> (Myrtaceae). <i>Botanical Journal of the Linnean Society</i> , 2019, 191, 1-17.	0.8	14
16	Evolutionary potential of a widespread clonal grass under changing climate. <i>Journal of Evolutionary Biology</i> , 2019, 32, 1057-1068.	0.8	5
17	Alternative selection methods and explicit or implied economic-worth functions for different traits in tree breeding. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	13
18	Field-scale variability in site conditions explain phenotypic plasticity in response to nitrogen source in <i>Pinus radiata</i> D. Don. <i>Plant and Soil</i> , 2019, 443, 353-368.	1.8	9

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19	A high-density exome capture genotype-by-sequencing panel for forestry breeding in <i>Pinus radiata</i> . PLoS ONE, 2019, 14, e0222640.	1.1	30
20	Evaluation of forest tree breeding strategies based on partial pedigree reconstruction through simulations: <i>Pinus pinaster</i> and <i>Eucalyptus nitens</i> as case studies. Canadian Journal of Forest Research, 2019, 49, 1504-1515.	0.8	9
21	Stand density and genetic improvement have site-specific effects on the economic returns from <i>Pinus radiata</i> plantations. Forest Ecology and Management, 2019, 446, 80-92.	1.4	10
22	A role for <i>SPEECHLESS</i> in the integration of leaf stomatal patterning with the growth vs disease trade-off in poplar. New Phytologist, 2019, 223, 1888-1903.	3.5	25
23	Modelling of population structure through contemporary groups in genetic evaluation. BMC Genetics, 2019, 20, 81.	2.7	4
24	Genomic selection for non-key traits in radiata pine when the documented pedigree is corrected using DNA marker information. BMC Genomics, 2019, 20, 1026.	1.2	27
25	Genomic selection of juvenile height across a single-generational gap in Douglas-fir. Heredity, 2019, 122, 848-863.	1.2	26
26	Multienvironment genomic variance decomposition analysis of open-pollinated Interior spruce (<i>Picea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	30
27	Genomic-based multiple-trait evaluation in <i>Eucalyptus grandis</i> using dominant DArT markers. Plant Science, 2018, 271, 27-33.	1.7	23
28	Effect of Hidden Relatedness on Single-Step Genetic Evaluation in an Advanced Open-Pollinated Breeding Program. Journal of Heredity, 2018, 109, 802-810.	1.0	28
29	Effect of genomic prediction on response to selection in forest tree breeding. Tree Genetics and Genomes, 2018, 14, 1.	0.6	12
30	Adaptive differentiation of <i>Festuca rubra</i> along a climate gradient revealed by molecular markers and quantitative traits. PLoS ONE, 2018, 13, e0194670.	1.1	17
31	Ecological genomics of variation in bud-break phenology and mechanisms of response to climate warming in <i>Populus trichocarpa</i> . New Phytologist, 2018, 220, 300-316.	3.5	40
32	Assessing the genetic variation of tolerance to red needle cast in a <i>Pinus radiata</i> breeding population. Tree Genetics and Genomes, 2018, 14, 1.	0.6	9
33	Single-Step BLUP with Varying Genotyping Effort in Open-Pollinated <i>Picea glauca</i> . G3: Genes, Genomes, Genetics, 2017, 7, 935-942.	0.8	50
34	Sexual homomorphism in dioecious trees: extensive tests fail to detect sexual dimorphism in <i>Populus</i> . Scientific Reports, 2017, 7, 1831.	1.6	54
35	Improving accuracy of breeding values by incorporating genomic information in spatial-competition mixed models. Molecular Breeding, 2017, 37, 1.	1.0	32
36	Practical application of genomic selection in a doubled-haploid winter wheat breeding program. Molecular Breeding, 2017, 37, 117.	1.0	45

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37	Genomic prediction accuracies in space and time for height and wood density of Douglas-fir using exome capture as the genotyping platform. <i>BMC Genomics</i> , 2017, 18, 930.	1.2	52
38	Exploration of genetic architecture through sib-ship reconstruction in advanced breeding population of <i>Eucalyptus nitens</i> . <i>PLoS ONE</i> , 2017, 12, e0185137.	1.1	34
39	SSRs, SNPs and DArTs comparison on estimation of relatedness and genetic parametersâ€™ precision from a small half-sib sample population of <i>Eucalyptus grandis</i> . <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	9
40	Implementation of the Realized Genomic Relationship Matrix to Open-Pollinated White Spruce Family Testing for Disentangling Additive from Nonadditive Genetic Effects. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 743-753.	0.8	73
41	Species-specific alleles at a β -tubulin gene show significant associations with leaf morphological variation within <i>Quercus petraea</i> and <i>Q. robur</i> populations. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	6
42	Evolutionary potential in the Alpine: trait heritabilities and performance variation of the dwarf willow <i>Salix herbacea</i> from different elevations and microhabitats. <i>Ecology and Evolution</i> , 2016, 6, 3940-3952.	0.8	98
43	Evolutionary Quantitative Genomics of <i>Populus trichocarpa</i> . <i>PLoS ONE</i> , 2015, 10, e0142864.	1.1	31
44	A comparison of genomic selection models across time in interior spruce (<i>Picea engelmannii</i> – <i>glauca</i>) using unordered SNP imputation methods. <i>Heredity</i> , 2015, 115, 547-555.	1.2	84
45	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
46	Prediction accuracies for growth and wood attributes of interior spruce in space using genotyping-by-sequencing. <i>BMC Genomics</i> , 2015, 16, 370.	1.2	86
47	Association genetics, geography and ecophysiology link stomatal patterning in <i>Populus trichocarpa</i> with carbon gain and disease resistance trade-offs. <i>Molecular Ecology</i> , 2014, 23, 5771-5790.	2.0	103
48	Extensive Functional Pleiotropy of REVOLUTA Substantiated through Forward Genetics. <i>Plant Physiology</i> , 2014, 164, 548-554.	2.3	17
49	Genetics of wood quality attributes in Western Larch. <i>Annals of Forest Science</i> , 2014, 71, 415-424.	0.8	12
50	Estimates of genetic parameters and breeding values from western larch open-pollinated families using marker-based relationship. <i>Tree Genetics and Genomes</i> , 2014, 10, 241-249.	0.6	24
51	Randomized, replicated, staggered clonal-row (R2SCR) seed orchard design. <i>Tree Genetics and Genomes</i> , 2014, 10, 555-563.	0.6	12
52	Geographical and environmental gradients shape phenotypic trait variation and genetic structure in <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2014, 201, 1263-1276.	3.5	185
53	Genome-wide association implicates numerous genes underlying ecological trait variation in natural populations of <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2014, 203, 535-553.	3.5	171
54	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

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55	Comparison of genetic parameters from marker-based relationship, sibship, and combined models in Scots pine multi-site open-pollinated tests. <i>Tree Genetics and Genomes</i> , 2013, 9, 1227-1235.	0.6	18
56	A 34K <i>SNP</i> 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
57	<i>Populus trichocarpa</i> cell wall chemistry and ultrastructure trait variation, genetic control and genetic correlations. <i>New Phytologist</i> , 2013, 197, 777-790.	3.5	100
58	Network analysis reveals the relationship among wood properties, gene expression levels and genotypes of natural <i>Populus trichocarpa</i> accessions. <i>New Phytologist</i> , 2013, 200, 727-742.	3.5	37
59	Association Analysis Identifies <i>Melampsora columbiae</i> Poplar Leaf Rust Resistance SNPs. <i>PLoS ONE</i> , 2013, 8, e78423.	1.1	31
60	Optimization of genetic gain and diversity in seed orchard crops considering variation in seed germination. <i>Scandinavian Journal of Forest Research</i> , 2012, 27, 787-793.	0.5	4
61	Breeding without breeding: selection using the genomic best linear unbiased predictor method (GBLUP). <i>New Forests</i> , 2012, 43, 631-637.	0.7	27
62	Breeding without Breeding. <i>Tree Genetics and Genomes</i> , 2012, 8, 873-877.	0.6	11
63	Breeding without Breeding: Is a Complete Pedigree Necessary for Efficient Breeding?. <i>PLoS ONE</i> , 2011, 6, e25737.	1.1	76
64	Breeding without breeding: minimum fingerprinting effort with respect to the effective population size. <i>Tree Genetics and Genomes</i> , 2011, 7, 1069-1078.	0.6	12
65	Pollination dynamics in a Douglas-fir seed orchard as revealed by pedigree reconstruction. <i>Annals of Forest Science</i> , 2010, 67, 808-808.	0.8	27
66	Production impacts of forest tree breeding on an example of Norway spruce. <i>Journal of Forest Science</i> , 2010, 56, 348-352.	0.5	0
67	Optimization of combined genetic gain and diversity for collection and deployment of seed orchard crops. <i>Tree Genetics and Genomes</i> , 2009, 5, 583-593.	0.6	28
68	Addressing spatial variability in provenance experiments exemplified in two trials with black spruce. <i>Journal of Forest Science</i> , 2007, 53, 47-56.	0.5	7