

Igor Chybicki

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

1,504
citations

430442

18
h-index

329751

37
g-index

40
all docs

40
docs citations

40
times ranked

1785
citing authors

#	ARTICLE	IF	CITATIONS
1	Simultaneous Estimation of Null Alleles and Inbreeding Coefficients. <i>Journal of Heredity</i> , 2009, 100, 106-113.	1.0	535
2	Using Genetic Markers to Directly Estimate Gene Flow and Reproductive Success Parameters in Plants on the Basis of Naturally Regenerated Seedlings. <i>Genetics</i> , 2006, 173, 363-372.	1.2	108
3	Increased inbreeding and strong kinship structure in <i>Taxus baccata</i> estimated from both AFLP and SSR data. <i>Heredity</i> , 2011, 107, 589-600.	1.2	76
4	Realized gene flow within mixed stands of <i>Quercus robur</i> L. and <i>Q. petraea</i> (Matt.) L. revealed at the stage of naturally established seedling. <i>Molecular Ecology</i> , 2010, 19, 2137-2151.	2.0	65
5	NM+: software implementing parentage-based models for estimating gene dispersal and mating patterns in plants. <i>Molecular Ecology Resources</i> , 2010, 10, 1071-1075.	2.2	60
6	Comparison of direct and indirect genetic methods for estimating seed and pollen dispersal in <i>Fagus sylvatica</i> and <i>Fagus crenata</i> . <i>Forest Ecology and Management</i> , 2010, 259, 2151-2159.	1.4	53
7	Nuclear and mitochondrial patterns of introgression into native dark bees (<i>Apis mellifera mellifera</i>) in Poland. <i>Journal of Apicultural Research</i> , 2011, 50, 116-129.	0.7	46
8	Isolation by distance in saproxylic beetles may increase with niche specialization. <i>Journal of Insect Conservation</i> , 2013, 17, 219-233.	0.8	44
9	CAUTIONS ON DIRECT GENE FLOW ESTIMATION IN PLANT POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 956-963.	1.1	42
10	Presence of Triploids among Oak Species. <i>Annals of Botany</i> , 2007, 99, 959-964.	1.4	42
11	Seeing the forest through the trees: comprehensive inference on individual mating patterns in a mixed stand of <i>Quercus robur</i> and <i>Q. petraea</i> . <i>Annals of Botany</i> , 2013, 112, 561-574.	1.4	35
12	Seed and pollen gene dispersal in <i>Taxus baccata</i> , a dioecious conifer in the face of strong population fragmentation. <i>Annals of Botany</i> , 2018, 122, 409-421.	1.4	35
13	Isolation-by-distance within naturally established populations of European beech (<i>Fagus sylvatica</i>). <i>Journal of Ecology</i> , 2010, 98, 1071-1081.	0.5	27
14	NM+ improved reimplementation of NM+, a software for estimating gene dispersal and mating patterns. <i>Molecular Ecology Resources</i> , 2018, 18, 159-168.	2.2	26
15	No reduction in genetic diversity of Swiss stone pine (<i>Pinus cembra</i> L.) in Tatra Mountains despite high fragmentation and small population size. <i>Conservation Genetics</i> , 2014, 15, 1433-1445.	0.8	25
16	Rural avenues as dispersal corridors for the vulnerable saproxylic beetle <i>Elatér ferrugineus</i> in a fragmented agricultural landscape. <i>Journal of Insect Conservation</i> , 2015, 19, 567-580.	0.8	25
17	Chloroplast microsatellites as a tool for phylogeographic studies: the case of white oaks in Poland. <i>Forest Ecology and Management</i> , 2015, 8, 765-771.	0.5	22
18	Partial reproductive isolation between European subspecies of honey bees. <i>Apidologie</i> , 2013, 44, 611-619.	0.9	21

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19	Clonality as a driver of spatial genetic structure in populations of clonal tree species. <i>Journal of Plant Research</i> , 2015, 128, 731-745.	1.2	19
20	Variable rates of random genetic drift in protected populations of English yew: implications for gene pool conservation. <i>Conservation Genetics</i> , 2012, 13, 899-911.	0.8	18
21	Beech roots are simultaneously colonized by multiple genets of the ectomycorrhizal fungus <i>Laccaria amethystina</i> clustered in two genetic groups. <i>Molecular Ecology</i> , 2012, 21, 2116-2129.	2.0	18
22	PCR multiplexing of nuclear microsatellite loci in <i>Quercus</i> species. <i>Plant Molecular Biology Reporter</i> , 2005, 23, 121-128.	1.0	14
23	Gene Flow, Spatial Structure, Local Adaptation, and Assisted Migration in Trees. , 2012, , 71-116.		14
24	The evolutionary heritage and ecological uniqueness of Scots pine in the Caucasus ecoregion is at risk of climate changes. <i>Scientific Reports</i> , 2021, 11, 22845.	1.6	14
25	Population at the edge: increased divergence but not inbreeding towards northern range limit in <i>Acer campestre</i> . <i>Tree Genetics and Genomes</i> , 2014, 10, 1739-1753.	0.6	13
26	Climatic oscillations in Quaternary have shaped the co-evolutionary patterns between the Norway spruce and its host-associated herbivore. <i>Scientific Reports</i> , 2020, 10, 16524.	1.6	13
27	Genetic evidence of reproductive isolation in a remote enclave of <i>Quercus pubescens</i> in the presence of cross-fertile species. <i>Plant Systematics and Evolution</i> , 2012, 298, 1045-1056.	0.3	12
28	Relative strength of fine-scale spatial genetic structure in paternally vs biparentally inherited DNA in a dioecious plant depends on both sex proportions and pollen-to-seed dispersal ratio. <i>Heredity</i> , 2016, 117, 449-459.	1.2	11
29	Spatial Genetic Structure Within Two Contrasting Stands of Scots Pine (<i>Pinus sylvestris</i> L.). <i>Silvae Genetica</i> , 2008, 57, 193-202.	0.4	11
30	Assessment of genetic diversity in two-species oak seed stands and their progeny populations. <i>Scandinavian Journal of Forest Research</i> , 2012, 27, 2-9.	0.5	10
31	Phenological match drives pollen-mediated gene flow in a temporally dimorphic tree. <i>Plant Biology</i> , 2018, 20, 93-100.	1.8	10
32	Gene flow and reproductive success in ash (<i>Fraxinus excelsior</i> L.) in the face of ash dieback: restoration and conservation. <i>Annals of Forest Science</i> , 2021, 78, 1.	0.8	10
33	Note on the Applicability of the F-model in Analysis of Pollen Pool Heterogeneity. <i>Journal of Heredity</i> , 2013, 104, 578-585.	1.0	8
34	Bayesian approach reveals confounding effects of population size and seasonality on outcrossing rates in a fragmented subalpine conifer. <i>Tree Genetics and Genomes</i> , 2014, 10, 1723-1737.	0.6	7
35	Bayesian quantification of ecological determinants of outcrossing in natural plant populations: Computer simulations and the case study of biparental inbreeding in English yew. <i>Molecular Ecology</i> , 2019, 28, 4077-4096.	2.0	6
36	CAUTIONS ON DIRECT GENE FLOW ESTIMATION IN PLANT POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 956.	1.1	3

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37	Identification of determinants of pollen donor fecundity using the hierarchical neighborhood model. <i>Molecular Ecology Resources</i> , 2021, 21, 781-800.	2.2	3
38	Genetic diversity of <i>Dactylorhiza incarnata</i> (Orchidaceae) in northern Poland. <i>Acta Societatis Botanicorum Poloniae</i> , 2016, 85, .	0.8	3
39	Trunk perimeter correlates with genetic bottleneck intensity and the level of genetic diversity in populations of <i>Taxus baccata</i> L. <i>Annals of Forest Science</i> , 2021, 78, 1.	0.8	0
40	High genetic diversity promotes a common-garden trial of <i>Quercus robur</i> as a potential seed source. <i>Dendrobiology</i> , 0, 79, 1-9.	0.6	0