

# Bernd Degen

## List of Publications by Year in descending order

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57  
papers

1,587  
citations

430874

18  
h-index

315739

38  
g-index

59  
all docs

59  
docs citations

59  
times ranked

1894  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fine-scale genetic structure and gene dispersal inferences in 10 Neotropical tree species. <i>Molecular Ecology</i> , 2005, 15, 559-571.	3.9	277
2	Modelling exploration of the future of European beech ( <i>Fagus sylvatica</i> L.) under climate change – Range, abundance, genetic diversity and adaptive response. <i>Forest Ecology and Management</i> , 2010, 259, 2213-2222.	3.2	206
3	Forensic timber identification: It's time to integrate disciplines to combat illegal logging. <i>Biological Conservation</i> , 2015, 191, 790-798.	4.1	176
4	Modelling the long-term impacts of selective logging on genetic diversity and demographic structure of four tropical tree species in the Amazon forest. <i>Forest Ecology and Management</i> , 2008, 254, 335-349.	3.2	96
5	Efficient Long-Distance Gene Flow into an Isolated Relict Oak Stand. <i>Journal of Heredity</i> , 2011, 102, 464-472.	2.4	82
6	Opportunities for Improved Transparency in the Timber Trade through Scientific Verification. <i>BioScience</i> , 2016, 66, 990-998.	4.9	60
7	Fine-scale spatial genetic structure of eight tropical tree species as analysed by RAPDs. <i>Heredity</i> , 2001, 87, 497-507.	2.6	58
8	Comparative study of genetic variation and differentiation of two pedunculate oak ( <i>Quercus robur</i> ) stands using microsatellite and allozyme loci. <i>Heredity</i> , 1999, 83, 597-603.	2.6	48
9	Complete Chloroplast Genome Sequences of Four Meliaceae Species and Comparative Analyses. <i>International Journal of Molecular Sciences</i> , 2018, 19, 701.	4.1	37
10	Revealing hidden species diversity in closely related species using nuclear SNPs, SSRs and DNA sequences – a case study in the tree genus <i>Milicia</i> . <i>BMC Evolutionary Biology</i> , 2016, 16, 259.	3.2	36
11	Development of Molecular Markers for Determining Continental Origin of Wood from White Oaks ( <i>Quercus</i> L. sect. <i>Quercus</i> ). <i>PLoS ONE</i> , 2016, 11, e0158221.	2.5	34
12	Effects of Animal Pollination on Pollen Dispersal, Selfing, and Effective Population Size of Tropical Trees: A Simulation Study. <i>Biotropica</i> , 2004, 36, 165-179.	1.6	32
13	Low Interannual Variation of Mating System and Gene Flow of <i>Symphonia globulifera</i> in the Brazilian Amazon. <i>Biotropica</i> , 2007, 39, 628-636.	1.6	29
14	High levels of pollen dispersal detected through paternity analysis from a continuous <i>Symphonia globulifera</i> population in the Brazilian Amazon. <i>Forest Ecology and Management</i> , 2009, 258, 1260-1266.	3.2	27
15	Geographic Influence on Genetic Structure in the Widespread Neotropical Tree <i>Simarouba amara</i> (Simaroubaceae). <i>Tropical Plant Biology</i> , 2010, 3, 28-39.	1.9	22
16	Low Inbreeding and High Pollen Dispersal Distances in Populations of Two Amazonian Forest Tree Species. <i>Biotropica</i> , 2007, 39, 406-415.	1.6	20
17	A set of SNP markers for timber tracking of <i>Larix</i> spp. in Europe and Russia. <i>Forestry</i> , 2018, 91, 614-628.	2.3	20
18	Spatial genetic structure in wild cherry ( <i>Prunus avium</i> L.): I. variation among natural populations of different density. <i>Tree Genetics and Genomes</i> , 2011, 7, 271-283.	1.6	18

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19	Spatial genetic structure in populations of the green oak leaf roller, <i>Tortrix viridana</i> L. (Lepidoptera), <i>Tj ETQq1 1 0.784314 rgBT /Overl</i>	2.5	16
20	A nearest neighbour approach by genetic distance to the assignment of individual trees to geographic origin. <i>Forensic Science International: Genetics</i> , 2017, 27, 132-141.	3.1	16
21	<i>Genetics and Tropical Forests.</i> , 2014, , 1-30.		16
22	Genetic structure of the green oak leaf roller ( <i>Tortrix viridana</i> L.) and one of its hosts, <i>Quercus robur</i> L. <i>Forest Ecology and Management</i> , 2008, 256, 1270-1279.	3.2	15
23	Genetic variation for growth, morphological, and physiological traits in a wild population of the Neotropical shade-tolerant rainforest tree <i>Sextonia rubra</i> (Mez) van der Werff (Lauraceae). <i>Tree Genetics and Genomes</i> , 2010, 6, 319-329.	1.6	14
24	Development of DNA-based methods to identify CITES-protected timber species: a case study in the Meliaceae family. <i>Holzforschung</i> , 2012, 66, .	1.9	14
25	Mating patterns and pollen dispersal in four contrasting wild cherry populations ( <i>Prunus avium</i> L.). <i>European Journal of Forest Research</i> , 2012, 131, 1055-1069.	2.5	13
26	Development of nuclear, chloroplast and mitochondrial SNP markers for <i>Khaya</i> sp.. <i>Conservation Genetics Resources</i> , 2016, 8, 283-297.	0.8	13
27	Development of a set of SNP markers for population genetics studies of Ipe ( <i>Handroanthus</i> sp.), a valuable tree genus from Latin America. <i>Conservation Genetics Resources</i> , 2018, 10, 779-781.	0.8	13
28	Impact of Gene Flow and Introgression on the Range Wide Genetic Structure of <i>Quercus robur</i> (L.) in Europe. <i>Forests</i> , 2021, 12, 1425.	2.1	13
29	Spatial genetic structure in wild cherry ( <i>Prunus avium</i> L.): II. Effect of density and clonal propagation on spatial genetic structure based on simulation studies. <i>Tree Genetics and Genomes</i> , 2011, 7, 541-552.	1.6	11
30	Assessing the Ability of Chloroplast and Nuclear DNA Gene Markers to Verify the Geographic Origin of Jatoba ( <i>Hymenaea courbaril</i> L.) Timber. <i>Journal of Heredity</i> , 2018, 109, 543-552.	2.4	11
31	Development of nuclear and plastid SNP markers for genetic studies of <i>Dipteryx</i> tree species in Amazonia. <i>Conservation Genetics Resources</i> , 2019, 11, 333-336.	0.8	11
32	Applying targeted genotyping by sequencing with a new set of nuclear and plastid SNP and indel loci for <i>Quercus robur</i> and <i>Quercus petraea</i> . <i>Conservation Genetics Resources</i> , 2021, 13, 345-347.	0.8	11
33	Development of nuclear SNP markers for the timber tracking of the African tree species <i>Sapelli</i> , <i>Entandrophragma cylindricum</i> . <i>Conservation Genetics Resources</i> , 2018, 10, 539-541.	0.8	10
34	Genetic differentiation of <i>Quercus robur</i> in the South-Ural. <i>Silvae Genetica</i> , 2019, 68, 111-115.	0.8	10
35	Use of DNA-Fingerprints to Control the Origin of Forest Reproductive Material. <i>Silvae Genetica</i> , 2010, 59, 268-273.	0.8	9
36	DNA taxonomy in the timber genus <i>Milicia</i> : evidence of unidirectional introgression in the West African contact zone. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	8

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37	Nuclear and chloroplastic SNP markers for genetic studies of timber origin for <i>Hymenaea</i> trees. <i>Conservation Genetics Resources</i> , 2019, 11, 329-331.	0.8	8
38	Development of new SNPs loci on <i>Quercus robur</i> and <i>Quercus petraea</i> for genetic studies covering the whole species'™ distribution range. <i>Conservation Genetics Resources</i> , 2020, 12, 597-600.	0.8	8
39	Forest ecosystem genomics and adaptation: EVOLTREE conference report. <i>Tree Genetics and Genomes</i> , 2011, 7, 869-875.	1.6	7
40	Nuclear and plastidial SNP and INDEL markers for genetic tracking studies of <i>Jacaranda copaia</i> . <i>Conservation Genetics Resources</i> , 2019, 11, 341-343.	0.8	7
41	Genetic diversity and differentiation among the species of African mahogany ( <i>Khaya</i> spp.) based on a large SNP array. <i>Conservation Genetics</i> , 2019, 20, 1035-1044.	1.5	7
42	An assessment of heterozygosity and fitness in Chir pine ( <i>Pinus roxburghii</i> Sarg.) using isozymes. <i>New Forests</i> , 2007, 34, 153-162.	1.7	6
43	SNP Markers as a Successful Molecular Tool for Assessing Species Identity and Geographic Origin of Trees in the Economically Important South American Legume Genus <i>Dipteryx</i> . <i>Journal of Heredity</i> , 2020, 111, 346-356.	2.4	6
44	A Very Small and Isolated Population of the Green Oak Leaf Roller, <i>Tortrix viridana</i> L., with High Genetic Diversity'™How Does This Work?. <i>Journal of Heredity</i> , 2010, 101, 780-783.	2.4	5
45	Development of nuclear and plastid SNP and INDEL markers for population genetic studies and timber traceability of <i>Carapa</i> species. <i>Conservation Genetics Resources</i> , 2019, 11, 337-339.	0.8	4
46	Nuclear and plastid SNP markers for tracing <i>Cedrela</i> timber in the tropics. <i>Conservation Genetics Resources</i> , 2020, 12, 239-244.	0.8	4
47	Genetic diversity and differentiation among populations of the pedunculate oak ( <i>Quercus robur</i> ) at the eastern margin of its range based on a new set of 95 SNP loci. <i>Journal of Forestry Research</i> , 2021, 32, 2237-2243.	3.6	4
48	When does habitat fragmentation lead to changes in populations gene pool of pedunculate oak ( <i>Quercus robur</i> L.)?. <i>Forest Ecology and Management</i> , 2021, 499, 119617.	3.2	4
49	Genetic comparison of planted and natural <i>Quercus robur</i> stands in Russia. <i>Silvae Genetica</i> , 2021, 70, 1-8.	0.8	3
50	Development of D-Loop mitochondrial markers for amplification of prey DNA from wolf scat. <i>Conservation Genetics Resources</i> , 2021, 13, 1-4.	0.8	2
51	Development of new SNP and INDEL loci for the valuable African timber species <i>Lophira alata</i> . <i>Conservation Genetics Resources</i> , 2021, 13, 85-87.	0.8	2
52	Short note: Development of a new set of SNP markers to measure genetic diversity and genetic differentiation of Mongolian oak ( <i>Quercus mongolica</i> Fisch. ex Ledeb.) in the Far East of Russia. <i>Silvae Genetica</i> , 2019, 68, 85-91.	0.8	2
53	<i>Khaya</i> revisited: Genetic markers and morphological analysis reveal six species in the widespread taxon <i>K. Anthotheca</i> . <i>Taxon</i> , 0, , .	0.7	2
54	Development of nuclear SNP markers for Mahogany ( <i>Swietenia</i> spp.). <i>Conservation Genetics Resources</i> , 2020, 12, 585-587.	0.8	1

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55	Genetics and Tropical Forests. , 2016, , 885-920.		1
56	Development of SNP markers for the African timber species <i>Nauclea diderrichii</i> . Conservation Genetics Resources, 2020, 12, 357-359.	0.8	0
57	Large-scale genetic structure of <i>Quercus robur</i> in its eastern distribution range enables assignment of unknown seed sources. Forestry, 0, , .	2.3	0