

Richard Buggs

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

5,273
citations

186265
28
h-index

114465
63
g-index

77
all docs

77
docs citations

77
times ranked

6231
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic structure and diversity of oak populations in British parklands. <i>Plants People Planet</i> , 2022, 4, 167-181.	3.3	7
2	Uses and benefits of digital sequence information from plant genetic resources: Lessons learnt from botanical collections. <i>Plants People Planet</i> , 2022, 4, 33-43.	3.3	10
3	A high-quality reference genome for <i>Fraxinus pennsylvanica</i> for ash species restoration and research. <i>Molecular Ecology Resources</i> , 2022, 22, 1284-1302.	4.8	12
4	Reconfiguring Darwin's abominable mystery. <i>Nature Plants</i> , 2022, 8, 194-195.	9.3	1
5	A chromosome-scale genome assembly of European hazel (<i>Corylus avellana</i> L.) reveals targets for crop improvement. <i>Plant Journal</i> , 2021, 105, 1413-1430.	5.7	32
6	Introgression between <i>Betula tianshanica</i> and <i>Betula microphylla</i> and its implications for conservation. <i>Plants People Planet</i> , 2021, 3, 363-374.	3.3	5
7	Resolving phylogeny and polyploid parentage using genus-wide genome-wide sequence data from birch trees. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 107126.	2.7	26
8	Unraveling Genetic Diversity Amongst European Hazelnut (<i>Corylus avellana</i> L.) Varieties in Turkey. <i>Frontiers in Plant Science</i> , 2021, 12, 661274.	3.6	8
9	The origin of Darwin's 'abominable mystery'. <i>American Journal of Botany</i> , 2021, 108, 22-36.	1.7	10
10	Extraction and high-throughput sequencing of oak heartwood DNA: Assessing the feasibility of genome-wide DNA methylation profiling. <i>PLoS ONE</i> , 2021, 16, e0254971.	2.5	1
11	Evidence for the Widespread Occurrence of Bacteria Implicated in Acute Oak Decline from Incidental Genetic Sampling. <i>Forests</i> , 2021, 12, 1683.	2.1	7
12	The viability of a breeding programme for ash in the British Isles in the face of ash dieback. <i>Plants People Planet</i> , 2020, 2, 29-40.	3.3	15
13	Genomic assessment of local adaptation in dwarf birch to inform assisted gene flow. <i>Evolutionary Applications</i> , 2020, 13, 161-175.	3.1	37
14	Resistance of European ash (<i>Fraxinus excelsior</i>) saplings to larval feeding by the emerald ash borer (<i>Agrilus planipennis</i>). <i>Plants People Planet</i> , 2020, 2, 41-46.	3.3	9
15	Genetic diversity and domestication of hazelnut (<i>Corylus avellana</i> L.) in Turkey. <i>Plants People Planet</i> , 2020, 2, 326-339.	3.3	16
16	Changing perceptions of tree resistance research. <i>Plants People Planet</i> , 2020, 2, 2-4.	3.3	9
17	FluentDNA: Nucleotide Visualization of Whole Genomes, Annotations, and Alignments. <i>Frontiers in Genetics</i> , 2020, 11, 292.	2.3	3
18	Convergent molecular evolution among ash species resistant to the emerald ash borer. <i>Nature Ecology and Evolution</i> , 2020, 4, 1116-1128.	7.8	26

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19	The Origin of Novel Genes. <i>Inference</i> , 2020, 5, .	0.0	0
20	Estimating mortality rates of European ash (<i>Fraxinus excelsior</i>) under the ash dieback (<i>Hymenoscyphus fraxineus</i>) epidemic. <i>Plants People Planet</i> , 2019, 1, 48-58.	3.3	87
21	Population structure of <i>Betula albosinensis</i> and <i>Betula platyphylla</i> : evidence for hybridization and a cryptic lineage. <i>Annals of Botany</i> , 2019, 123, 1179-1189.	2.9	28
22	Genomic basis of European ash tree resistance to ash dieback fungus. <i>Nature Ecology and Evolution</i> , 2019, 3, 1686-1696.	7.8	50
23	Repeated long-distance dispersal and convergent evolution in hazel. <i>Scientific Reports</i> , 2019, 9, 16016.	3.3	8
24	Mitigating pest and pathogen impacts using resistant trees: a framework and overview to inform development and deployment in Europe and North America. <i>Forestry</i> , 2018, 91, 1-16.	2.3	25
25	Genetic diversity maintained among fragmented populations of a tree undergoing range contraction. <i>Heredity</i> , 2018, 121, 304-318.	2.6	22
26	Genome-wide epigenetic variation among ash trees differing in susceptibility to a fungal disease. <i>BMC Genomics</i> , 2018, 19, 502.	2.8	14
27	The deepening of Darwin's abominable mystery. <i>Nature Ecology and Evolution</i> , 2017, 1, 169.	7.8	15
28	Genome sequence and genetic diversity of European ash trees. <i>Nature</i> , 2017, 541, 212-216.	27.8	166
29	A first assessment of <i>Fraxinus excelsior</i> (common ash) susceptibility to <i>Hymenoscyphus fraxineus</i> (ash) Tj ETQq1 1 0,784314 rgBT /Over	3.3	18
30	Ash leaf metabolomes reveal differences between trees tolerant and susceptible to ash dieback disease. <i>Scientific Data</i> , 2017, 4, 170190.	5.3	13
31	Unidirectional diploid-tetraploid introgression among British birch trees with shifting ranges shown by restriction site-associated markers. <i>Molecular Ecology</i> , 2016, 25, 2413-2426.	3.9	78
32	Emerging Genomics of Angiosperm Trees. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 85-99.	0.3	0
33	Molecular markers for tolerance of European ash (<i>Fraxinus excelsior</i>) to dieback disease identified using Associative Transcriptomics. <i>Scientific Reports</i> , 2016, 6, 19335.	3.3	85
34	Molecular phylogeny and genome size evolution of the genus <i>Betula</i> (Betulaceae). <i>Annals of Botany</i> , 2016, 117, 1023-1035.	2.9	69
35	250 years of hybridization between two biennial herb species without speciation. <i>AoB PLANTS</i> , 2015, 7, plv081.	2.3	6
36	The potential for field studies and genomic technologies to enhance resistance and resilience of British tree populations to pests and pathogens. <i>Forestry</i> , 2015, 88, 27-40.	2.3	17

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37	Speciation by genome duplication: Repeated origins and genomic composition of the recently formed allopolyploid species <i>Mimulus peregrinus</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1487-1500.	2.3	72
38	Is the Atkinson discriminant function a reliable method for distinguishing between <i>Betula pendula</i> and <i>B. pubescens</i> (Betulaceae)? <i>New Journal of Botany</i> , 2014, 4, 90-94.	0.1	11
39	Molecular footprints of the Holocene retreat of dwarf birch in Britain. <i>Molecular Ecology</i> , 2014, 23, 2771-2782.	3.9	45
40	The legacy of diploid progenitors in allopolyploid gene expression patterns. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130354.	4.0	111
41	Hybridization and speciation. <i>Journal of Evolutionary Biology</i> , 2013, 26, 229-246.	1.7	1,735
42	Genome sequence of dwarf birch (<i>Betula nana</i>) and cross-species RAD markers. <i>Molecular Ecology</i> , 2013, 22, 3098-3111.	3.9	132
43	Unravelling gene expression of complex crop genomes. <i>Heredity</i> , 2013, 110, 97-98.	2.6	17
44	Next-generation sequencing and genome evolution in allopolyploids. <i>American Journal of Botany</i> , 2012, 99, 372-382.	1.7	77
45	Monkeying around with ploidy. <i>Molecular Ecology</i> , 2012, 21, 5159-5161.	3.9	7
46	The Early Stages of Polyploidy: Rapid and Repeated Evolution in <i>Tragopogon</i> . , 2012, , 271-292.		36
47	Rapid, Repeated, and Clustered Loss of Duplicate Genes in Allopolyploid Plant Populations of Independent Origin. <i>Current Biology</i> , 2012, 22, 248-252.	3.9	159
48	Biosystematic relationships and the formation of polyploids. <i>Taxon</i> , 2011, 60, 324-332.	0.7	28
49	Transcriptomic Shock Generates Evolutionary Novelty in a Newly Formed, Natural Allopolyploid Plant. <i>Current Biology</i> , 2011, 21, 551-556.	3.9	192
50	Tissue-specific silencing of homoeologs in natural populations of the recent allopolyploid <i>Tragopogon mirus</i> . <i>New Phytologist</i> , 2010, 186, 175-183.	7.3	108
51	Characterization of duplicate gene evolution in the recent natural allopolyploid <i>Tragopogon miscellus</i> by next-generation sequencing and Sequenom iPLEX MassARRAY genotyping. <i>Molecular Ecology</i> , 2010, 19, 132-146.	3.9	167
52	What we still don't know about polyploidy. <i>Taxon</i> , 2010, 59, 1387-1403.	0.7	300
53	Synthetic polyploids of <i>Tragopogon miscellus</i> and <i>T. mirus</i> (Asteraceae): 60 Years after Ownbey's discovery. <i>American Journal of Botany</i> , 2009, 96, 979-988.	1.7	70
54	Does hybridization between divergent progenitors drive whole-genome duplication?. <i>Molecular Ecology</i> , 2009, 18, 3334-3339.	3.9	49

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55	Gene loss and silencing in <i>Tragopogon miscellus</i> (Asteraceae): comparison of natural and synthetic allotetraploids. <i>Heredity</i> , 2009, 103, 73-81.	2.6	138
56	On the Origins of Species: Does Evolution Repeat Itself in Polyploid Populations of Independent Origin?. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2009, 74, 215-23.	1.1	20
57	Towards natural polyploid model organisms. <i>Molecular Ecology</i> , 2008, 17, 1875-1876.	3.9	7
58	Does Phylogenetic Distance Between Parental Genomes Govern the Success of Polyploids. <i>Castanea</i> , 2008, 73, 74-93.	0.1	43
59	Empirical study of hybrid zone movement. <i>Heredity</i> , 2007, 99, 301-312.	2.6	297
60	ECOLOGICAL DIFFERENTIATION AND DIPLOID SUPERIORITY ACROSS A MOVING PLOIDY CONTACT ZONE. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 125-140.	2.3	107
61	HYBRIDIZATION, POLYPLOIDY, AND THE EVOLUTION OF SEXUAL SYSTEMS IN <i>MERCURIALIS</i> (EUPHORBIACEAE). <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 1801-1815.	2.3	83
62	Rapid Displacement of a Monoecious Plant Lineage Is Due to Pollen Swamping by a Dioecious Relative. <i>Current Biology</i> , 2006, 16, 996-1000.	3.9	69
63	HYBRIDIZATION, POLYPLOIDY, AND THE EVOLUTION OF SEXUAL SYSTEMS IN <i>MERCURIALIS</i> (EUPHORBIACEAE). <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 1801.	2.3	5
64	Hybridization, polyploidy, and the evolution of sexual systems in <i>Mercurialis</i> (Euphorbiaceae). <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 1801-15.	2.3	21
65	Development of anonymous cDNA microarrays to study changes to the <i>Senecio</i> floral transcriptome during hybrid speciation. <i>Molecular Ecology</i> , 2005, 14, 2493-2510.	3.9	106
66	Polyploidy and the sexual system: what can we learn from <i>Mercurialis annua</i> ?. <i>Biological Journal of the Linnean Society</i> , 2004, 82, 547-560.	1.6	121
67	Next generation apomorphy: the ubiquity of taxonomically restricted genes. , 0, , 237-263.		0