Richard Buggs

List of Publications by Year
in descending order

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	Hybridization and speciation. Journal of Evolutionary Biology, 2013, 26, 229-246.	1.7	1,735
2	What we still don't know about polyploidy. Taxon, 2010, 59, 1387-1403.	0.7	300
3	Empirical study of hybrid zone movement. Heredity, 2007, 99, 301-312.	2.6	297
4	Transcriptomic Shock Generates Evolutionary Novelty in a Newly Formed, Natural Allopolyploid Plant. Current Biology, 2011, 21, 551-556.	3.9	192
5	Characterization of duplicate gene evolution in the recent natural allopolyploid <i>Tragopogon miscellus</i> by nextâ€generation sequencing and Sequenom iPLEX MassARRAY genotyping. Molecular Ecology, 2010, 19, 132-146.	3.9	167
6	Genome sequence and genetic diversity of European ash trees. Nature, 2017, 541, 212-216.	27.8	166
7	Rapid, Repeated, and Clustered Loss of Duplicate Genes in Allopolyploid Plant Populations of Independent Origin. Current Biology, 2012, 22, 248-252.	3.9	159
8	Gene loss and silencing in Tragopogon miscellus (Asteraceae): comparison of natural and synthetic allotetraploids. Heredity, 2009, 103, 73-81.	2.6	138
9	Genome sequence of dwarf birch (<i>Betula nana</i>) and crossâ€species <scp>RAD</scp> markers. Molecular Ecology, 2013, 22, 3098-3111.	3.9	132
10	Polyploidy and the sexual system: what can we learn from Mercurialis annua?. Biological Journal of the Linnean Society, 2004, 82, 547-560.	1.6	121
11	The legacy of diploid progenitors in allopolyploid gene expression patterns. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130354.	4.0	111
12	Tissueâ€specific silencing of homoeologs in natural populations of the recent allopolyploid <i>Tragopogon mirus</i>. New Phytologist, 2010, 186, 175-183.	7.3	108
13	ECOLOGICAL DIFFERENTIATION AND DIPLOID SUPERIORITY ACROSS A MOVING PLOIDY CONTACT ZONE. Evolution; International Journal of Organic Evolution, 2007, 61, 125-140.	2.3	107
14	Development of anonymous cDNA microarrays to study changes to the Senecio floral transcriptome during hybrid speciation. Molecular Ecology, 2005, 14, 2493-2510.	3.9	106
15	Estimating mortality rates of European ash (<i>Fraxinus excelsior</i>) under the ash dieback (<i>Hymenoscyphus fraxineus</i>) epidemic. Plants People Planet, 2019, 1, 48-58.	3.3	87
16	Molecular markers for tolerance of European ash (Fraxinus excelsior) to dieback disease identified using Associative Transcriptomics. Scientific Reports, 2016, 6, 19335.	3.3	85
17	HYBRIDIZATION, POLYPLOIDY, AND THE EVOLUTION OF SEXUAL SYSTEMS IN MERCURIALIS (EUPHORBIACEAE). Evolution; International Journal of Organic Evolution, 2006, 60, 1801-1815.	2.3	83
18	Unidirectional diploidâ€“tetraploid introgression among British birch trees with shifting ranges shown by restriction siteâ€associated markers. Molecular Ecology, 2016, 25, 2413-2426.	3.9	78

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19	Nextâ€generation sequencing and genome evolution in allopolyploids. American Journal of Botany, 2012, 99, 372-382.	1.7	77
20	Speciation by genome duplication: Repeated origins and genomic composition of the recently formed allopolyploid species<i>Mimulus peregrinus</i>. Evolution; International Journal of Organic Evolution, 2015, 69, 1487-1500.	2.3	72
21	Synthetic polyploids of <i>Tragopogon miscellus</i> and <i>T. mirus</i> (Asteraceae): 60 Years after Ownbey's discovery. American Journal of Botany, 2009, 96, 979-988.	1.7	70
22	Rapid Displacement of a Monoecious Plant Lineage Is Due to Pollen Swamping by a Dioecious Relative. Current Biology, 2006, 16, 996-1000.	3.9	69
23	Molecular phylogeny and genome size evolution of the genus<i>Betula</i>(Betulaceae). Annals of Botany, 2016, 117, 1023-1035.	2.9	69
24	Genomic basis of European ash tree resistance to ash dieback fungus. Nature Ecology and Evolution, 2019, 3, 1686-1696.	7.8	50
25	Does hybridization between divergent progenitors drive wholeâ€genome duplication?. Molecular Ecology, 2009, 18, 3334-3339.	3.9	49
26	Molecular footprints of the <scp>H</scp>olocene retreat of dwarf birch in <scp>B</scp>ritain. Molecular Ecology, 2014, 23, 2771-2782.	3.9	45
27	Does Phylogenetic Distance Between Parental Genomes Govern the Success of Polyploids. Castanea, 2008, 73, 74-93.	0.1	43
28	Genomic assessment of local adaptation in dwarf birch to inform assisted gene flow. Evolutionary Applications, 2020, 13, 161-175.	3.1	37
29	The Early Stages of Polyploidy: Rapid and Repeated Evolution in Tragopogon. , 2012, , 271-292.		36
30	A chromosomeâ€scale genome assembly of European hazel (<i>Corylus avellana</i>Â L.) reveals targets for crop improvement. Plant Journal, 2021, 105, 1413-1430.	5.7	32
31	Biosystematic relationships and the formation of polyploids. Taxon, 2011, 60, 324-332.	0.7	28
32	Population structure of Betula albosinensis and Betula platyphylla: evidence for hybridization and a cryptic lineage. Annals of Botany, 2019, 123, 1179-1189.	2.9	28
33	Resolving phylogeny and polyploid parentage using genus-wide genome-wide sequence data from birch trees. Molecular Phylogenetics and Evolution, 2021, 160, 107126.	2.7	26
34	Convergent molecular evolution among ash species resistant to the emerald ash borer. Nature Ecology and Evolution, 2020, 4, 1116-1128.	7.8	26
35	Mitigating pest and pathogen impacts using resistant trees: a framework and overview to inform development and deployment in Europe and North America. Forestry, 2018, 91, 1-16.	2.3	25
36	Genetic diversity maintained among fragmented populations of a tree undergoing range contraction. Heredity, 2018, 121, 304-318.	2.6	22

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37	Hybridization, polyploidy, and the evolution of sexual systems in Mercurialis (Euphorbiaceae). Evolution; International Journal of Organic Evolution, 2006, 60, 1801-15.	2.3	21
38	On the Origins of Species: Does Evolution Repeat Itself in Polyploid Populations of Independent Origin?. Cold Spring Harbor Symposia on Quantitative Biology, 2009, 74, 215-23.	1.1	20
39	A first assessment of Fraxinus excelsior (common ash) susceptibility to Hymenoscyphus fraxineus (ash) Tj ETQq1 1 0.784314 rgBT /Ove	3.3	18
40	Unravelling gene expression of complex crop genomes. Heredity, 2013, 110, 97-98.	2.6	17
41	The potential for field studies and genomic technologies to enhance resistance and resilience of British tree populations to pests and pathogens. Forestry, 2015, 88, 27-40.	2.3	17
42	Genetic diversity and domestication of hazelnut (<i>Corylus avellana</i> L.) in Turkey. Plants People Planet, 2020, 2, 326-339.	3.3	16
43	The deepening of Darwin's abominable mystery. Nature Ecology and Evolution, 2017, 1, 169.	7.8	15
44	The viability of a breeding programme for ash in the British Isles in the face of ash dieback. Plants People Planet, 2020, 2, 29-40.	3.3	15
45	Genome-wide epigenetic variation among ash trees differing in susceptibility to a fungal disease. BMC Genomics, 2018, 19, 502.	2.8	14
46	Ash leaf metabolomes reveal differences between trees tolerant and susceptible to ash dieback disease. Scientific Data, 2017, 4, 170190.	5.3	13
47	A highâ€quality reference genome for <i>Fraxinus pennsylvanica</i> for ash species restoration and research. Molecular Ecology Resources, 2022, 22, 1284-1302.	4.8	12
48	Is the Atkinson discriminant function a reliable method for distinguishing between<i>Betula pendula</i>and<i>B. pubescens</i>(Betulaceae)?. New Journal of Botany, 2014, 4, 90-94.	0.1	11
49	Uses and benefits of digital sequence information from plant genetic resources: Lessons learnt from botanical collections. Plants People Planet, 2022, 4, 33-43.	3.3	10
50	The origin of Darwinâ€™s â€œabominable mysteryâ€. American Journal of Botany, 2021, 108, 22-36.	1.7	10
51	Resistance of European ash (<i>Fraxinus excelsior</i>) saplings to larval feeding by the emerald ash borer (<i>Agrilus planipennis</i>). Plants People Planet, 2020, 2, 41-46.	3.3	9
52	Changing perceptions of tree resistance research. Plants People Planet, 2020, 2, 2-4.	3.3	9
53	Repeated long-distance dispersal and convergent evolution in hazel. Scientific Reports, 2019, 9, 16016.	3.3	8
54	Unraveling Genetic Diversity Amongst European Hazelnut (Corylus avellana L.) Varieties in Turkey. Frontiers in Plant Science, 2021, 12, 661274.	3.6	8

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55	Towards natural polyploid model organisms. Molecular Ecology, 2008, 17, 1875-1876.	3.9	7
56	Monkeying around with ploidy. Molecular Ecology, 2012, 21, 5159-5161.	3.9	7
57	Genomic structure and diversity of oak populations in British parklands. Plants People Planet, 2022, 4, 167-181.	3.3	7
58	Evidence for the Widespread Occurrence of Bacteria Implicated in Acute Oak Decline from Incidental Genetic Sampling. Forests, 2021, 12, 1683.	2.1	7
59	250 years of hybridization between two biennial herb species without speciation. AoB PLANTS, 2015, 7, plv081.	2.3	6
60	HYBRIDIZATION, POLYPLOIDY, AND THE EVOLUTION OF SEXUAL SYSTEMS IN MERCURIALIS (EUPHORBIACEAE). Evolution; International Journal of Organic Evolution, 2006, 60, 1801.	2.3	5
61	Introgression between <i>Betula tianshanica</i> and <i>Betula microphylla</i> and its implications for conservation. Plants People Planet, 2021, 3, 363-374.	3.3	5
62	FluentDNA: Nucleotide Visualization of Whole Genomes, Annotations, and Alignments. Frontiers in Genetics, 2020, 11, 292.	2.3	3
63	Extraction and high-throughput sequencing of oak heartwood DNA: Assessing the feasibility of genome-wide DNA methylation profiling. PLoS ONE, 2021, 16, e0254971.	2.5	1
64	Reconfiguring Darwinâ€™s abominable mystery. Nature Plants, 2022, 8, 194-195.	9.3	1
65	Emerging Genomics of Angiosperm Trees. Plant Genetics and Genomics: Crops and Models, 2016, , 85-99.	0.3	0
66	Next generation apomorphy: the ubiquity of taxonomically restricted genes. , 0, , 237-263.		0
67	The Origin of Novel Genes. Inference, 2020, 5, .	0.0	0