LorenÂ H Rieseberg

List of Publications by Year
in descending order

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441

papers

45,524

citations

1877

105

h-index

3343

190

g-index

511

all docs

511

docs citations

511

times ranked

32064

citing authors

#	Article	IF	Citations
1	Rapid evolution of post-zygotic reproductive isolation is widespread in Arctic plant lineages. Annals of Botany, 2022, 129, 171-184.	1.4	9
2	Genetic basis and dual adaptive role of floral pigmentation in sunflowers. ELife, 2022, 11, .	2.8	24
3	Parental Population Range Expansion before Secondary Contact Promotes Heterosis. American Naturalist, 2022, 200, E1-E15.	1.0	12
4	Editorial 2022. Molecular Ecology, 2022, 31, 1-30.	2.0	5
5	Expression complementation of gene presence/absence polymorphisms in hybrids contributes importantly to heterosis in sunflower. Journal of Advanced Research, 2022, 42, 83-98.	4.4	12
6	Mutation Load in Sunflower Inversions Is Negatively Correlated with Inversion Heterozygosity. Molecular Biology and Evolution, 2022, 39, .	3.5	18
7	Using landscape genomics to delineate seed and breeding zones for lodgepole pine. New Phytologist, 2022, 235, 1653-1664.	3.5	8
8	Hybrid evolution repeats itself across environmental contexts in Texas sunflowers () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 Td (<i>He	1.1	5
9	The genomic basis of the plant island syndrome in Darwinâ€™s giant daisies. Nature Communications, 2022, 13, .	5.8	6
10	Three problems in the genetics of speciation by selection. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	31
11	Research priorities for global food security under extreme events. One Earth, 2022, 5, 756-766.	3.6	27
12	The genome of <i>Draba nivalis</i> shows signatures of adaptation to the extreme environmental stresses of the Arctic. Molecular Ecology Resources, 2021, 21, 661-676.	2.2	14
13	Sharing and reporting benefits from biodiversity research. Molecular Ecology, 2021, 30, 1103-1107.	2.0	19
14	Patterns, Predictors, and Consequences of Dominance in Hybrids. American Naturalist, 2021, 197, E72-E88.	1.0	45
15	The tip of the iceberg: Genome wide marker analysis reveals hidden hybridization during invasion. Molecular Ecology, 2021, 30, 810-825.	2.0	3
16	From bits to bites: Advancement of the Germinate platform to support prebreeding informatics for crop wild relatives. Crop Science, 2021, 61, 1538-1566.	0.8	26
17	Genome-Wide Expression and Alternative Splicing in Domesticated Sunflowers (Helianthus annuus L.) under Flooding Stress. Agronomy, 2021, 11, 92.	1.3	7
18	Laying the groundwork for crop wild relative conservation in the United States. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	7

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19	Genome-wide shifts in climate-related variation underpin responses to selective breeding in a widespread conifer. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	17
20	Microsatellites as Agents of Adaptive Change: An RNA-Seq-Based Comparative Study of Transcriptomes from Five Helianthus Species. Symmetry, 2021, 13, 933.	1.1	11
21	Standing variation rather than recent adaptive introgression probably underlies differentiation of the <i>texanus</i> subspecies of <i>Helianthus annuus</i>. Molecular Ecology, 2021, 30, 6229-6245.	2.0	13
22	Arabidopsis-Based Dual-Layered Biological Network Analysis Elucidates Fully Modulated Pathways Related to Sugarcane Resistance on Biotrophic Pathogen Infection. Frontiers in Plant Science, 2021, 12, 707904.	1.7	0
23	Aberrant RNA splicing due to genetic incompatibilities in sunflower hybrids. Evolution; International Journal of Organic Evolution, 2021, 75, 2747-2758.	1.1	7
24	Genomic Analyses of Phenotypic Differences Between Native and Invasive Populations of Diffuse Knapweed (Centaurea diffusa). Frontiers in Ecology and Evolution, 2021, 8, .	1.1	7
25	Editorial 2021. Molecular Ecology, 2021, 30, 1-25.	2.0	4
26	Genome report: a draft genome of <i>Alliaria petiolata</i> (garlic mustard) as a model system for invasion genetics. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	5
27	While neither universally applicable nor practical operationally, the biological species concept continues to offer a compelling framework for studying species and speciation. National Science Review, 2020, 7, 1398-1400.	4.6	9
28	Genetically Based Trait Differentiation but Lack of Trade-offs between Stress Tolerance and Performance in Introduced Canada Thistle. Plant Communications, 2020, 1, 100116.	3.6	4
29	The Genomic Observatories Metadatabase. Molecular Ecology Resources, 2020, 20, 1453-1454.	2.2	8
30	Mobilizing Crop Biodiversity. Molecular Plant, 2020, 13, 1341-1344.	3.9	50
31	Population Genomics of Speciation and Adaptation in Sunflowers. Population Genomics, 2020, , 1.	0.2	2
32	Plant Evolutionary Adaptation. Plant Communications, 2020, 1, 100118.	3.6	0
33	Ancestral Reconstruction of Karyotypes Reveals an Exceptional Rate of Nonrandom Chromosomal Evolution in Sunflower. Genetics, 2020, 214, 1031-1045.	1.2	31
34	Gene banks for wild and cultivated sunflower genetic resources. OCL - Oilseeds and Fats, Crops and Lipids, 2020, 27, 9.	0.6	20
35	Frequency, Origins, and Evolutionary Role of Chromosomal Inversions in Plants. Frontiers in Plant Science, 2020, 11, 296.	1.7	89
36	Multiple chromosomal inversions contribute to adaptive divergence of a dune sunflower ecotype. Molecular Ecology, 2020, 29, 2535-2549.	2.0	100

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37	Massive haplotypes underlie ecotypic differentiation in sunflowers. Nature, 2020, 584, 602-607.	13.7	263
38	Editorial 2020. Molecular Ecology, 2020, 29, 1-19.	2.0	3
39	An evaluation of alternative explanations for widespread cytonuclear discordance in annual sunflowers (<i>Helianthus</i>). New Phytologist, 2019, 221, 515-526.	3.5	118
40	Intraspecific genetic divergence within Helianthus niveus and the status of two new morphotypes from Mexico. American Journal of Botany, 2019, 106, 1229-1239.	0.8	7
41	Mapping footprints of past genetic exchange. Science, 2019, 366, 570-571.	6.0	3
42	Contemporary evolution of maize landraces and their wild relatives influenced by gene flow with modern maize varieties. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 21302-21311.	3.3	25
43	Some perspective on <i>Molecular Ecology</i> perspectives: Are women being left out?. Molecular Ecology, 2019, 28, 2451-2455.	2.0	5
44	Hybridization speeds adaptive evolution in an eight-year field experiment. Scientific Reports, 2019, 9, 6746.	1.6	47
45	Genetic and phenotypic analyses indicate that resistance to flooding stress is uncoupled from performance in cultivated sunflower. New Phytologist, 2019, 223, 1657-1670.	3.5	14
46	Genetic dissection of epistatic and QTL by environment interaction effects in three bread wheat genetic backgrounds for yield-related traits under saline conditions. Euphytica, 2019, 215, 1.	0.6	13
47	Shifts in the abiotic and biotic environment of cultivated sunflower under future climate change. OCL - Oilseeds and Fats, Crops and Lipids, 2019, 26, 9.	0.6	11
48	BSA-seq mapping reveals major QTL for broomrape resistance in four sunflower lines. Molecular Breeding, 2019, 39, 1.	1.0	34
49	Skim-Sequencing Reveals the Likely Origin of the Enigmatic Endangered Sunflower Helianthus schweinitzii. Genes, 2019, 10, 1040.	1.0	3
50	The genomics of domestication special issue editorial. Evolutionary Applications, 2019, 12, 3-5.	1.5	3
51	Sunflower pan-genome analysis shows that hybridization altered gene content and disease resistance. Nature Plants, 2019, 5, 54-62.	4.7	172
52	A new model of speciation. National Science Review, 2019, 6, 289-290.	4.6	7
53	Phylogenetic trends and environmental correlates of nuclear genome size variation in <i>Helianthus</i> sunflowers. New Phytologist, 2019, 221, 1609-1618.	3.5	39
54	Genomic sequence and copy number evolution during hybrid crop development in sunflowers. Evolutionary Applications, 2019, 12, 54-65.	1.5	27

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55	Trends in Global Agricultural Land Use: Implications for Environmental Health and Food Security. Annual Review of Plant Biology, 2018, 69, 789-815.	8.6	559
56	Homogenization of Populations in the Wildflower, Texas Bluebonnet (Lupinus texensis). Journal of Heredity, 2018, 109, 152-161.	1.0	5
57	Editorial 2018. Molecular Ecology, 2018, 27, 1-34.	2.0	6
58	A novel post hoc method for detecting index switching finds no evidence for increased switching on the Illumina HiSeq X. Molecular Ecology Resources, 2018, 18, 169-175.	2.2	25
59	Gene flow in Argentinian sunflowers as revealed by genotypingâ€byâ€sequencing data. Evolutionary Applications, 2018, 11, 193-204.	1.5	23
60	Speciation and the City. Trends in Ecology and Evolution, 2018, 33, 815-826.	4.2	62
61	Evolution of invasiveness by genetic accommodation. Nature Ecology and Evolution, 2018, 2, 991-999.	3.4	53
62	Neo-Domestication of an Interspecific Tetraploid Helianthus annuus Ã— Helianthus tuberous Population That Segregates for Perennial Habit. Genes, 2018, 9, 422.	1.0	10
63	Genetics of alternative splicing evolution during sunflower domestication. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6768-6773.	3.3	40
64	Editorial 2017. Molecular Ecology, 2017, 26, 383-412.	2.0	2
65	Both mechanism and age of duplications contribute to biased gene retention patterns in plants. BMC Genomics, 2017, 18, 46.	1.2	30
66	Gene expression and drought response in an invasive thistle. Biological Invasions, 2017, 19, 875-893.	1.2	16
67	The genetic architecture of UV floral patterning in sunflower. Annals of Botany, 2017, 120, 39-50.	1.4	19
68	Genetic admixture and heterosis may enhance the invasiveness of common ragweed. Evolutionary Applications, 2017, 10, 241-250.	1.5	35
69	The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. Nature, 2017, 546, 148-152.	13.7	579
70	The Genetics and Genomics of Plant Domestication. BioScience, 2017, 67, 971-982.	2.2	83
71	Multiple introductions, admixture and bridgehead invasion characterize the introduction history of <i>Ambrosia artemisiifolia</i> in Europe and Australia. Molecular Ecology, 2017, 26, 5421-5434.	2.0	116
72	Bioinformatically predicted deleterious mutations reveal complementation in the interior spruce hybrid complex. BMC Genomics, 2017, 18, 970.	1.2	16

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73	Remarkable life history polymorphism may be evolving under divergent selection in the silverleaf sunflower. Molecular Ecology, 2016, 25, 3817-3830.	2.0	17
74	A genomic perspective on hybridization and speciation. Molecular Ecology, 2016, 25, 2337-2360.	2.0	458
75	Revisiting a classic case of introgression: hybridization and gene flow in Californian sunflowers. Molecular Ecology, 2016, 25, 2630-2643.	2.0	49
76	Genome-wide genotyping-by-sequencing data provide a high-resolution view of wild Helianthus diversity, genetic structure, and interspecies gene flow. American Journal of Botany, 2016, 103, 2170-2177.	0.8	48
77	Genomics of <i>Cynara cardunculus</i> through the exploitation of NGS technologies. Acta Horticulturae, 2016, , 1-8.	0.1	0
78	Genetic structure reveals a history of multiple independent origins followed by admixture in the allopolyploid weed <i>Salsola ryanii</i>. Evolutionary Applications, 2016, 9, 871-878.	1.5	10
79	Editorial 2016. Molecular Ecology, 2016, 25, 433-449.	2.0	0
80	Convergent local adaptation to climate in distantly related conifers. Science, 2016, 353, 1431-1433.	6.0	303
81	Multiple reproductive barriers separate recently diverged sunflower ecotypes. Evolution; International Journal of Organic Evolution, 2016, 70, 2322-2335.	1.1	53
82	Hybridization and extinction. Evolutionary Applications, 2016, 9, 892-908.	1.5	517
83	Evolutionary and social consequences of introgression of nontransgenic herbicide resistance from rice to weedy rice in Brazil. Evolutionary Applications, 2016, 9, 837-846.	1.5	67
84	The genome sequence of the outbreeding globe artichoke constructed de novo incorporating a phase-aware low-pass sequencing strategy of F1 progeny. Scientific Reports, 2016, 6, 19427.	1.6	106
85	Complete Mitochondrial Genome Sequence of Sunflower (<i>Helianthus annuus</i> L.). Genome Announcements, 2016, 4, .	0.8	13
86	Applying gene flow science to environmental policy needs: a boundary work perspective. Evolutionary Applications, 2016, 9, 924-936.	1.5	9
87	When gene flow really matters: gene flow in applied evolutionary biology. Evolutionary Applications, 2016, 9, 833-836.	1.5	72
88	Exome capture from the spruce and pine gigaâ€genomes. Molecular Ecology Resources, 2016, 16, 1136-1146.	2.2	75
89	Transcriptomeâ€derived evidence supports recent polyploidization and a major phylogeographic division in T rithuria submersa (H ydatellaceae, N ymphaeales). New Phytologist, 2016, 210, 310-323.	3.5	10
90	Origins of food crops connect countries worldwide. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20160792.	1.2	125

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91	Most Compositae (Asteraceae) are descendants of a paleohexaploid and all share a paleotetraploid ancestor with the Calyceraceae. American Journal of Botany, 2016, 103, 1203-1211.	0.8	98
92	A Balanced Data Archiving Policy for Long-Term Studies. Trends in Ecology and Evolution, 2016, 31, 84-85.	4.2	17
93	Ambient insect pressure and recipient genotypes determine fecundity of transgenic cropâ€weed rice hybrid progeny: Implications for environmental biosafety assessment. Evolutionary Applications, 2016, 9, 847-856.	1.5	16
94	Fitness correlates of crop transgene flow into weedy populations: a case study of weedy rice in China and other examples. Evolutionary Applications, 2016, 9, 857-870.	1.5	38
95	Expression Divergence Is Correlated with Sequence Evolution but Not Positive Selection in Conifers. Molecular Biology and Evolution, 2016, 33, 1502-1516.	3.5	48
96	Recombination Rate Evolution and the Origin of Species. Trends in Ecology and Evolution, 2016, 31, 226-236.	4.2	165
97	The origins of reproductive isolation in plants. New Phytologist, 2015, 207, 968-984.	3.5	288
98	Evolution of invasiveness through increased resource use in a vacant niche. Nature Plants, 2015, 1, .	4.7	78
99	Ecogeography and utility to plant breeding of the crop wild relatives of sunflower (Helianthus) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.7	57
100	A Unified Single Nucleotide Polymorphism Map of Sunflower (Helianthus annuus L.) Derived from Current Genomic Resources. Crop Science, 2015, 55, 1696-1702.	0.8	16
101	Association mapping in sunflower (Helianthus annuus L.) reveals independent control of apical vs. basal branching. BMC Plant Biology, 2015, 15, 84.	1.6	43
102	Repetitive DNA and Plant Domestication: Variation in Copy Number and Proximity to Genes of LTR-Retrotransposons among Wild and Cultivated Sunflower (<i>Helianthus annuus</i>) Genotypes. Genome Biology and Evolution, 2015, 7, 3368-3382.	1.1	36
103	Adaptive plasticity and niche expansion in an invasive thistle. Ecology and Evolution, 2015, 5, 3183-3197.	0.8	42
104	What we still don't know about invasion genetics. Molecular Ecology, 2015, 24, 2277-2297.	2.0	344
105	Genome scans reveal candidate domestication and improvement genes in cultivated sunflower, as well as postâ€domestication introgression with wild relatives. New Phytologist, 2015, 206, 830-838.	3.5	79
106	Quantitative trait locus mapping identifies candidate alleles involved in adaptive introgression and range expansion in a wild sunflower. Molecular Ecology, 2015, 24, 2194-2211.	2.0	59
107	Methods for studying polyploid diversification and the dead end hypothesis: a reply to Soltis <i>etÂal</i>. (2014). New Phytologist, 2015, 206, 27-35.	3.5	82
108	Patterns of domestication in the Ethiopian oilâ€seed crop noug (Guizotia abyssinica). Evolutionary Applications, 2015, 8, 464-475.	1.5	16

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109	Professor Harry Smith (1935-2015). Molecular Ecology, 2015, 24, 2299-2300.	2.0	2
110	The Accumulation of Deleterious Mutations as a Consequence of Domestication and Improvement in Sunflowers and Other Compositae Crops. Molecular Biology and Evolution, 2015, 32, 2273-2283.	3.5	139
111	Editorial 2015. Molecular Ecology, 2015, 24, 1-17.	2.0	2
112	Early genome duplications in conifers and other seed plants. Science Advances, 2015, 1, e1501084.	4.7	236
113	Comparative genomics in the Asteraceae reveals little evidence for parallel evolutionary change in invasive taxa. Molecular Ecology, 2015, 24, 2226-2240.	2.0	38
114	Sequence-Based Analysis of Structural Organization and Composition of the Cultivated Sunflower (Helianthus annuus L.) Genome. Biology, 2014, 3, 295-319.	1.3	16
115	Bridging physiological and evolutionary timeâ€scales in a gene regulatory network. New Phytologist, 2014, 203, 685-696.	3.5	15
116	Shared selective pressure and local genomic landscape lead to repeatable patterns of genomic divergence in sunflowers. Molecular Ecology, 2014, 23, 311-324.	2.0	74
117	A target enrichment method for gathering phylogenetic information from hundreds of loci: An example from the Compositae. Applications in Plant Sciences, 2014, 2, 1300085.	0.8	178
118	Increasing homogeneity in global food supplies and the implications for food security. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4001-4006.	3.3	757
119	HYBRID INCOMPATIBILITY IS ACQUIRED FASTER IN ANNUAL THAN IN PERENNIAL SPECIES OF SUNFLOWER AND TARWEED. Evolution; International Journal of Organic Evolution, 2014, 68, 893-900.	1.1	26
120	Chromosomal Evolution and Patterns of Introgression in <i>Helianthus</i>. Genetics, 2014, 197, 969-979.	1.2	52
121	Conservation and divergence of gene expression plasticity following <i>c</i>. 140Âmillion years of evolution in lodgepole pine (<i><scp>P</scp>inus contorta</i>) and interior spruce (<i><scp>P</scp>icea glauca</i>ÂÃ—Â<i><scp>P</scp>icea engelmannii</i>). New Phytologist, 2014, 203, 578-591.	3.5	46
122	Genomics of <scp>C</scp>ompositae crops: reference transcriptome assemblies and evidence of hybridization with wild relatives. Molecular Ecology Resources, 2014, 14, 166-177.	2.2	45
123	Genome skimming reveals the origin of the Jerusalem Artichoke tuber crop species: neither from Jerusalem nor an artichoke. New Phytologist, 2014, 201, 1021-1030.	3.5	151
124	De Novo Genome Assembly of the Economically Important Weed Horseweed Using Integrated Data from Multiple Sequencing Platforms Â Â Â. Plant Physiology, 2014, 166, 1241-1254.	2.3	101
125	Rapid evolution of an invasive weed. New Phytologist, 2014, 202, 309-321.	3.5	78
126	Editorial 2014. Molecular Ecology, 2014, 23, 1-15.	2.0	1

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127	The role of homoploid hybridization in evolution: A century of studies synthesizing genetics and ecology. American Journal of Botany, 2014, 101, 1247-1258.	0.8	173
128	Genomics of homoploid hybrid speciation: diversity and transcriptional activity of long terminal repeat retrotransposons in hybrid sunflowers. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130345.	1.8	46
129	On the adaptive value of cytoplasmic genomes in plants. Molecular Ecology, 2014, 23, 4899-4911.	2.0	129
130	Genomic variation in Helianthus: learning from the past and looking to the future. Briefings in Functional Genomics, 2014, 13, 328-340.	1.3	10
131	Genetics of Cryptic Speciation within an Arctic Mustard, Draba nivalis. PLoS ONE, 2014, 9, e93834.	1.1	23
132	Genome-scale transcriptional analyses of first-generation interspecific sunflower hybrids reveals broad regulatory compatibility. BMC Genomics, 2013, 14, 342.	1.2	15
133	The genetic basis of speciation in the Giliopsis lineage of Ipomopsis (Polemoniaceae). Heredity, 2013, 111, 227-237.	1.2	33
134	The repetitive component of the sunflower genome as shown by different procedures for assembling next generation sequencing reads. BMC Genomics, 2013, 14, 686.	1.2	52
135	DIVERGENCE IS FOCUSED ON FEW GENOMIC REGIONS EARLY IN SPECIATION: INCIPIENT SPECIATION OF SUNFLOWER ECOTYPES. Evolution; International Journal of Organic Evolution, 2013, 67, 2468-2482.	1.1	97
136	Methodological challenges to realizing the potential of hybridization research. Journal of Evolutionary Biology, 2013, 26, 259-260.	0.8	11
137	Sunflower genetic, genomic and ecological resources. Molecular Ecology Resources, 2013, 13, 10-20.	2.2	59
138	The molecular basis of invasiveness: differences in gene expression of native and introduced common ragweed (<i><scp>A</scp>mbrosia artemisiifolia</i>) in stressful and benign environments. Molecular Ecology, 2013, 22, 2496-2510.	2.0	70
139	Recent nonhybrid origin of sunflower ecotypes in a novel habitat. Molecular Ecology, 2013, 22, 799-813.	2.0	47
140	Editorial 2013. Molecular Ecology, 2013, 22, 1-14.	2.0	1
141	A road map for molecular ecology. Molecular Ecology, 2013, 22, 2605-2626.	2.0	100
142	CONVERGENCE AND DIVERGENCE DURING THE ADAPTATION TO SIMILAR ENVIRONMENTS BY AN AUSTRALIAN GROUNDSEL. Evolution; International Journal of Organic Evolution, 2013, 67, 2515-2529.	1.1	66
143	Genomic evidence for the parallel evolution of coastal forms in the <i>Senecio lautus</i> complex. Molecular Ecology, 2013, 22, 2941-2952.	2.0	109
144	Genomic islands of divergence are not affected by geography of speciation in sunflowers. Nature Communications, 2013, 4, 1827.	5.8	263

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145	Feeding the future. Nature, 2013, 499, 23-24.	13.7	464
146	Divergence in Gene Expression Is Uncoupled from Divergence in Coding Sequence in a Secondarily Woody Sunflower. International Journal of Plant Sciences, 2013, 174, 1079-1089.	0.6	29
147	Association Mapping and the Genomic Consequences of Selection in Sunflower. PLoS Genetics, 2013, 9, e1003378.	1.5	116
148	RNA-Seq Analysis of Allele-Specific Expression, Hybrid Effects, and Regulatory Divergence in Hybrids Compared with Their Parents from Natural Populations. Genome Biology and Evolution, 2013, 5, 1309-1323.	1.1	131
149	Transcriptome divergence between introduced and native populations of Canada thistle, <i>Cirsium arvense</i>. New Phytologist, 2013, 199, 595-608.	3.5	34
150	Genomic Resources Notes accepted 1 February 2013â€"31 March 2013. Molecular Ecology Resources, 2013, 13, 759-759.	2.2	1
151	Allele Identification for Transcriptome-Based Population Genomics in the Invasive Plant<i>Centaurea solstitialis</i>. G3: Genes, Genomes, Genetics, 2013, 3, 359-367.	0.8	65
152	What can patterns of differentiation across plant genomes tell us about adaptation and speciation?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 364-373.	1.8	234
153	The sunflower (<i>Helianthus annuus</i> L.) genome reflects a recent history of biased accumulation of transposable elements. Plant Journal, 2012, 72, 142-153.	2.8	88
154	Largeâ€scale transcriptome characterization and mass discovery of SNPs in globe artichoke and its related taxa. Plant Biotechnology Journal, 2012, 10, 956-969.	4.1	33
155	Development of a 10,000 Locus Genetic Map of the Sunflower Genome Based on Multiple Crosses. G3: Genes, Genomes, Genetics, 2012, 2, 721-729.	0.8	96
156	Sorting through the chaff, nDNA gene trees for phylogenetic inference and hybrid identification of annual sunflowers (Helianthus sect. Helianthus). Molecular Phylogenetics and Evolution, 2012, 64, 145-155.	1.2	33
157	Genomics of Compositae weeds: EST libraries, microarrays, and evidence of introgression. American Journal of Botany, 2012, 99, 209-218.	0.8	80
158	Reproductive Isolation during Domestication. Plant Cell, 2012, 24, 2710-2717.	3.1	69
159	Preparation of Normalized cDNA Libraries for 454 Titanium Transcriptome Sequencing. Methods in Molecular Biology, 2012, 888, 119-133.	0.4	12
160	Response of Sunflower (Helianthus annuus L.) Leaf Surface Defenses to Exogenous Methyl Jasmonate. PLoS ONE, 2012, 7, e37191.	1.1	23
161	Development of an Ultra-Dense Genetic Map of the Sunflower Genome Based on Single-Feature Polymorphisms. PLoS ONE, 2012, 7, e51360.	1.1	12
162	Parallel Ecological Speciation in Plants?. International Journal of Ecology, 2012, 2012, 1-17.	0.3	47

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163	The Population Genomics of Sunflowers and Genomic Determinants of Protein Evolution Revealed by RNAseq. Biology, 2012, 1, 575-596.	1.3	34
164	Editorial 2012. Molecular Ecology, 2012, 21, 1-22.	2.0	14
165	Invasion history of North American Canada thistle, <i>Cirsium arvense</i>. Journal of Biogeography, 2012, 39, 1919-1931.	1.4	30
166	RECONCILING EXTREMELY STRONG BARRIERS WITH HIGH LEVELS OF GENE EXCHANGE IN ANNUAL SUNFLOWERS. Evolution; International Journal of Organic Evolution, 2012, 66, 1459-1473.	1.1	74
167	REDUCED DROUGHT TOLERANCE DURING DOMESTICATION AND THE EVOLUTION OF WEEDINESS RESULTS FROM TOLERANCE-GROWTH TRADE-OFFS. Evolution; International Journal of Organic Evolution, 2012, 66, 3803-3814.	1.1	80
168	Changes in the rootâ€associated fungal communities along a primary succession gradient analysed by 454 pyrosequencing. Molecular Ecology, 2012, 21, 1897-1908.	2.0	172
169	Metaâ€barcoding of â€˜dirtâ€™ DNA from soil reflects vertebrate biodiversity. Molecular Ecology, 2012, 21, 1966-1979.	2.0	276
170	Soil sampling and isolation of extracellular DNA from large amount of starting material suitable for metabarcoding studies. Molecular Ecology, 2012, 21, 1816-1820.	2.0	264
171	Two decades of describing the unseen majority of aquatic microbial diversity. Molecular Ecology, 2012, 21, 1878-1896.	2.0	180
172	Plant species richness belowground: higher richness and new patterns revealed by nextâ€generation sequencing. Molecular Ecology, 2012, 21, 2004-2016.	2.0	105
173	Tracking earthworm communities from soil DNA. Molecular Ecology, 2012, 21, 2017-2030.	2.0	109
174	Adaptation with gene flow across the landscape in a dune sunflower. Molecular Ecology, 2012, 21, 2078-2091.	2.0	106
175	Towards nextâ€generation biodiversity assessment using DNA metabarcoding. Molecular Ecology, 2012, 21, 2045-2050.	2.0	1,253
176	New environmental metabarcodes for analysing soil DNA: potential for studying past and present ecosystems. Molecular Ecology, 2012, 21, 1821-1833.	2.0	259
177	Environmental DNA. Molecular Ecology, 2012, 21, 1789-1793.	2.0	926
178	Bioinformatic challenges for DNA metabarcoding of plants and animals. Molecular Ecology, 2012, 21, 1834-1847.	2.0	243
179	Contributions of Flowering Time Genes to Sunflower Domestication and Improvement. Genetics, 2011, 187, 271-287.	1.2	82
180	Recently Formed Polyploid Plants Diversify at Lower Rates. Science, 2011, 333, 1257-1257.	6.0	424

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