

Martin Lascoux

List of Publications by Year in descending order

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103
papers

8,292
citations

101496

36
h-index

54882

84
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120
all docs

120
docs citations

120
times ranked

10790
citing authors

#	ARTICLE	IF	CITATIONS
1	Hunting for Beneficial Mutations: Conditioning on SIFT Scores When Estimating the Distribution of Fitness Effect of New Mutations. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	13
2	What does the distribution of fitness effects of new mutations reflect? Insights from plants. <i>New Phytologist</i> , 2022, 233, 1613-1619.	3.5	6
3	Genome-wide evolutionary response of European oaks during the Anthropocene. <i>Evolution Letters</i> , 2022, 6, 4-20.	1.6	24
4	Competitive ability depends on mating system and ploidy level across <i>Capsella</i> species. <i>Annals of Botany</i> , 2022, 129, 697-708.	1.4	2
5	The relative role of plasticity and demographic history in <i>Capsella bursa-pastoris</i> : a common garden experiment in Asia and Europe. <i>AoB PLANTS</i> , 2022, 14, .	1.2	4
6	Genome-wide analyses of introgression between two sympatric Asian oak species. <i>Nature Ecology and Evolution</i> , 2022, 6, 924-935.	3.4	32
7	Allorecognition genes drive reproductive isolation in <i>Podospora anserina</i> . <i>Nature Ecology and Evolution</i> , 2022, 6, 910-923.	3.4	15
8	The GenTree Leaf Collection: Inter- and intraspecific leaf variation in seven forest tree species in Europe. <i>Global Ecology and Biogeography</i> , 2021, 30, 590-597.	2.7	11
9	Analysis of diversity-dependent species evolution using concepts in population genetics. <i>Journal of Mathematical Biology</i> , 2021, 82, 22.	0.8	0
10	The GenTree Platform: growth traits and tree-level environmental data in 12 European forest tree species. <i>GigaScience</i> , 2021, 10, .	3.3	3
11	An introgressed gene causes meiotic drive in <i>Neurospora sitophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	26
12	Leveraging breeding programs and genomic data in Norway spruce (<i>Picea abies</i> L. Karst) for GWAS analysis. <i>Genome Biology</i> , 2021, 22, 179.	3.8	29
13	The GenTree Dendroecological Collection, tree-ring and wood density data from seven tree species across Europe. <i>Scientific Data</i> , 2020, 7, 1.	2.4	830
14	From Drift to Draft: How Much Do Beneficial Mutations Actually Contribute to Predictions of Ohta's Slightly Deleterious Model of Molecular Evolution?. <i>Genetics</i> , 2020, 214, 1005-1018.	1.2	25
15	Genomic insights on the contribution of balancing selection and local adaptation to the long-term survival of a widespread living fossil tree, <i>Cercidiphyllum japonicum</i> . <i>New Phytologist</i> , 2020, 228, 1674-1689.	3.5	22
16	Genetics to the rescue: managing forests sustainably in a changing world. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	11
17	Shift in ecological strategy helps marginal populations of shepherd's purse (<i>Capsella</i>) <i>Sciences</i> , 2020, 287, 20200463.	1.2	12
18	Survival in the Tropics despite isolation, inbreeding and asexual reproduction: insights from the genome of the world's southernmost poplar (<i>Populus ilicifolia</i>). <i>Plant Journal</i> , 2020, 103, 430-442.	2.8	23

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19	Cytoplasmic DNA variation does not support a recent contribution of <i>Pinus sylvestris</i> L. from the Caucasus to the main range. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	30
20	Genomic data provide new insights on the demographic history and the extent of recent material transfers in Norway spruce. <i>Evolutionary Applications</i> , 2019, 12, 1539-1551.	1.5	49
21	Towards the new normal: Transcriptomic convergence and genomic legacy of the two subgenomes of an allopolyploid weed (<i>Capsella bursa-pastoris</i>). <i>PLoS Genetics</i> , 2019, 15, e1008131.	1.5	27
22	Parental legacy, demography, and admixture influenced the evolution of the two subgenomes of the tetraploid <i>Capsella bursa-pastoris</i> (Brassicaceae). <i>PLoS Genetics</i> , 2019, 15, e1007949.	1.5	42
23	Assessing the potential for assisted gene flow using past introduction of Norway spruce in southern Sweden: Local adaptation and genetic basis of quantitative traits in trees. <i>Evolutionary Applications</i> , 2019, 12, 1946-1959.	1.5	36
24	Clinal variation in growth cessation and FTL2 expression in Siberian spruce. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	4
25	Modeling a trait-dependent diversification process coupled with molecular evolution on a random species tree. <i>Journal of Theoretical Biology</i> , 2019, 461, 189-203.	0.8	3
26	Competitive ability of <i>Capsella</i> species with different mating systems and ploidy levels. <i>Annals of Botany</i> , 2018, 121, 1257-1264.	1.4	13
27	Ancient polymorphisms and divergence hitchhiking contribute to genomic islands of divergence within a poplar species complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E236-E243.	3.3	126
28	From America to Eurasia: a multigenomes history of the genus <i>Abies</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 14-28.	1.2	31
29	Convergent evolution of complex genomic rearrangements in two fungal meiotic drive elements. <i>Nature Communications</i> , 2018, 9, 4242.	5.8	40
30	Paternally expressed imprinted genes associate with hybridization barriers in <i>Capsella</i> . <i>Nature Plants</i> , 2018, 4, 352-357.	4.7	81
31	Homeologue-specific expression divergence in the recently formed tetraploid <i>Capsella bursa-pastoris</i> (Brassicaceae). <i>New Phytologist</i> , 2018, 220, 624-635.	3.5	10
32	Demographic expansion and genetic load of the halophyte model plant <i>Eutrema salsugineum</i> . <i>Molecular Ecology</i> , 2018, 27, 2943-2955.	2.0	11
33	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	4.7	303
34	Genome sequencing and population genomic analyses provide insights into the adaptive landscape of silver birch. <i>Nature Genetics</i> , 2017, 49, 904-912.	9.4	221
35	Using the Ornstein-Uhlenbeck process to model the evolution of interacting populations. <i>Journal of Theoretical Biology</i> , 2017, 429, 35-45.	0.8	18
36	Genetic Diversity and the Efficacy of Purifying Selection across Plant and Animal Species. <i>Molecular Biology and Evolution</i> , 2017, 34, 1417-1428.	3.5	142

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37	Multispecies genetic structure and hybridization in the <i>Betula</i> genus across Eurasia. <i>Molecular Ecology</i> , 2017, 26, 589-605.	2.0	67
38	Fine- and local- scale genetic structure of <i>Dysoxylum malabaricum</i> , a late-successional canopy tree species in disturbed forest patches in the Western Ghats, India. <i>Conservation Genetics</i> , 2017, 18, 1-15.	0.8	24
39	Local Adaptation in European Firs Assessed through Extensive Sampling across Altitudinal Gradients in Southern Europe. <i>PLoS ONE</i> , 2016, 11, e0158216.	1.1	34
40	The influence of population structure on gene expression and flowering time variation in the ubiquitous weed <i>Capsella bursa-pastoris</i> (Brassicaceae). <i>Molecular Ecology</i> , 2016, 25, 1106-1121.	2.0	36
41	An informational transition in conditioned Markov chains: Applied to genetics and evolution. <i>Journal of Theoretical Biology</i> , 2016, 402, 158-170.	0.8	2
42	Identifying Genetic Signatures of Natural Selection Using Pooled Population Sequencing in <i>Picea abies</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1979-1989.	0.8	28
43	Different alleles of a gene encoding leucoanthocyanidin reductase (PaLAR3) influence resistance against the fungus <i>Heterobasidion parviporum</i> in <i>Picea abies</i> . <i>Plant Physiology</i> , 2016, 171, pp.00685.2016.	2.3	34
44	The extent and meaning of hybridization and introgression between Siberian spruce (<i>Picea</i>) and European spruce (<i>Picea</i>). <i>Molecular Ecology</i> , 2016, 25, 2773-2789.	2.0	54
45	Introgression maintains the genetic integrity of the mating-type determining chromosome of the fungus <i>Neurospora tetrasperma</i> . <i>Genome Research</i> , 2016, 26, 486-498.	2.4	39
46	Genetic and morphological evidence for introgression between three species of willows. <i>BMC Evolutionary Biology</i> , 2015, 15, 193.	3.2	29
47	Population structure and the rate of evolution. <i>Journal of Theoretical Biology</i> , 2015, 365, 486-495.	0.8	5
48	Hybrid origins and the earliest stages of diploidization in the highly successful recent polyploid <i>Capsella bursa-pastoris</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2806-2811.	3.3	128
49	High Rates of Gene Flow by Pollen and Seed in Oak Populations across Europe. <i>PLoS ONE</i> , 2014, 9, e85130.	1.1	92
50	Patterns of Nucleotide Diversity at Photoperiod Related Genes in Norway Spruce [<i>Picea abies</i> (L.) Karst.]. <i>PLoS ONE</i> , 2014, 9, e95306.	1.1	20
51	Amount of Information Needed for Model Choice in Approximate Bayesian Computation. <i>PLoS ONE</i> , 2014, 9, e99581.	1.1	5
52	A <i>Picea abies</i> Linkage Map Based on SNP Markers Identifies QTLs for Four Aspects of Resistance to <i>Heterobasidion parviporum</i> Infection. <i>PLoS ONE</i> , 2014, 9, e101049.	1.1	52
53	Clinal Variation at Phenology-Related Genes in Spruce: Parallel Evolution in <i>FTL2</i> and <i>Gigantea</i> ?. <i>Genetics</i> , 2014, 197, 1025-1038.	1.2	41
54	A global multilocus analysis of the model fungus <i>Neurospora</i> reveals a single recent origin of a novel genetic system. <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 136-147.	1.2	20

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55	Exact simulation of conditioned Wright-Fisher models. <i>Journal of Theoretical Biology</i> , 2014, 363, 419-426.	0.8	6
56	Investigating Population History Using Temporal Genetic Differentiation. <i>Molecular Biology and Evolution</i> , 2014, 31, 2516-2527.	3.5	50
57	The Hypomethylated Partial Restriction (HMPR) method reduces the repetitive content of genomic libraries in Norway spruce (<i>Picea abies</i>). <i>Tree Genetics and Genomes</i> , 2013, 9, 601-612.	0.6	3
58	Ecological genomics of local adaptation. <i>Nature Reviews Genetics</i> , 2013, 14, 807-820.	7.7	1,099
59	Genomic insights into salt adaptation in a desert poplar. <i>Nature Communications</i> , 2013, 4, 2797.	5.8	286
60	Southern montane populations did not contribute to the recolonization of <i>W</i> Iberian <i>P</i> lain by <i>S</i> iberian larch (<i>L</i> arix sibirica): a range-wide analysis of cytoplasmic markers. <i>Molecular Ecology</i> , 2013, 22, 4958-4971.	2.0	61
61	Distribution of Long-Range Linkage Disequilibrium and Tajima's D Values in Scandinavian Populations of Norway Spruce (<i>Picea abies</i>). <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 795-806.	0.8	26
62	Origin and demographic history of the endemic Taiwan spruce (<i>Picea morrisonicola</i>). <i>Ecology and Evolution</i> , 2013, 3, 3320-3333.	0.8	10
63	Nuclear and cytoplasmic genetic diversity reveals long-term population decline in <i>Abies semenovii</i> , an endemic fir of central Asia. <i>Canadian Journal of Forest Research</i> , 2012, 42, 2142-2152.	0.8	9
64	Flowering time and transcriptome variation in <i>Capsella bursa-pastoris</i> (Brassicaceae). <i>New Phytologist</i> , 2012, 194, 676-689.	3.5	22
65	Sequencing of the needle transcriptome from Norway spruce (<i>Picea abies</i> Karst L.) reveals lower substitution rates, but similar selective constraints in gymnosperms and angiosperms. <i>BMC Genomics</i> , 2012, 13, 589.	1.2	60
66	Disentangling the Roles of History and Local Selection in Shaping Clinal Variation of Allele Frequencies and Gene Expression in Norway Spruce (<i>Picea abies</i>). <i>Genetics</i> , 2012, 191, 865-881.	1.2	195
67	Joint analysis of demography and selection in population genetics: where do we stand and where could we go?. <i>Molecular Ecology</i> , 2012, 21, 28-44.	2.0	138
68	POPULATION GENETIC EVIDENCE FOR COMPLEX EVOLUTIONARY HISTORIES OF FOUR HIGH ALTITUDE JUNIPER SPECIES IN THE QINGHAI-TIBETAN PLATEAU. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 831-845.	1.1	70
69	Post-glacial history and introgression in <i>Abies</i> (Pinaceae) species of the Russian Far East inferred from both nuclear and cytoplasmic markers. <i>Journal of Biogeography</i> , 2011, 38, 326-340.	1.4	40
70	The Pleistocene demography of an alpine juniper of the Qinghai-Tibetan Plateau: tabula rasa, cryptic refugia or something else?. <i>Journal of Biogeography</i> , 2011, 38, 31-43.	1.4	27
71	Contrasting demographic history and population structure in <i>Capsella rubella</i> and <i>Capsella grandiflora</i> , two closely related species with different mating systems. <i>Molecular Ecology</i> , 2011, 20, 3306-3320.	2.0	63
72	Direction and extent of organelle DNA introgression between two spruce species in the Qinghai-Tibetan Plateau. <i>New Phytologist</i> , 2011, 192, 1024-1033.	3.5	88

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73	A sample view of the pedunculate oak (<i>Quercus robur</i>) genome from the sequencing of hypomethylated and random genomic libraries. <i>Tree Genetics and Genomes</i> , 2011, 7, 1277-1285.	0.6	7
74	Polymorphism and Divergence in Two Willow Species, <i>Salix viminalis</i> L. and <i>Salix schwerinii</i> E. Wolf. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 387-400.	0.8	30
75	The "New Wave"™ in plant demographic inference: more loci and more individuals. <i>Molecular Ecology</i> , 2010, 19, 1075-1078.	2.0	9
76	Cytoplasmic DNA variation and biogeography of <i>Larix</i> Mill. in Northeast Asia. <i>Molecular Ecology</i> , 2010, 19, 1239-1252.	2.0	59
77	Demographic histories of four spruce (<i>Picea</i>) species of the Qinghai-Tibetan Plateau and neighboring areas inferred from multiple nuclear loci. <i>Molecular Biology and Evolution</i> , 2010, 27, 1001-1014.	3.5	113
78	Recent speciation of <i>Capsella rubella</i> from <i>Capsella grandiflora</i> , associated with loss of self-incompatibility and an extreme bottleneck. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5246-5251.	3.3	204
79	Polymorphism and Divergence at Three Duplicate Genes in <i>Brassica nigra</i> . <i>Journal of Molecular Evolution</i> , 2008, 66, 581-590.	0.8	7
80	Past demography in forest trees: what can we learn from nuclear DNA sequences that we do not already know?. <i>Plant Ecology and Diversity</i> , 2008, 1, 209-215.	1.0	17
81	Polyploid Speciation Did Not Confer Instant Reproductive Isolation in <i>Capsella</i> (Brassicaceae). <i>Molecular Biology and Evolution</i> , 2008, 25, 1472-1481.	3.5	93
82	RAPD-derived, PCR-based mitochondrial markers for <i>Larix</i> species and their usefulness in phylogeny. <i>Conservation Genetics</i> , 2006, 7, 621-625.	0.8	13
83	Multilocus Patterns of Nucleotide Diversity, Linkage Disequilibrium and Demographic History of Norway Spruce [<i>Picea abies</i> (L.) Karst]. <i>Genetics</i> , 2006, 174, 2095-2105.	1.2	241
84	Bayesian inference of evolutionary history from chloroplast microsatellites in the cosmopolitan weed <i>Capsella bursa-pastoris</i> (Brassicaceae). <i>Molecular Ecology</i> , 2005, 14, 4221-4233.	2.0	41
85	Impact of Ice Ages on the genetic structure of trees and shrubs. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2004, 359, 197-207.	1.8	111
86	Phylogenetic relationships of <i>Betula</i> species (Betulaceae) based on nuclear <i>ADH</i> and chloroplast <i>matK</i> sequences. <i>American Journal of Botany</i> , 2004, 91, 1834-1845.	0.8	76
87	Glacial Refugia: Hotspots But Not Melting Pots of Genetic Diversity. <i>Science</i> , 2003, 300, 1563-1565.	6.0	1,569
88	Conflicting phylogenies of <i>Larix</i> (Pinaceae) based on cytoplasmic and nuclear DNA. <i>Molecular Phylogenetics and Evolution</i> , 2003, 27, 173-184.	1.2	43
89	Nuclear and cytoplasmic variation within and between Eurasian <i>Larix</i> (Pinaceae) species. <i>American Journal of Botany</i> , 2003, 90, 1113-1123.	0.8	61
90	Sequence Variation and Haplotype Structure at the Putative Flowering-Time Locus COL1 of <i>Brassica nigra</i> . <i>Molecular Biology and Evolution</i> , 2002, 19, 1474-1482.	3.5	22

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91	Naturally Occurring Indel Variation in the <i>Brassica nigra</i> COL1 Gene Is Associated With Variation in Flowering Time. <i>Genetics</i> , 2002, 161, 299-306.	1.2	63
92	Title is missing!. <i>European Journal of Plant Pathology</i> , 2001, 107, 871-881.	0.8	17
93	A Study of Deleterious Gene Structure in Plants Using Markov Chain Monte Carlo. <i>Biometrics</i> , 1999, 55, 376-386.	0.8	1
94	Intra- and interspecific allozyme variability in Eurasian <i>Larix</i> Mill. species. <i>Heredity</i> , 1999, 82, 193-204.	1.2	48
95	Genetic relationship among Eurasian and American <i>Larix</i> species based on allozymes. <i>Heredity</i> , 1999, 83, 62-70.	1.2	48
96	Low isozyme diversity in Nordic and central European populations of <i>Vicia pisiformis</i> and <i>V. dumetorum</i> (Fabaceae). <i>Nordic Journal of Botany</i> , 1999, 19, 643-652.	0.2	5
97	Probability of Identity by Descent in Metapopulations. <i>Genetics</i> , 1999, 152, 1217-1228.	1.2	2
98	One step beyond lethal equivalents: characterization of deleterious loci in the rapid cycling <i>Brassica rapa</i> L. base population. , 1998, 104, 161-170.		5
99	The infinite island model with sex-differentiated gene flow. <i>Heredity</i> , 1998, 81, 63-68.	1.2	30
100	The infinite island model with sex-differentiated gene flow. <i>Heredity</i> , 1998, 81, 63-68.	1.2	8
101	UNPREDICTABILITY OF CORRELATED RESPONSE TO SELECTION: LINKAGE AND INITIAL FREQUENCY ALSO MATTER. <i>Evolution; International Journal of Organic Evolution</i> , 1997, 51, 1394-1400.	1.1	11
102	Population structure of a riparian willow species, <i>Salix viminalis</i> L.. <i>Genetical Research</i> , 1996, 68, 45-54.	0.3	30
103	Growth of 24 full-sib families of <i>Pinus sylvestris</i> L. At six relative nutrient addition rates. <i>Scandinavian Journal of Forest Research</i> , 1994, 9, 115-123.	0.5	7