Patrick Mardulyn

List of Publications by Year
in descending order

53	3,573	304743 22	175258 52
papers	citations	h-index	g-index

53	53	53	4826
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Diversification of the orchid genus Tridactyle : Origin of endemism on the oceanic islands of SÃ£o TomÃ© & PrÃncipe in the Gulf of Guinea. Journal of Biogeography, 2022, 49, 523-536.	3.0	1
2	Evolutionary history of inquiline social parasitism in Plagiolepis ants. Molecular Phylogenetics and Evolution, 2021, 155, 107016.	2.7	12
3	At the Gate of Mutualism: Identification of Genomic Traits Predisposing to Insect-Bacterial Symbiosis in Pathogenic Strains of the Aphid Symbiont Serratia symbiotica. Frontiers in Cellular and Infection Microbiology, 2021, 11, 660007.	3.9	14
4	Genome Assembly of the Cold-Tolerant Leaf BeetleGonioctena quinquepunctata, an Important Resource for Studying Its Evolution and Reproductive Barriers between Species. Genome Biology and Evolution, 2021, 13, .	2.5	2
5	Wholeâ€genome sequencing reveals asymmetric introgression between two sister species of coldâ€resistant leaf beetles. Molecular Ecology, 2021, 30, 4077-4089.	3.9	3
6	Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Genome Sequencing from Post-Mortem Formalin-Fixed, Paraffin-Embedded Lung Tissues. Journal of Molecular Diagnostics, 2021, 23, 1065-1077.	2.8	2
7	Estimating Migration of Gonioctena quinquepunctata (Coleoptera: Chrysomelidae) Inside a Mountain Range in a Spatially Explicit Context. Insect Systematics and Diversity, 2021, 5, .	1.7	0
8	Unraveling heteroplasmy patterns with NOVOPlasty. NAR Genomics and Bioinformatics, 2020, 2, lqz011.	3.2	36
9	What do tropical cryptogams reveal? Strong genetic structure in Amazonian bryophytes. New Phytologist, 2020, 228, 640-650.	7.3	10
10	Mitonuclear mismatch alters performance and reproductive success in naturally introgressed populations of a montane leaf beetle*. Evolution; International Journal of Organic Evolution, 2020, 74, 1724-1740.	2.3	27
11	Limited gene exchange between two sister species of leaf beetles within a hybrid zone in the Alps. Journal of Evolutionary Biology, 2019, 32, 1406-1417.	1.7	6
12	Molecular phylogeny and taxonomic synopsis of the angraecoid genus Ypsilopus (Orchidaceae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30	0.7	6
13	Maintenance of genetic and morphological identity in two sibling Syrrhopodon species (Calymperaceae, Bryopsida) despite extensive introgression. Journal of Systematics and Evolution, 2019, 57, 395-403.	3.1	4
14	Divergent geographic patterns of genetic diversity among wild bees: Conservation implications. Diversity and Distributions, 2018, 24, 1860-1868.	4.1	4
15	Molecular chaperoning helps safeguarding mitochondrial integrity and motor functions in the Sahara silver ant Cataglyphis bombycina. Scientific Reports, 2018, 8, 9220.	3.3	11
16	NOVOPlasty:de novoassembly of organelle genomes from whole genome data. Nucleic Acids Research, 2017, 45, gkw955.	14.5	2,079
17	Ecological niche modelling and coalescent simulations to explore the recent geographical range history of five widespread bumblebee species in Europe. Journal of Biogeography, 2017, 44, 39-50.	3.0	30
18	Glacial survival of trophically linked boreal species in northern Europe. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20162799.	2.6	13

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19	Widespread co-occurrence of two distantly related mitochondrial genomes in individuals of the leaf beetle Gonioctena intermedia. Biology Letters, 2017, 13, 20170570.	2.3	8
20	Evolution of reproductive traits in Cataglyphis desert ants: mating frequency, queen number, and thelytoky. Behavioral Ecology and Sociobiology, 2016, 70, 1367-1379.	1.4	27
21	High migration rates shape the postglacial history of amphiâ€Atlantic bryophytes. Molecular Ecology, 2016, 25, 5568-5584.	3.9	22
22	Improving intraspecific allele networks inferred by maximum parsimony. Methods in Ecology and Evolution, 2016, 7, 90-95.	5.2	3
23	Mitochondrial DNA hyperdiversity and its potential causes in the marine periwinkleMelarhaphe neritoides(Mollusca: Gastropoda). PeerJ, 2016, 4, e2549.	2.0	15
24	Comparative multilocus phylogeography of two Palaearctic spruce bark beetles: influence of contrasting ecological strategies on genetic variation. Molecular Ecology, 2015, 24, 1292-1310.	3.9	34
25	Approximate Bayesian Computation Reveals the Crucial Role of Oceanic Islands for the Assembly of Continental Biodiversity. Systematic Biology, 2015, 64, 579-589.	5.6	63
26	Impact of past climatic changes and resource availability on the population demography of three foodâ€specialist bees. Molecular Ecology, 2015, 24, 1074-1090.	3.9	21
27	Theoretical expectations of the Isolationâ€“Migration model of population evolution for inferring demographic parameters. Methods in Ecology and Evolution, 2015, 6, 610-620.	5.2	6
28	Late Pleistocene molecular dating of past population fragmentation and demographic changes in African rain forest tree species supports the forest refuge hypothesis. Journal of Biogeography, 2015, 42, 1443-1454.	3.0	54
29	Comparative phylogeography of five bumblebees: impact of range fragmentation, range size and diet specialization. Biological Journal of the Linnean Society, 2015, 116, 926-939.	1.6	20
30	Multi-locus DNA sequence variation in a complex of four leaf beetle species with parapatric distributions: Mitochondrial and nuclear introgressions reveal recent hybridization. Molecular Phylogenetics and Evolution, 2014, 78, 14-24.	2.7	12
31	Molecular phylogeny, biogeography, and host plant shifts in the bee genus Melitta (Hymenoptera:) Tj ETQq1 1 0.784314 rgBT /Overlo	2.7	34
32	<scp>spads</scp> 1.0: a toolbox to perform spatial analyses on <scp>DNA</scp> sequence data sets. Molecular Ecology Resources, 2014, 14, 647-651.	4.8	91
33	INFERRING THE PAST AND PRESENT CONNECTIVITY ACROSS THE RANGE OF A NORTH AMERICAN LEAF BEETLE: COMBINING ECOLOGICAL NICHE MODELING AND A GEOGRAPHICALLY EXPLICIT MODEL OF COALESCENCE. Evolution; International Journal of Organic Evolution, 2014, 68, n/a-n/a.	2.3	19
34	Comparing Phylogeographic Hypotheses by Simulating DNA Sequences under a Spatially Explicit Model of Coalescence. Molecular Biology and Evolution, 2014, 31, 3359-3372.	8.9	14
35	Climate change and the spread of vectorâ€borne diseases: using approximate <scp>B</scp>ayesian computation to compare invasion scenarios for the bluetongue virus vector <scp>C</scp>ulicoides imicola in <scp>I</scp>taly. Molecular Ecology, 2013, 22, 2456-2466.	3.9	28
36	Pre-adaptations and the evolution of pollination by sexual deception: Cope's rule of specialization revisited. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 4786-4794.	2.6	72

#	Article	IF	Citations
37	Trees and/or networks to display intraspecific DNA sequence variation?. Molecular Ecology, 2012, 21, 3385-3390.	3.9	30
38	Conflicting mitochondrial and nuclear phylogeographic signals and evolution of host-plant shifts in the boreo-montane leaf beetle Chrysomela lapponica. Molecular Phylogenetics and Evolution, 2011, 61, 686-696.	2.7	23
39	TESTING PHYLOGEOGRAPHIC HYPOTHESES IN A EURO-SIBERIAN COLD-ADAPTED LEAF BEETLE WITH COALESCENT SIMULATIONS. Evolution; International Journal of Organic Evolution, 2009, 63, 2717-2729.	2.3	42
40	Genetic differentiation among European samples of the arcticâ€alpine leaf beetle, ChrysomelaÂlapponica. Entomologia Experimentalis Et Applicata, 2008, 129, 181-188.	1.4	6
41	Morphological and mitochondrial DNA analyses indicate the presence of a hybrid zone between two species of leaf beetle (Coleoptera; Chrysomelidae) in Southern Spain. Biological Journal of the Linnean Society, 2008, 94, 105-114.	1.6	1
42	Controlling Population Evolution in the Laboratory to Evaluate Methods of Historical Inference. PLoS ONE, 2008, 3, e2960.	2.5	9
43	PROGRAM NOTE: TREES SIFTER 1.0: an approximate method to estimate the time to the most recent common ancestor of a sample of DNA sequences. Molecular Ecology Notes, 2007, 7, 418-421.	1.7	3
44	Inferring contemporary levels of gene flow and demographic history in a local population of the leaf beetle Gonioctena olivacea from mitochondrial DNA sequence variation. Molecular Ecology, 2005, 14, 1641-1653.	3.9	17
45	Evaluating Intraspecific â€œNetworkâ€•Construction Methods Using Simulated Sequence Data: Do Existing Algorithms Outperform the Global Maximum Parsimony Approach?. Systematic Biology, 2005, 54, 363-372.	5.6	132
46	Structure and Evolution of the Mitochondrial Control Region of Leaf Beetles (Coleoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 387 Td Evolution, 2003, 56, 38-45.	1.8	23
47	The major opsin gene is useful for inferring higher level phylogenetic relationships of the corbiculate bees. Molecular Phylogenetics and Evolution, 2003, 28, 610-613.	2.7	21
48	Phylogenetic relationships among microgastrine braconid wasp genera based on data from the 16S, COI and 28S genes and morphology. Systematic Entomology, 2002, 27, 337-359.	3.9	54
49	Phylogeography of the Vosges mountains populations of Gonioctena pallida (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 1751-1763.	3.9	36
50	Multiple Molecular Data Sets Suggest Independent Origins of Highly Eusocial Behavior in Bees (Hymenoptera:Apinae). Systematic Biology, 2001, 50, 194-214.	5.6	85
51	The Major Opsin in Bees (Insecta: Hymenoptera): A Promising Nuclear Gene for Higher Level Phylogenetics. Molecular Phylogenetics and Evolution, 1999, 12, 168-176.	2.7	89
52	Phylogenetic Signal in the COI, 16S, and 28S Genes for Inferring Relationships among Genera of Microgastrinae (Hymenoptera; Braconidae): Evidence of a High Diversification Rate in This Group of Parasitoids. Molecular Phylogenetics and Evolution, 1999, 12, 282-294.	2.7	131
53	Phylogenetic Analyses of DNA and Allozyme Data Suggest that Gonioctena Leaf Beetles (Coleoptera;) Tj ETQq1 1 0.784314 rgBT /Ove Systematic Biology, 1997, 46, 722-747.	5.6	68