

Markus Pfenninger

List of Publications by Year in descending order

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Version: 2024-02-01

110
papers

6,312
citations

94381

37
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76872

74
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134
all docs

134
docs citations

134
times ranked

8599
citing authors

#	ARTICLE	IF	CITATIONS
1	Photoperiod is an important seasonal selection factor in <i>Chironomus riparius</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 101	0.7	7
2	Whole genome sequencing and RNA-seq evaluation allowed to detect Cd adaptation footprint in <i>Chironomus riparius</i> . <i>Science of the Total Environment</i> , 2022, 819, 152843.	3.9	6
3	On the use of population genomic time series for environmental monitoring. <i>American Journal of Botany</i> , 2022, 109, 497-499.	0.8	3
4	Spontaneous rate of clonal single nucleotide mutations in <i>Daphnia galeata</i> . <i>PLoS ONE</i> , 2022, 17, e0265632.	1.1	2
5	Polyamide microplastic exposure elicits rapid, strong and genome-wide evolutionary response in the freshwater non-biting midge <i>Chironomus riparius</i> . <i>Chemosphere</i> , 2022, 299, 134452.	4.2	8
6	ModEst: Accurate estimation of genome size from next generation sequencing data. <i>Molecular Ecology Resources</i> , 2022, 22, 1454-1464.	2.2	17
7	Population Genomic Time Series Data of a Natural Population Suggests Adaptive Tracking of Fluctuating Environmental Changes. <i>Integrative and Comparative Biology</i> , 2022, 62, 1812-1826.	0.9	4
8	Measuring mutagenicity in ecotoxicology: A case study of Cd exposure in <i>Chironomus riparius</i> . <i>Environmental Pollution</i> , 2021, 272, 116004.	3.7	13
9	A multigenerational approach can detect early Cd pollution in <i>Chironomus riparius</i> . <i>Chemosphere</i> , 2021, 262, 127815.	4.2	9
10	Little parallelism in genomic signatures of local adaptation in two sympatric, cryptic sister species. <i>Journal of Evolutionary Biology</i> , 2021, 34, 937-952.	0.8	9
11	Genomic divergence landscape in recurrently hybridizing <i>Chironomus</i> sister taxa suggests stable steady state between mutual gene flow and isolation. <i>Evolution Letters</i> , 2021, 5, 86-100.	1.6	5
12	De novo Genome Assembly of the Raccoon Dog (<i>Nyctereutes procyonoides</i>). <i>Frontiers in Genetics</i> , 2021, 12, 658256.	1.1	11
13	Whole-genome re-sequencing data to infer historical demography and speciation processes in land snails: the study of two <i>Candidula</i> sister species. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200156.	1.8	8
14	De novo genome assembly of the land snail <i>Candidula unifasciata</i> (Mollusca: Gastropoda). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	8
15	Genomic basis for drought resistance in European beech forests threatened by climate change. <i>ELife</i> , 2021, 10, .	2.8	33
16	Temperature dependence of spontaneous mutation rates. <i>Genome Research</i> , 2021, 31, 1582-1589.	2.4	31
17	A Chromosome-Level Genome Assembly of the European Beech (<i>Fagus sylvatica</i>) Reveals Anomalies for Organelle DNA Integration, Repeat Content and Distribution of SNPs. <i>Frontiers in Genetics</i> , 2021, 12, 691058.	1.1	17
18	Hybridization Dynamics and Extensive Introgression in the <i>Daphnia longispina</i> Species Complex: New Insights from a High-Quality <i>Daphnia galeata</i> Reference Genome. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	11

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19	Combining environmental DNA and species distribution modeling to evaluate reintroduction success of a freshwater fish. <i>Ecological Applications</i> , 2020, 30, e02034.	1.8	18
20	A comprehensive phylogeographic study of <i>Arion vulgaris</i> Moquin-Tandon, 1855 (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70).	0.7	11
21	Genomic processes underlying rapid adaptation of a natural <i>Chironomus riparius</i> population to unintendedly applied experimental selection pressures. <i>Molecular Ecology</i> , 2020, 29, 536-548.	2.0	29
22	Climate Change Genomics Calls for Standardized Data Reporting. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	26
23	Range-wide patterns of human-mediated hybridisation in European wildcats. <i>Conservation Genetics</i> , 2020, 21, 247-260.	0.8	31
24	Evolutionary genomics can improve prediction of species' responses to climate change. <i>Evolution Letters</i> , 2020, 4, 4-18.	1.6	190
25	A High-Quality Genome Assembly from Short and Long Reads for the Non-biting Midge <i>Chironomus riparius</i> (Diptera). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1151-1157.	0.8	22
26	Hybrid Genome Assembly of a Neotropical Mutualistic Ant. <i>Genome Biology and Evolution</i> , 2019, 11, 2306-2311.	1.1	11
27	Establishing laboratory cultures and performing ecological and evolutionary experiments with the emerging model species <i>Chironomus riparius</i> . <i>Journal of Applied Entomology</i> , 2019, 143, 584-592.	0.8	12
28	An experimental assessment of reproductive isolation and its consequences for seasonal hybridization dynamics. <i>Biological Journal of the Linnean Society</i> , 2019, 126, 327-337.	0.7	4
29	Modelling seasonal dynamics, population stability, and pest control in <i>Aedes japonicus japonicus</i> (Diptera: Culicidae). <i>Parasites and Vectors</i> , 2019, 12, 142.	1.0	16
30	The genomic footprint of climate adaptation in <i>Chironomus riparius</i> . <i>Molecular Ecology</i> , 2018, 27, 1439-1456.	2.0	54
31	First insights into the phylogeny of deep-sea glass sponges (Hexactinellida) from polymetallic nodule fields in the Clarion-Clipperton Fracture Zone (CCFZ), northeastern Pacific. <i>Hydrobiologia</i> , 2018, 811, 283-293.	1.0	9
32	Molecular phylogeny of <i>Candidula</i> (Geomitridae) land snails inferred from mitochondrial and nuclear markers reveals the polyphyly of the genus. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 357-368.	1.2	13
33	Transcriptomic responses to predator kairomones in embryos of the aquatic snail <i>Radix balthica</i> . <i>Ecology and Evolution</i> , 2018, 8, 11071-11082.	0.8	1
34	Rapid adaptation to high temperatures in <i>Chironomus riparius</i> . <i>Ecology and Evolution</i> , 2018, 8, 12780-12789.	0.8	18
35	Environmental DNA Time Series in Ecology. <i>Trends in Ecology and Evolution</i> , 2018, 33, 945-957.	4.2	152
36	Thermal experiments with the Asian bush mosquito (<i>Aedes japonicus japonicus</i>) (Diptera: Culicidae) and implications for its distribution in Germany. <i>Parasites and Vectors</i> , 2018, 11, 81.	1.0	42

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37	A reference genome of the European beech (<i>Fagus sylvatica</i> L.). <i>GigaScience</i> , 2018, 7, .	3.3	58
38	The evolutionary history of bears is characterized by gene flow across species. <i>Scientific Reports</i> , 2017, 7, 46487.	1.6	176
39	Global patterns of thermal tolerances and vulnerability of endotherms to climate change remain robust irrespective of varying data suitability criteria. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170232.	1.2	5
40	Adaptive differentiation coincides with local bioclimatic conditions along an elevational cline in populations of a lichen-forming fungus. <i>BMC Evolutionary Biology</i> , 2017, 17, 93.	3.2	39
41	The influence of thermal tolerances on geographical ranges of endotherms. <i>Global Ecology and Biogeography</i> , 2017, 26, 650-668.	2.7	36
42	<i>Chironomus riparius</i> (Diptera) genome sequencing reveals the impact of minisatellite transposable elements on population divergence. <i>Molecular Ecology</i> , 2017, 26, 3256-3275.	2.0	15
43	Combining De Novo Peptide Sequencing Algorithms, A Synergistic Approach to Boost Both Identifications and Confidence in Bottom-up Proteomics. <i>Journal of Proteome Research</i> , 2017, 16, 3209-3218.	1.8	14
44	Direct estimation of the spontaneous mutation rate by short-term mutation accumulation lines in <i>Chironomus riparius</i> . <i>Evolution Letters</i> , 2017, 1, 86-92.	1.6	56
45	DISMS2: A flexible algorithm for direct proteome-wide distance calculation of LC-MS/MS runs. <i>BMC Bioinformatics</i> , 2017, 18, 148.	1.2	15
46	An Annotated Draft Genome for <i>Radix auricularia</i> (Gastropoda, Mollusca). <i>Genome Biology and Evolution</i> , 2017, 9, 585-592.	1.1	57
47	Positive selection on panpulmonate mitogenomes provide new clues on adaptations to terrestrial life. <i>BMC Evolutionary Biology</i> , 2016, 16, 164.	3.2	41
48	Support for the evolutionary speed hypothesis from intraspecific population genetic data in the non-biting midge <i>Chironomus riparius</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152413.	1.2	41
49	Phylogenetic analyses of gazelles reveal repeated transitions of key ecological traits and provide novel insights into the origin of the genus <i>Gazella</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 1-10.	1.2	13
50	Molecular phylogeny of the Ellobiidae (Gastropoda: Panpulmonata) supports independent terrestrial invasions. <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 43-54.	1.2	25
51	Standardized Laboratory Feeding of Larval <i>Aedes japonicus japonicus</i> (Diptera: Culicidae). <i>Journal of Insect Science</i> , 2015, 15, 144.	0.6	6
52	Unique evolutionary trajectories in repeated adaptation to hydrogen sulphide-toxic habitats of a neotropical fish (<i>Poecilia mexicana</i>). <i>Molecular Ecology</i> , 2015, 24, 5446-5459.	2.0	49
53	Global variation in thermal physiology of birds and mammals: evidence for phylogenetic niche conservatism only in the tropics. <i>Journal of Biogeography</i> , 2015, 42, 2187-2196.	1.4	73
54	Positive selection in development and growth rate regulation genes involved in species divergence of the genus <i>Radix</i> . <i>BMC Evolutionary Biology</i> , 2015, 15, 164.	3.2	13

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55	Relocation, high-latitude warming and host genetic identity shape the foliar fungal microbiome of poplars. <i>Molecular Ecology</i> , 2015, 24, 235-248.	2.0	125
56	Characterizing a hybrid zone between a cryptic species pair of freshwater snails. <i>Molecular Ecology</i> , 2015, 24, 643-655.	2.0	19
57	Misperceived invasion: the Lusitanian slug (<i>Ariolimax lusitanicus</i> auct.) Tj ETQq1 1 0.784314 rgBT /Overlo <C>entral <E>urope. <i>Evolutionary Applications</i> , 2014, 7, 702-713.	1.5	48
58	Noninvasive genetic assessment of brown bear population structure in Bulgarian mountain regions. <i>Mammalian Biology</i> , 2014, 79, 268-276.	0.8	48
59	Control Region Length Dynamics Potentially Drives Amino Acid Evolution in Tarsier Mitochondrial Genomes. <i>Journal of Molecular Evolution</i> , 2014, 79, 40-51.	0.8	8
60	Global variation in thermal tolerances and vulnerability of endotherms to climate change. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141097.	1.2	217
61	Parallel evolution of cox genes in H ₂ S-tolerant fish as key adaptation to a toxic environment. <i>Nature Communications</i> , 2014, 5, 3873.	5.8	75
62	Utility of island populations in reintroduction programmes – relationships between Arabian gazelles (<i>Gazella arabica</i>) from the Farasan Archipelago and endangered mainland populations. <i>Molecular Ecology</i> , 2014, 23, 1910-1922.	2.0	8
63	Genomic basis of ecological niche divergence among cryptic sister species of non-biting midges. <i>BMC Genomics</i> , 2013, 14, 384.	1.2	25
64	GENETIC DIFFERENTIATION AND SELECTION AGAINST MIGRANTS IN EVOLUTIONARILY REPLICATED EXTREME ENVIRONMENTS. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2647-2661.	1.1	58
65	Evolutionary determinants of population differences in population growth rate – habitat temperature interactions in <i>Chironomus riparius</i> . <i>Oecologia</i> , 2013, 172, 585-594.	0.9	20
66	Phylogenetic and population genetic analyses suggest a potential species boundary between Mountain (Gazella gazella) and Arabian Gazelles (G. arabica) in the Levant. <i>Mammalian Biology</i> , 2013, 78, 383-386.	0.8	19
67	The impact of global climate change on genetic diversity within populations and species. <i>Molecular Ecology</i> , 2013, 22, 925-946.	2.0	500
68	Twelve new microsatellite loci for the sulphur molly (Poecilia sulphuraria) and the related Atlantic molly (P. mexicana). <i>Conservation Genetics Resources</i> , 2012, 4, 935-937.	0.4	6
69	Taxonomic assessment of Lumbricidae (Oligochaeta) earthworm genera using DNA barcodes. <i>European Journal of Soil Biology</i> , 2012, 48, 41-47.	1.4	35
70	Methodological framework for projecting the potential loss of intraspecific genetic diversity due to global climate change. <i>BMC Evolutionary Biology</i> , 2012, 12, 224.	3.2	29
71	On the Processes Shaping Small-Scale Population Structure in <i>Radix balthica</i> (Linnaeus 1758). <i>Malacologia</i> , 2012, 55, 219-233.	0.2	12
72	Experimental evidence for niche segregation in a sister species pair of non-biting midges. <i>Hydrobiologia</i> , 2012, 691, 203-212.	1.0	12

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73	Impact of genetic diversity and inbreeding on the life-history of Chironomus midges over consecutive generations. <i>Chemosphere</i> , 2012, 88, 988-993.	4.2	8
74	Alpine Crossroads or Origin of Genetic Diversity? Comparative Phylogeography of Two Sympatric Microgastropod Species. <i>PLoS ONE</i> , 2012, 7, e37089.	1.1	17
75	A new approach to an old conundrum—DNA barcoding sheds new light on phenotypic plasticity and morphological stasis in microsnails (Gastropoda, Pulmonata, Carychiidae). <i>Molecular Ecology Resources</i> , 2011, 11, 255-265.	2.2	52
76	A genetic basis for intraspecific differences in developmental timing?. <i>Evolution & Development</i> , 2011, 13, 542-548.	1.1	22
77	A phylogeographic framework for the conservation of Saharan and Arabian Dorcas gazelles (<i>Artiodactyla: Bovidae</i>). <i>Organisms Diversity and Evolution</i> , 2011, 11, 317-329.	0.7	29
78	Factors and processes shaping the population structure and distribution of genetic variation across the species range of the freshwater snail <i>radix balthica</i> (Pulmonata, Basommatophora). <i>BMC Evolutionary Biology</i> , 2011, 11, 135.	3.2	56
79	Short read Illumina data for the de novo assembly of a non-model snail species transcriptome (<i>Radix</i>). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> 2011, 12, 317.	1.2	137
80	Evolution of freshwater crab diversity in the Aegean region (Crustacea: Brachyura: Potamidae). <i>Molecular Phylogenetics and Evolution</i> , 2011, 59, 23-33.	1.2	47
81	Phylogeography of a Land Snail Suggests Trans-Mediterranean Neolithic Transport. <i>PLoS ONE</i> , 2011, 6, e20734.	1.1	23
82	When Indian crabs were not yet Asian - biogeographic evidence for Eocene proximity of India and Southeast Asia. <i>BMC Evolutionary Biology</i> , 2010, 10, 287.	3.2	63
83	Temporal speciation pattern in the western Mediterranean genus <i>Tudorella</i> P. Fischer, 1885 (Gastropoda, Pomatiidae) supports the Tyrrhenian vicariance hypothesis. <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 427-436.	1.2	48
84	A species delimitation approach in the <i>Trochulus sericeus/hispidus</i> complex reveals two cryptic species within a sharp contact zone. <i>BMC Evolutionary Biology</i> , 2009, 9, 171.	3.2	49
85	Disjunct distribution of the Mediterranean freshwater crab <i>Potamon fluviatile</i> —natural expansion or human introduction?. <i>Biological Invasions</i> , 2009, 11, 2209-2221.	1.2	33
86	Rapid genetic erosion in pollutant-exposed experimental chironomid populations. <i>Environmental Pollution</i> , 2009, 157, 881-886.	3.7	66
87	Climate-driven range dynamics of the freshwater limpet, <i>Ancylus fluviatilis</i> (Pulmonata). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> 2009, 11, 2209-2221.	1.4	29
88	Reproductive Isolation and Ecological Niche Partition among Larvae of the Morphologically Cryptic Sister Species <i>Chironomus riparius</i> and <i>C. piger</i> . <i>PLoS ONE</i> , 2008, 3, e2157.	1.1	30
89	Intraspecific range dynamics and niche evolution in <i>Candidula</i> land snail species. <i>Biological Journal of the Linnean Society</i> , 2007, 90, 303-317.	0.7	33
90	Utility of DNA taxonomy and barcoding for the inference of larval community structure in morphologically cryptic <i>Chironomus</i> (Diptera) species. <i>Molecular Ecology</i> , 2007, 16, 1957-1968.	2.0	143

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91	Cryptic animal species are homogeneously distributed among taxa and biogeographical regions. BMC Evolutionary Biology, 2007, 7, 121.	3.2	512
92	Comparing the efficacy of morphologic and DNA-based taxonomy in the freshwater gastropod genus Radix (Basommatophora, Pulmonata). BMC Evolutionary Biology, 2006, 6, 100.	3.2	105
93	Rangewide phylogeography of a terrestrial slug in Europe: evidence for Alpine refugia and rapid colonization after the Pleistocene glaciations. Molecular Ecology, 2005, 14, 1133-1150.	2.0	92
94	INFERENCE OF A RADIATION IN MASTUS (GASTROPODA, PULMONATA, ENIDAE) ON THE ISLAND OF CRETE. Evolution; International Journal of Organic Evolution, 2005, 59, 991-1005.	1.1	23
95	Why do snails have hairs? A Bayesian inference of character evolution. BMC Evolutionary Biology, 2005, 5, 59.	3.2	55
96	INFERENCE OF A RADIATION IN MASTUS (GASTROPODA, PULMONATA, ENIDAE) ON THE ISLAND OF CRETE. Evolution; International Journal of Organic Evolution, 2005, 59, 991.	1.1	59
97	A new Trochulus species from Switzerland (Gastropoda: Pulmonata: Hygromiidae). Archiv Fur Molluskenkunde, 2005, 134, 261-269.	0.1	7
98	Impact of a flood disaster on sediment toxicity in a major river system – the Elbe flood 2002 as a case study. Environmental Pollution, 2005, 134, 87-95.	3.7	44
99	Inference of a radiation in Mastus (Gastropoda, Pulmonata, Enidae) on the island of Crete. Evolution; International Journal of Organic Evolution, 2005, 59, 991-1005.	1.1	11
100	Molecular phylogeny and character evolution in the Western Palaearctic Helicidae s.l. (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.2	51
101	Evidence for survival of Pleistocene climatic changes in Northern refugia by the land snail Trochoidea geyeri (SoÅ³s 1926) (Helicellinae, Stylommatophora). BMC Evolutionary Biology, 2003, 3, 8.	3.2	47
102	Ecological and morphological differentiation among cryptic evolutionary lineages in freshwater limpets of the nominal formâ€”group Ancyclus fluviatilis (O.F. MÃ¼ller, 1774). Molecular Ecology, 2003, 12, 2731-2745.	2.0	58
103	Evidence for ecological speciation in the sister species Candidula unifasciata (Poiret, 1801) and C.â€”frugosiuscula (Michaud, 1831) (Helicellinae, Gastropoda). Biological Journal of the Linnean Society, 2003, 79, 611-628.	0.7	32
104	Simulated bottlenecks and loss of rare alleles: implications on the conservation genetics of two gastropod species. Journal for Nature Conservation, 2003, 11, 77-81.	0.8	4
105	PHYLOGEOGRAPHIC HISTORY OF THE LAND SNAIL CANDIDULA UNIFASCIATA (HELICELLINAE,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 International Journal of Organic Evolution, 2002, 56, 1776.	1.1	59
106	Relationship between microspatial population genetic structure and habitat heterogeneity in Pomatias elegans (O.F. MÃ¼ller 1774) (Caenogastropoda, Pomatiasidae). Biological Journal of the Linnean Society, 2002, 76, 565-575.	0.7	33
107	PHYLOGEOGRAPHIC HISTORY OF THE LAND SNAIL CANDIDULA UNIFASCIATA (HELICELLINAE,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 International Journal of Organic Evolution, 2002, 56, 1776-1788.	1.1	1,274
108	Phenotypic evolution and hidden speciation in Candidula unifasciata ssp. (Helicellinae, Gastropoda) inferred by 16S variation and quantitative shell traits. Molecular Ecology, 2001, 10, 2541-2554.	2.0	55

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109	Dynamic microsatellites in transcribed regions of gastropod mitochondrial 16S rDNA. <i>Genome</i> , 2001, 44, 163-166.	0.9	2
110	Northern blot analysis of simple repetitive sequence transcription in plants. <i>Electrophoresis</i> , 1996, 17, 1183-1189.	1.3	4