

SÃ©bastien J Puechmaille

List of Publications by Year in descending order

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Version: 2024-02-01

91
papers

4,279
citations

147786

31
h-index

128286

60
g-index

99
all docs

99
docs citations

99
times ranked

5597
citing authors

#	ARTICLE	IF	CITATIONS
1	Population genetics as a tool to elucidate pathogen reservoirs: Lessons from <i>Pseudogymnoascus destructans</i> , the causative agent of White-Nose disease in bats. <i>Molecular Ecology</i> , 2022, 31, 675-690.	3.9	7
2	Misconceptions and misinformation about bats and viruses. <i>International Journal of Infectious Diseases</i> , 2021, 105, 606-607.	3.3	4
3	Determinants of defence strategies of a hibernating European bat species towards the fungal pathogen <i>Pseudogymnoascus destructans</i> . <i>Developmental and Comparative Immunology</i> , 2021, 119, 104017.	2.3	14
4	Bat Overpasses Help Bats to Cross Roads Safely by Increasing Their Flight Height. <i>Acta Chiropterologica</i> , 2021, 23, .	0.6	0
5	A Rapid, in-Situ Minimally-Invasive Technique to Assess Infections with <i>Pseudogymnoascus destructans</i> in Bats. <i>Acta Chiropterologica</i> , 2021, 23, .	0.6	4
6	Heterothermy and antifungal responses in bats. <i>Current Opinion in Microbiology</i> , 2021, 62, 61-67.	5.1	3
7	Genetic diversity in a long-lived mammal is explained by the past's demographic shadow and current connectivity. <i>Molecular Ecology</i> , 2021, 30, 5048-5063.	3.9	7
8	Mating type determination within a microsatellite multiplex for the fungal pathogen <i>Pseudogymnoascus destructans</i> , the causative agent of white-nose disease in bats. <i>Conservation Genetics Resources</i> , 2020, 12, 45-48.	0.8	6
9	Six reference-quality genomes reveal evolution of bat adaptations. <i>Nature</i> , 2020, 583, 578-584.	27.8	210
10	Timescale and colony-dependent relationships between environmental conditions and plasma oxidative markers in a long-lived bat species. , 2020, 8, coaa083.		1
11	Seasonal patterns of <i>Pseudogymnoascus destructans</i> germination indicate host-pathogen coevolution. <i>Biology Letters</i> , 2020, 16, 20200177.	2.3	9
12	Drivers of longitudinal telomere dynamics in a long-lived bat species, <i>Myotis myotis</i> . <i>Molecular Ecology</i> , 2020, 29, 2963-2977.	3.9	39
13	Did you wash your caving suit? Cavers' role in the potential spread of <i>Pseudogymnoascus destructans</i> , the causative agent of White-Nose Disease. <i>International Journal of Speleology</i> , 2020, 49, 149-159.	1.0	16
14	Mehely's Horseshoe Bat <i>Rhinolophus mehelyi</i> Matschie, 1901. <i>Handbook of the Mammals of Europe</i> , 2020, , 1-28.	0.3	0
15	The patterns and possible causes of global geographical variation in the body size of the greater horseshoe bat (<i>Rhinolophus ferrumequinum</i>). <i>Journal of Biogeography</i> , 2019, 46, 2363-2377.	3.0	15
16	Range expansion is associated with increased survival and fecundity in a long-lived bat species. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190384.	2.6	13
17	Two New Cryptic Bat Species within the <i>Myotis nattereri</i> Species Complex (Vespertilionidae.) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.8	26
18	Unavailable names in the <i>Myotis nattereri</i> species complex. <i>Journal of Biogeography</i> , 2019, 46, 2145-2146.	3.0	3

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19	A continent-scale study of the social structure and phylogeography of the bent-wing bat, <i>Miniopterus schreibersii</i> (Mammalia: Chiroptera), using new microsatellite data. <i>Journal of Mammalogy</i> , 2019, , .	1.3	3
20	Phenotypic plasticity closely linked to climate at origin and resulting in increased mortality under warming and frost stress in a common grass. <i>Ecology and Evolution</i> , 2019, 9, 1344-1352.	1.9	17
21	Longitudinal comparative transcriptomics reveals unique mechanisms underlying extended healthspan in bats. <i>Nature Ecology and Evolution</i> , 2019, 3, 1110-1120.	7.8	70
22	Considering adaptive genetic variation in climate change vulnerability assessment reduces species range loss projections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10418-10423.	7.1	308
23	Major roads have important negative effects on insectivorous bat activity. <i>Biological Conservation</i> , 2019, 235, 53-62.	4.1	35
24	Bat overpasses as an alternative solution to restore habitat connectivity in the context of road requalification. <i>Ecological Engineering</i> , 2019, 131, 34-38.	3.6	11
25	Integrating population genetics to define conservation units from the core to the edge of <i>Rhinolophus ferrumequinum</i> western range. <i>Ecology and Evolution</i> , 2019, 9, 12272-12290.	1.9	12
26	Bat overpasses: An insufficient solution to restore habitat connectivity across roads. <i>Journal of Applied Ecology</i> , 2019, 56, 573-584.	4.0	20
27	Screening and Biosecurity for White-Nose Fungus <i>Pseudogymnoascus destructans</i> (Ascomycota): Tj ETQq1 1 0.784314 rgBT ₅ /Overlo 0.6	0.6	0
28	Identifying unusual mortality events in bats: a baseline for bat hibernation monitoring and whiteâ€nose syndrome research. <i>Mammal Review</i> , 2018, 48, 224-228.	4.8	20
29	SARS-CoV related Betacoronavirus and diverse Alphacoronavirus members found in western old-world. <i>Virology</i> , 2018, 517, 88-97.	2.4	71
30	Growing old, yet staying young: The role of telomeres in batsâ€™ exceptional longevity. <i>Science Advances</i> , 2018, 4, eaao0926.	10.3	120
31	Mycobiomes of sympatric <i>Amorphophallus albispatus</i> (Araceae) and <i>Camellia sinensis</i> (Theaceae) â€ a case study reveals clear tissue preferences and differences in diversity and composition. <i>Mycological Progress</i> , 2018, 17, 489-500.	1.4	7
32	Combining noninvasive genetics and a new mammalian sexâ€linked marker provides new tools to investigate population size, structure and individual behaviour: An application to bats. <i>Molecular Ecology Resources</i> , 2018, 18, 217-228.	4.8	18
33	Population level mitogenomics of long-lived bats reveals dynamic heteroplasmy and challenges the Free Radical Theory of Ageing. <i>Scientific Reports</i> , 2018, 8, 13634.	3.3	24
34	Using Approximate Bayesian Computation to infer sex ratios from acoustic data. <i>PLoS ONE</i> , 2018, 13, e0199428.	2.5	15
35	Maleâ€biased dispersal and the potential impact of humanâ€induced habitat modifications on the Neotropical bat <i>Trachops cirrhosus</i> . <i>Ecology and Evolution</i> , 2018, 8, 6065-6080.	1.9	7
36	Is there a link between aging and microbiome diversity in exceptional mammalian longevity?. <i>PeerJ</i> , 2018, 6, e4174.	2.0	28

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37	The complete mitochondrial genome of the Greater Mouse-Eared bat, <i>Myotis myotis</i> (Chiroptera: Vespertilionidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 347-349.	0.7	7
38	Evidence for genetic variation in Natterer's bats (<i>Myotis nattereri</i>) across three regions in Germany but no evidence for co-variation with their associated astroviruses. BMC Evolutionary Biology, 2017, 17, 5.	3.2	14
39	Characterization of Microsatellites in <i>Pseudogymnoascus destructans</i> for White-nose Syndrome Genetic Analysis. Journal of Wildlife Diseases, 2017, 53, 869.	0.8	10
40	Towards Navigating the Minotaur's Labyrinth: Cryptic Diversity and Taxonomic Revision within the Speciose Genus <i>Hipposideros</i> (Hipposideridae). Acta Chiropterologica, 2017, 19, 1-18.	0.6	34
41	Conspecific and heterospecific social groups affect each other's resource use: a study on roost sharing among bat colonies. Animal Behaviour, 2017, 123, 329-338.	1.9	22
42	Stabilization of a bat-pitcher plant mutualism. Scientific Reports, 2017, 7, 13170.	3.3	1
43	Which temporal resolution to consider when investigating the impact of climatic data on population dynamics? The case of the lesser horseshoe bat (<i>Rhinolophus hipposideros</i>). Oecologia, 2017, 184, 749-761.	2.0	14
44	A Potent Anti-Inflammatory Response in Bat Macrophages May Be Linked to Extended Longevity and Viral Tolerance. Acta Chiropterologica, 2017, 19, 219-228.	0.6	46
45	Phylogenetics of a Fungal Invasion: Origins and Widespread Dispersal of White-Nose Syndrome. MBio, 2017, 8, .	4.1	70
46	The program <code>structure</code> does not reliably recover the correct population structure when sampling is uneven: subsampling and new estimators alleviate the problem. Molecular Ecology Resources, 2016, 16, 608-627.	4.8	672
47	Phylogeographic-based conservation implications for the New Zealand long-tailed bat, (<i>Chalinolobus</i>) Tj ETQq1 1 0.784314 rgBT /Ove Conservation Genetics, 2016, 17, 1067-1079.	1.5	14
48	A nonlethal sampling method to obtain, generate and assemble whole blood transcriptomes from small, wild mammals. Molecular Ecology Resources, 2016, 16, 150-162.	4.8	38
49	The Effects of Human-Mediated Habitat Fragmentation on a Sedentary Woodland-Associated Species (<i>Rhinolophus hipposideros</i>) at Its Range Margin. Acta Chiropterologica, 2016, 18, 377.	0.6	18
50	Patterns of orofacial clefting in the facial morphology of bats: a possible naturally occurring model of cleft palate. Journal of Anatomy, 2016, 229, 657-672.	1.5	11
51	Acoustic identification of Mexican bats based on taxonomic and ecological constraints on call design. Methods in Ecology and Evolution, 2016, 7, 1082-1091.	5.2	51
52	Circum-Mediterranean phylogeography of a bat coupled with past environmental niche modeling: A new paradigm for the recolonization of Europe?. Molecular Phylogenetics and Evolution, 2016, 99, 323-336.	2.7	19
53	Nuclear introns outperform mitochondrial DNA in inter-specific phylogenetic reconstruction: Lessons from horseshoe bats (<i>Rhinolophidae</i> : Chiroptera). Molecular Phylogenetics and Evolution, 2016, 97, 196-212.	2.7	77
54	White-Nose Syndrome in Bats. , 2016, , 245-262.		57

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55	Will reduced host connectivity curb the spread of a devastating epidemic?. <i>Molecular Ecology</i> , 2015, 24, 5491-5494.	3.9	3
56	White-Nose Syndrome fungus introduced from Europe to North America. <i>Current Biology</i> , 2015, 25, R217-R219.	3.9	125
57	Disease alters macroecological patterns of North American bats. <i>Global Ecology and Biogeography</i> , 2015, 24, 741-749.	5.8	206
58	How and Why Overcome the Impediments to Resolution: Lessons from rhinolophid and hipposiderid Bats. <i>Molecular Biology and Evolution</i> , 2015, 32, 313-333.	8.9	82
59	Bats Are Acoustically Attracted to Mutualistic Carnivorous Plants. <i>Current Biology</i> , 2015, 25, 1911-1916.	3.9	39
60	A new species of the <i>Miniopterus</i> species complex (Chiroptera: Miniopteridae) from the Maghreb Region, North Africa. <i>Zootaxa</i> , 2014, 3794, 108.	0.5	25
61	Further Evidence for Cryptic North-Western Refugia in Europe? Mitochondrial Phylogeography of the Sibling Species <i>Pipistrellus pipistrellus</i> and <i>Pipistrellus pygmaeus</i> . <i>Acta Chiropterologica</i> , 2014, 16, 263-277.	0.6	15
62	Female Mate Choice Can Drive the Evolution of High Frequency Echolocation in Bats: A Case Study with <i>Rhinolophus mehelyi</i> . <i>PLoS ONE</i> , 2014, 9, e103452.	2.5	63
63	Non-invasive genetics can help find rare species: a case study with <i>Rhinolophus mehelyi</i> and <i>R. euryale</i> (Rhinolophidae: Chiroptera) in Western Europe. <i>Mammalia</i> , 2014, 78, .	0.7	14
64	Scale-dependent effects of landscape variables on gene flow and population structure in bats. <i>Diversity and Distributions</i> , 2014, 20, 1173-1185.	4.1	34
65	The shaping of genetic variation in edge populations under past and future climate change. <i>Ecology Letters</i> , 2013, 16, 1258-1266.	6.4	99
66	Phylogeography and postglacial recolonization of Europe by <i>Rhinolophus hipposideros</i> : evidence from multiple genetic markers. <i>Molecular Ecology</i> , 2013, 22, 4055-4070.	3.9	56
67	Factors Affecting Geographic Variation in Echolocation Calls of the Endemic <i>Myotis davidii</i> in China. <i>Ethology</i> , 2013, 119, 881-890.	1.1	17
68	Skin Lesions in European Hibernating Bats Associated with <i>Geomyces destructans</i> , the Etiologic Agent of White-Nose Syndrome. <i>PLoS ONE</i> , 2013, 8, e74105.	2.5	40
69	Empirical Assessment of Non-Invasive Population Genetics in Bats: Comparison of DNA Quality from Faecal and Tissue Samples. <i>Acta Chiropterologica</i> , 2012, 14, 45-52.	0.6	29
70	A continental-scale tool for acoustic identification of European bats. <i>Journal of Applied Ecology</i> , 2012, 49, 1064-1074.	4.0	144
71	Biogeography of Old World emballonurine bats (Chiroptera: Emballonuridae) inferred with mitochondrial and nuclear DNA. <i>Molecular Phylogenetics and Evolution</i> , 2012, 64, 204-211.	2.7	25
72	Genetic analyses reveal further cryptic lineages within the <i>Myotis nattereri</i> species complex. <i>Mammalian Biology</i> , 2012, 77, 224-228.	1.5	47

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73	Phylogeny of the Emballonurini (Emballonuridae) with descriptions of a new genus and species from Madagascar. <i>Journal of Mammalogy</i> , 2012, 93, 1440-1455.	1.3	18
74	A new species of <i>Hipposideros</i> (Chiroptera: Hipposideridae) from Vietnam. <i>Journal of Mammalogy</i> , 2012, 93, 1-11.	1.3	26
75	Horseshoe Bats Recognise the Sex of Conspecifics from Their Echolocation Calls. <i>Acta Chiropterologica</i> , 2012, 14, 161-166.	0.6	32
76	Resolving a mammal mystery: the identity of <i>Paracoelops megalotis</i> (Chiroptera: Hipposideridae). <i>Zootaxa</i> , 2012, 3505, 75.	0.5	7
77	Systematics of the <i>Hipposideros turpis</i> complex and a description of a new subspecies from Vietnam. <i>Mammal Review</i> , 2012, 42, 166-192.	4.8	39
78	A Taxonomic Review of <i>Rhinolophus coelophyllus</i> Peters 1867 and <i>R. shameli</i> Tate 1943 (Chiroptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	8
79	Effect of Sample Preservation Methods on the Viability of <i>Geomyces destructans</i> , the Fungus Associated with White-Nose Syndrome in Bats. <i>Acta Chiropterologica</i> , 2011, 13, 217-221.	0.6	8
80	Pan-European Distribution of White-Nose Syndrome Fungus (<i>Geomyces destructans</i>) Not Associated with Mass Mortality. <i>PLoS ONE</i> , 2011, 6, e19167.	2.5	180
81	White-nose syndrome: is this emerging disease a threat to European bats?. <i>Trends in Ecology and Evolution</i> , 2011, 26, 570-576.	8.7	82
82	SARS-Coronavirus ancestor's foot-prints in South-East Asian bat colonies and the refuge theory. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1690-1702.	2.3	66
83	A rapid PCR-based assay for identification of cryptic <i>Myotis</i> spp. (<i>M. mystacinus</i> , <i>M. brandtii</i> and <i>M.</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	10
84	The evolution of sensory divergence in the context of limited gene flow in the bumblebee bat. <i>Nature Communications</i> , 2011, 2, 573.	12.8	85
85	White-Nose Syndrome Fungus (<i>Geomyces destructans</i>) in Bat, France. <i>Emerging Infectious Diseases</i> , 2010, 16, 290-293.	4.3	103
86	A Taxonomic Review of <i>Hipposideros halophyllus</i> , with Additional Information on <i>H. ater</i> and <i>H. cineraceus</i> (Chiroptera: Hipposideridae) from Thailand and Myanmar. <i>Acta Chiropterologica</i> , 2010, 12, 29-50.	0.6	11
87	Characterization and multiplex genotyping of 16 polymorphic microsatellite loci in the endangered bumble-bee bat, <i>Craseonycteris thonglongyai</i> (Chiroptera: Craseonycteridae). <i>Conservation Genetics</i> , 2009, 10, 1073-1076.	1.5	3
88	Population size, distribution, threats and conservation status of two endangered bat species <i>Craseonycteris thonglongyai</i> and <i>Hipposideros turpis</i> . <i>Endangered Species Research</i> , 2009, 8, 15-23.	2.4	11
89	Good DNA from bat droppings. <i>Acta Chiropterologica</i> , 2007, 9, 269-276.	0.6	40
90	Empirical evaluation of non-invasive capture-mark-recapture estimation of population size based on a single sampling session. <i>Journal of Applied Ecology</i> , 2007, 44, 843-852.	4.0	96

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91	Characterization of 14 polymorphic microsatellite loci for the lesser horseshoe bat, <i>Rhinolophus hipposideros</i> (Rhinolophidae, Chiroptera). <i>Molecular Ecology Notes</i> , 2005, 5, 941-944.	1.7	25