SÃ©bastien J Puechmaille

List of Publications by Year
in descending order

91 papers	4,279 citations	147726 31 h-index	128225 60 g-index
99 all docs	99 docs citations	99 times ranked	5597 citing authors

#	Article	IF	Citations
1	The program <scp>structure</scp> 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.	2.2	672
2	Considering adaptive genetic variation in climate change vulnerability assessment reduces species range loss projections. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10418-10423.	3.3	308
3	Six reference-quality genomes reveal evolution of bat adaptations. Nature, 2020, 583, 578-584.	13.7	210
4	Disease alters macroecological patterns of <scp>N</scp>orth <scp>A</scp>merican bats. Global Ecology and Biogeography, 2015, 24, 741-749.	2.7	206
5	Pan-European Distribution of White-Nose Syndrome Fungus (Geomyces destructans) Not Associated with Mass Mortality. PLoS ONE, 2011, 6, e19167.	1.1	180
6	A continentalâ€scale tool for acoustic identification of <scp>E</scp>uropean bats. Journal of Applied Ecology, 2012, 49, 1064-1074.	1.9	144
7	White-Nose Syndrome fungus introduced from Europe to North America. Current Biology, 2015, 25, R217-R219.	1.8	125
8	Growing old, yet staying young: The role of telomeres in batsâ€™ exceptional longevity. Science Advances, 2018, 4, eaao0926.	4.7	120
9	White-Nose Syndrome Fungus (<i>Geomyces destructans</i>) in Bat, France. Emerging Infectious Diseases, 2010, 16, 290-293.	2.0	103
10	The shaping of genetic variation in edgeâ€ofâ€range populations under past and future climate change. Ecology Letters, 2013, 16, 1258-1266.	3.0	99
11	Empirical evaluation of non-invasive capture-mark-recapture estimation of population size based on a single sampling session. Journal of Applied Ecology, 2007, 44, 843-852.	1.9	96
12	The evolution of sensory divergence in the context of limited gene flow in the bumblebee bat. Nature Communications, 2011, 2, 573.	5.8	85
13	White-nose syndrome: is this emerging disease a threat to European bats?. Trends in Ecology and Evolution, 2011, 26, 570-576.	4.2	82
14	How and Why Overcome the Impediments to Resolution: Lessons from rhinolophid and hipposiderid Bats. Molecular Biology and Evolution, 2015, 32, 313-333.	3.5	82
15	Nuclear introns outperform mitochondrial DNA in inter-specific phylogenetic reconstruction: Lessons from horseshoe bats (Rhinolophidae: Chiroptera). Molecular Phylogenetics and Evolution, 2016, 97, 196-212.	1.2	77
16	SARS-CoV related Betacoronavirus and diverse Alphacoronavirus members found in western old-world. Virology, 2018, 517, 88-97.	1.1	71
17	Phylogenetics of a Fungal Invasion: Origins and Widespread Dispersal of White-Nose Syndrome. MBio, 2017, 8, .	1.8	70
18	Longitudinal comparative transcriptomics reveals unique mechanisms underlying extended healthspan in bats. Nature Ecology and Evolution, 2019, 3, 1110-1120.	3.4	70

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19	SARS-Coronavirus ancestorâ€™s foot-prints in South-East Asian bat colonies and the refuge theory. Infection, Genetics and Evolution, 2011, 11, 1690-1702.	1.0	66
20	Female Mate Choice Can Drive the Evolution of High Frequency Echolocation in Bats: A Case Study with Rhinolophus mehelyi. PLoS ONE, 2014, 9, e103452.	1.1	63
21	White-Nose Syndrome in Bats. , 2016, , 245-262.		57
22	Phylogeography and postglacial recolonization of Europe by <i>Rhinolophus hipposideros</i>: evidence from multiple genetic markers. Molecular Ecology, 2013, 22, 4055-4070.	2.0	56
23	Acoustic identification of Mexican bats based on taxonomic and ecological constraints on call design. Methods in Ecology and Evolution, 2016, 7, 1082-1091.	2.2	51
24	Genetic analyses reveal further cryptic lineages within the Myotis nattereri species complex. Mammalian Biology, 2012, 77, 224-228.	0.8	47
25	A Potent Anti-Inflammatory Response in Bat Macrophages May Be Linked to Extended Longevity and Viral Tolerance. Acta Chiropterologica, 2017, 19, 219-228.	0.2	46
26	Good DNA from bat droppings. Acta Chiropterologica, 2007, 9, 269-276.	0.2	40
27	Skin Lesions in European Hibernating Bats Associated with Geomyces destructans, the Etiologic Agent of White-Nose Syndrome. PLoS ONE, 2013, 8, e74105.	1.1	40
28	Systematics of the <i>Hipposideros turpis</i> complex and a description of a new subspecies from Vietnam. Mammal Review, 2012, 42, 166-192.	2.2	39
29	Bats Are Acoustically Attracted to Mutualistic Carnivorous Plants. Current Biology, 2015, 25, 1911-1916.	1.8	39
30	Drivers of longitudinal telomere dynamics in a longâ€lived bat species, Myotis myotis. Molecular Ecology, 2020, 29, 2963-2977.	2.0	39
31	A nonlethal sampling method to obtain, generate and assemble whole blood transcriptomes from small, wild mammals. Molecular Ecology Resources, 2016, 16, 150-162.	2.2	38
32	Major roads have important negative effects on insectivorous bat activity. Biological Conservation, 2019, 235, 53-62.	1.9	35
33	Scaleâ€dependent effects of landscape variables on gene flow and population structure in bats. Diversity and Distributions, 2014, 20, 1173-1185.	1.9	34
34	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.	0.2	34
35	Horseshoe Bats Recognise the Sex of Conspecifics from Their Echolocation Calls. Acta Chiropterologica, 2012, 14, 161-166.	0.2	32
36	Empirical Assessment of Non-Invasive Population Genetics in Bats: Comparison of DNA Quality from Faecal and Tissue Samples. Acta Chiropterologica, 2012, 14, 45-52.	0.2	29

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37	Is there a link between aging and microbiome diversity in exceptional mammalian longevity?. PeerJ, 2018, 6, e4174.	0.9	28
38	A new species of<i>Hipposideros</i>(Chiroptera: Hipposideridae) from Vietnam. Journal of Mammalogy, 2012, 93, 1-11.	0.6	26
39	Two New Cryptic Bat Species within the Myotis nattereri Species Complex (Vespertilionidae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.2	26
40	Characterization of 14 polymorphic microsatellite loci for the lesser horseshoe bat, Rhinolophus hipposideros (Rhinolophidae, Chiroptera). Molecular Ecology Notes, 2005, 5, 941-944.	1.7	25
41	Biogeography of Old World emballonurine bats (Chiroptera: Emballonuridae) inferred with mitochondrial and nuclear DNA. Molecular Phylogenetics and Evolution, 2012, 64, 204-211.	1.2	25
42	<p class="HeadingRunIn">A new species of the Miniopterus schreibersii species complex (Chiroptera: Miniopteridae) from the Maghreb Region, North Africa</p>. Zootaxa, 2014, 3794, 108.	0.2	25
43	Population level mitogenomics of long-lived bats reveals dynamic heteroplasmy and challenges the Free Radical Theory of Ageing. Scientific Reports, 2018, 8, 13634.	1.6	24
44	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.	0.8	22
45	Identifying unusual mortality events in bats: a baseline for bat hibernation monitoring and whiteâ€nose syndrome research. Mammal Review, 2018, 48, 224-228.	2.2	20
46	Bat overpasses: An insufficient solution to restore habitat connectivity across roads. Journal of Applied Ecology, 2019, 56, 573-584.	1.9	20
47	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.	1.2	19
48	Phylogeny of the Emballonurini (Emballonuridae) with descriptions of a new genus and species from Madagascar. Journal of Mammalogy, 2012, 93, 1440-1455.	0.6	18
49	The Effects of Human-Mediated Habitat Fragmentation on a Sedentary Woodland-Associated Species (Rhinolophus hipposideros) at Its Range Margin. Acta Chiropterologica, 2016, 18, 377.	0.2	18
50	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. Molecular Ecology Resources, 2018, 18, 217-228.	2.2	18
51	Factors Affecting Geographic Variation in Echolocation Calls of the Endemic <i>Myotis davidii</i> in China. Ethology, 2013, 119, 881-890.	0.5	17
52	Phenotypic plasticity closely linked to climate at origin and resulting in increased mortality under warming and frost stress in a common grass. Ecology and Evolution, 2019, 9, 1344-1352.	0.8	17
53	Did you wash your caving suit? Caversâ€™ role in the potential spread of Pseudogymnoascus destructans, the causative agent of White-Nose Disease. International Journal of Speleology, 2020, 49, 149-159.	0.4	16
54	Further Evidence for Cryptic North-Western Refugia in Europe? Mitochondrial Phylogeography of the Sibling Species<i>Pipistrellus pipistrellus</i>and<i>Pipistrellus pygmaeus</i>. Acta Chiropterologica, 2014, 16, 263-277.	0.2	15

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55	Using Approximate Bayesian Computation to infer sex ratios from acoustic data. PLoS ONE, 2018, 13, e0199428.	1.1	15
56	The patterns and possible causes of global geographical variation in the body size of the greater horseshoe bat (<i>Rhinolophus ferrumequinum</i>). Journal of Biogeography, 2019, 46, 2363-2377.	1.4	15
57	Non-invasive genetics can help find rare species: a case study with Rhinolophus mehelyi and R. euryale (Rhinolophidae: Chiroptera) in Western Europe. Mammalia, 2014, 78, .	0.3	14
58	Phylogeographic-based conservation implications for the New Zealand long-tailed bat, (Chalinolobus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Conservation Genetics, 2016, 17, 1067-1079.	0.8	14
59	Evidence for genetic variation in Nattererâ€™s bats (Myotis nattereri) across three regions in Germany but no evidence for co-variation with their associated astroviruses. BMC Evolutionary Biology, 2017, 17, 5.	3.2	14
60	Which temporal resolution to consider when investigating the impact of climatic data on population dynamics? The case of the lesser horseshoe bat (Rhinolophus hipposideros). Oecologia, 2017, 184, 749-761.	0.9	14
61	Determinants of defence strategies of a hibernating European bat species towards the fungal pathogen Pseudogymnoascus destructans. Developmental and Comparative Immunology, 2021, 119, 104017.	1.0	14
62	Range expansion is associated with increased survival and fecundity in a long-lived bat species. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190384.	1.2	13
63	Integrating population genetics to define conservation units from the core to the edge of <i>Rhinolophus ferrumequinum</i> western range. Ecology and Evolution, 2019, 9, 12272-12290.	0.8	12
64	A Taxonomic Review ofHipposideros halophyllus, with Additional Information onH. aterandH. cineraceus(Chiroptera: Hipposideridae) from Thailand and Myanmar. Acta Chiropterologica, 2010, 12, 29-50.	0.2	11
65	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.	0.9	11
66	Bat overpasses as an alternative solution to restore habitat connectivity in the context of road requalification. Ecological Engineering, 2019, 131, 34-38.	1.6	11
67	Population size, distribution, threats and conservation status of two endangered bat species Craseonycteris thonglongyai and Hipposideros turpis. Endangered Species Research, 2009, 8, 15-23.	1.2	11
68	A rapid PCR-based assay for identification of cryptic Myotis spp. (M. mystacinus, M. brandtii and M.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.4	10
69	Characterization of Microsatellites in Pseudogymnoascus destructans for White-nose Syndrome Genetic Analysis. Journal of Wildlife Diseases, 2017, 53, 869.	0.3	10
70	Seasonal patterns of <i>Pseudogymnoascus destructans</i> germination indicate hostâ€“pathogen coevolution. Biology Letters, 2020, 16, 20200177.	1.0	9
71	A Taxonomic Review ofRhinolophus coelophyllusPeters 1867 andR. shameliTate 1943 (Chiroptera:) Tj ETQq1 1 0.784314 rgBT /Overlock	0.2	8
72	Effect of Sample Preservation Methods on the Viability ofGeomyces destructans, the Fungus Associated with White-Nose Syndrome in Bats. Acta Chiropterologica, 2011, 13, 217-221.	0.2	8

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73	Resolving a mammal mystery: the identity of Paracoelops megalotis (Chiroptera: Hipposideridae). Zootaxa, 2012, 3505, 75.	0.2	7
74	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
75	Mycobiomes of sympatric Amorphophallus albispathus (Araceae) and Camellia sinensis (Theaceae) â€“ a case study reveals clear tissue preferences and differences in diversity and composition. Mycological Progress, 2018, 17, 489-500.	0.5	7
76	Maleâ€biased dispersal and the potential impact of humanâ€induced habitat modifications on the Neotropical bat <i>Trachops cirrhosus</i>. Ecology and Evolution, 2018, 8, 6065-6080.	0.8	7
77	Genetic diversity in a longâ€lived mammal is explained by the pastâ€™s demographic shadow and current connectivity. Molecular Ecology, 2021, 30, 5048-5063.	2.0	7
78	Population genetics as a tool to elucidate pathogen reservoirs: Lessons from <i>Pseudogymnoascus destructans</i>, the causative agent of Whiteâ€Nose disease in bats. Molecular Ecology, 2022, 31, 675-690.	2.0	7
79	Mating type determination within a microsatellite multiplex for the fungal pathogen Pseudogymnoascus destructans, the causative agent of white-nose disease in bats. Conservation Genetics Resources, 2020, 12, 45-48.	0.4	6
80	Screening and Biosecurity for White-Nose Fungus Pseudogymnoascus destructans (Ascomycota:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.2	5
81	Misconceptions and misinformation about bats and viruses. International Journal of Infectious Diseases, 2021, 105, 606-607.	1.5	4
82	A Rapid, in-Situ Minimally-Invasive Technique to Assess Infections with Pseudogymnoascus destructans in Bats. Acta Chiropterologica, 2021, 23, .	0.2	4
83	Characterization and multiplex genotyping of 16 polymorphic microsatellite loci in the endangered bumble-bee bat, Craseonycteris thonglongyai (Chiroptera: Craseonycteridae). Conservation Genetics, 2009, 10, 1073-1076.	0.8	3
84	Will reduced host connectivity curb the spread of a devastating epidemic?. Molecular Ecology, 2015, 24, 5491-5494.	2.0	3
85	Unavailable names in the Myotis nattereri species complex. Journal of Biogeography, 2019, 46, 2145-2146.	1.4	3
86	A continent-scale study of the social structure and phylogeography of the bent-wing bat, Miniopterus schreibersii (Mammalia: Chiroptera), using new microsatellite data. Journal of Mammalogy, 2019, , .	0.6	3
87	Heterothermy and antifungal responses in bats. Current Opinion in Microbiology, 2021, 62, 61-67.	2.3	3
88	Stabilization of a bat-pitcher plant mutualism. Scientific Reports, 2017, 7, 13170.	1.6	1
89	Timescale and colony-dependent relationships between environmental conditions and plasma oxidative markers in a long-lived bat species. , 2020, 8, coaa083.		1
90	Bat Overpasses Help Bats to Cross Roads Safely by Increasing Their Flight Height. Acta Chiropterologica, 2021, 23, .	0.2	0

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91	Mehelyâ€™s Horseshoe Bat Rhinolophus mehelyi Matschie, 1901. Handbook of the Mammals of Europe, 2020, , 1-28.	0.1	0