

# Vitor C Sousa

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

4,471  
citations

201674

27  
h-index

289244

40  
g-index

51  
all docs

51  
docs citations

51  
times ranked

7270  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fasterâ€chaplodiploid evolution under divergenceâ€withâ€geneâ€flow: Simulations and empirical data from pineâ€feeding hymenopterans. <i>Molecular Ecology</i> , 2022, 31, 2348-2366.	3.9	9
2	Wholeâ€genome analysis of multiple wood ant population pairs supports similar speciation histories, but different degrees of gene flow, across their European ranges. <i>Molecular Ecology</i> , 2022, 31, 3416-3431.	3.9	7
3	Adaptation and convergence in circadianâ€related genes in Iberian freshwater fish. <i>Bmc Ecology and Evolution</i> , 2021, 21, 38.	1.6	3
4	Reply to â€œRe-evaluating the evidence for facilitation of stickleback speciation by admixture in the Lake Constance basinâ€: <i>Nature Communications</i> , 2021, 12, 2807.	12.8	3
5	The genomic history of the Aegean palatial civilizations. <i>Cell</i> , 2021, 184, 2565-2586.e21.	28.9	43
6	<i>fastsimcoal2</i> : demographic inference under complex evolutionary scenarios. <i>Bioinformatics</i> , 2021, 37, 4882-4885.	4.1	148
7	Genomic data and multi-species demographic modelling uncover past hybridization between currently allopatric freshwater species. <i>Heredity</i> , 2021, 127, 401-412.	2.6	2
8	Rapid host-plant adaptation in the herbivorous spider mite <i>Tetranychus urticae</i> occurs at low cost. <i>Current Opinion in Insect Science</i> , 2019, 36, 82-89.	4.4	28
9	Admixture between old lineages facilitated contemporary ecological speciation in Lake Constance stickleback. <i>Nature Communications</i> , 2019, 10, 4240.	12.8	49
10	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019, 570, 182-188.	27.8	259
11	Ancient admixture from an extinct ape lineage into bonobos. <i>Nature Ecology and Evolution</i> , 2019, 3, 957-965.	7.8	59
12	Genomic signatures of introgression between commercial and native bumblebees, <i>Bombus terrestris</i> , in western Iberian Peninsulaâ€Implications for conservation and trade regulation. <i>Evolutionary Applications</i> , 2019, 12, 679-691.	3.1	24
13	The Evolutionary History of Nebraska Deer Mice: Local Adaptation in the Face of Strong Gene Flow. <i>Molecular Biology and Evolution</i> , 2018, 35, 792-806.	8.9	76
14	Different Genomic Changes Underlie Adaptive Evolution in Populations of Contrasting History. <i>Molecular Biology and Evolution</i> , 2018, 35, 549-563.	8.9	32
15	Phylogeny Estimation by Integration over Isolation with Migration Models. <i>Molecular Biology and Evolution</i> , 2018, 35, 2805-2818.	8.9	89
16	History, geography and host use shape genomewide patterns of genetic variation in the redheaded pine sawfly ( <i>Neodiprion lecontei</i> ). <i>Molecular Ecology</i> , 2017, 26, 1022-1044.	3.9	46
17	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	12.6	263
18	Demographic modelling with wholeâ€genome data reveals parallel origin of similar <i>Pundamilia</i> cichlid species after hybridization. <i>Molecular Ecology</i> , 2017, 26, 123-141.	3.9	106

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19	The population genomics of rapid adaptation: disentangling signatures of selection and demography in white sands lizards. <i>Molecular Ecology</i> , 2016, 25, 306-323.	3.9	56
20	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	27.8	439
21	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016, 7, 11693.	12.8	222
22	Chimpanzee genomic diversity reveals ancient admixture with bonobos. <i>Science</i> , 2016, 354, 477-481.	12.6	230
23	Long-Distance Dispersal Shaped Patterns of Human Genetic Diversity in Eurasia. <i>Molecular Biology and Evolution</i> , 2016, 33, 946-958.	8.9	36
24	Impact of range expansions on current human genomic diversity. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 22-30.	3.3	40
25	Understanding the origin of species with genome-scale data: modelling gene flow. <i>Nature Reviews Genetics</i> , 2013, 14, 404-414.	16.3	246
26	Identifying Loci Under Selection Against Gene Flow in Isolation-with-Migration Models. <i>Genetics</i> , 2013, 194, 211-233.	2.9	58
27	Robust Demographic Inference from Genomic and SNP Data. <i>PLoS Genetics</i> , 2013, 9, e1003905.	3.5	1,185
28	Investigating sex-biased migration during the Neolithic transition in Europe, using an explicit spatial simulation framework. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 2409-2416.	2.6	37
29	Population divergence with or without admixture: selecting models using an ABC approach. <i>Heredity</i> , 2012, 108, 521-530.	2.6	44
30	Signature of a Pre-Human Population Decline in the Critically Endangered Reunion Island Endemic Forest Bird <i>Coracina newtoni</i> . <i>PLoS ONE</i> , 2012, 7, e43524.	2.5	22
31	On the nonidentifiability of migration time estimates in isolation with migration models. <i>Molecular Ecology</i> , 2011, 20, 3956-3962.	3.9	47
32	Migration patterns counteract seasonal isolation of <i>Squalius torgalensis</i> , a critically endangered freshwater fish inhabiting a typical Circum-Mediterranean small drainage. <i>Conservation Genetics</i> , 2010, 11, 1859-1870.	1.5	19
33	Conservation genetics of a critically endangered Iberian minnow: evidence of population decline and extirpations. <i>Animal Conservation</i> , 2010, 13, 162-171.	2.9	22
34	The Confounding Effects of Population Structure, Genetic Diversity and the Sampling Scheme on the Detection and Quantification of Population Size Changes. <i>Genetics</i> , 2010, 186, 983-995.	2.9	263
35	2BAD: an application to estimate the parental contributions during two independent admixture events. <i>Molecular Ecology Resources</i> , 2010, 10, 538-541.	4.8	10
36	Approximate Bayesian Computation Without Summary Statistics: The Case of Admixture. <i>Genetics</i> , 2009, 181, 1507-1519.	2.9	56

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37	Influence of forest fragmentation on an endangered large-bodied lemur in northwestern Madagascar. <i>Biological Conservation</i> , 2009, 142, 2862-2871.	4.1	59
38	SPAMs: A user-friendly software to simulate population genetics data under complex demographic models. <i>Molecular Ecology Resources</i> , 2009, 9, 749-753.	4.8	8
39	Genetic structure and signature of population decrease in the critically endangered freshwater cyprinid <i>Chondrostoma lusitanicum</i> . <i>Conservation Genetics</i> , 2008, 9, 791-805.	1.5	29
40	From genetic diversity and structure to conservation: Genetic signature of recent population declines in three mouse lemur species ( <i>Microcebus</i> spp.). <i>Biological Conservation</i> , 2008, 141, 1257-1271.	4.1	82