

Vitor C Sousa

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8892430/publications.pdf>

Version: 2024-02-01

40
papers

4,471
citations

201575

27
h-index

289141

40
g-index

51
all docs

51
docs citations

51
times ranked

7270
citing authors

#	ARTICLE	IF	CITATIONS
1	Fasterâ€ˆhaplodiploid evolution under divergenceâ€ˆwithâ€ˆgeneâ€ˆflow: Simulations and empirical data from pineâ€ˆfeeding hymenopterans. <i>Molecular Ecology</i> , 2022, 31, 2348-2366.	2.0	9
2	Wholeâ€ˆgenome 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.	2.0	7
3	Adaptation and convergence in circadianâ€ˆrelated genes in Iberian freshwater fish. <i>Bmc Ecology and Evolution</i> , 2021, 21, 38.	0.7	3
4	Reply to â€œRe-evaluating the evidence for facilitation of stickleback speciation by admixture in the Lake Constance basinâ€ˆ. <i>Nature Communications</i> , 2021, 12, 2807.	5.8	3
5	The genomic history of the Aegean palatial civilizations. <i>Cell</i> , 2021, 184, 2565-2586.e21.	13.5	43
6	<i>fastsimcoal2</i> : demographic inference under complex evolutionary scenarios. <i>Bioinformatics</i> , 2021, 37, 4882-4885.	1.8	148
7	Genomic data and multi-species demographic modelling uncover past hybridization between currently allopatric freshwater species. <i>Heredity</i> , 2021, 127, 401-412.	1.2	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.	2.2	28
9	Admixture between old lineages facilitated contemporary ecological speciation in Lake Constance stickleback. <i>Nature Communications</i> , 2019, 10, 4240.	5.8	49
10	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019, 570, 182-188.	13.7	259
11	Ancient admixture from an extinct ape lineage into bonobos. <i>Nature Ecology and Evolution</i> , 2019, 3, 957-965.	3.4	59
12	Genomic signatures of introgression between commercial and native bumblebees, <i>Bombus terrestris</i> , in western Iberian Peninsulaâ€ˆImplications for conservation and trade regulation. <i>Evolutionary Applications</i> , 2019, 12, 679-691.	1.5	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.	3.5	76
14	Different Genomic Changes Underlie Adaptive Evolution in Populations of Contrasting History. <i>Molecular Biology and Evolution</i> , 2018, 35, 549-563.	3.5	32
15	Phylogeny Estimation by Integration over Isolation with Migration Models. <i>Molecular Biology and Evolution</i> , 2018, 35, 2805-2818.	3.5	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.	2.0	46
17	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	6.0	263
18	Demographic modelling with wholeâ€ˆgenome data reveals parallel origin of similar <i>Pundamilia</i> cichlid species after hybridization. <i>Molecular Ecology</i> , 2017, 26, 123-141.	2.0	106

#	ARTICLE	IF	CITATIONS
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.	2.0	56
20	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	13.7	439
21	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016, 7, 11693.	5.8	222
22	Chimpanzee genomic diversity reveals ancient admixture with bonobos. <i>Science</i> , 2016, 354, 477-481.	6.0	230
23	Long-Distance Dispersal Shaped Patterns of Human Genetic Diversity in Eurasia. <i>Molecular Biology and Evolution</i> , 2016, 33, 946-958.	3.5	36
24	Impact of range expansions on current human genomic diversity. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 22-30.	1.5	40
25	Understanding the origin of species with genome-scale data: modelling gene flow. <i>Nature Reviews Genetics</i> , 2013, 14, 404-414.	7.7	246
26	Identifying Loci Under Selection Against Gene Flow in Isolation-with-Migration Models. <i>Genetics</i> , 2013, 194, 211-233.	1.2	58
27	Robust Demographic Inference from Genomic and SNP Data. <i>PLoS Genetics</i> , 2013, 9, e1003905.	1.5	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.	1.2	37
29	Population divergence with or without admixture: selecting models using an ABC approach. <i>Heredity</i> , 2012, 108, 521-530.	1.2	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.	1.1	22
31	On the nonidentifiability of migration time estimates in isolation with migration models. <i>Molecular Ecology</i> , 2011, 20, 3956-3962.	2.0	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.	0.8	19
33	Conservation genetics of a critically endangered Iberian minnow: evidence of population decline and extirpations. <i>Animal Conservation</i> , 2010, 13, 162-171.	1.5	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.	1.2	263
35	2BAD: an application to estimate the parental contributions during two independent admixture events. <i>Molecular Ecology Resources</i> , 2010, 10, 538-541.	2.2	10
36	Approximate Bayesian Computation Without Summary Statistics: The Case of Admixture. <i>Genetics</i> , 2009, 181, 1507-1519.	1.2	56

#	ARTICLE	IF	CITATIONS
37	Influence of forest fragmentation on an endangered large-bodied lemur in northwestern Madagascar. <i>Biological Conservation</i> , 2009, 142, 2862-2871.	1.9	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.	2.2	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.	0.8	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.	1.9	82