

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 | Robust Demographic Inference from Genomic and SNP Data. <i>PLoS Genetics</i> , 2013, 9, e1003905. | 3.5 | 1,185 |
| 2 | A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214. | 27.8 | 439 |
| 3 | 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 |
| 4 | Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662. | 12.6 | 263 |
| 5 | The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019, 570, 182-188. | 27.8 | 259 |
| 6 | Understanding the origin of species with genome-scale data: modelling gene flow. <i>Nature Reviews Genetics</i> , 2013, 14, 404-414. | 16.3 | 246 |
| 7 | Chimpanzee genomic diversity reveals ancient admixture with bonobos. <i>Science</i> , 2016, 354, 477-481. | 12.6 | 230 |
| 8 | Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016, 7, 11693. | 12.8 | 222 |
| 9 | <i>fastsimcoal2</i> : demographic inference under complex evolutionary scenarios. <i>Bioinformatics</i> , 2021, 37, 4882-4885. | 4.1 | 148 |
| 10 | Demographic modelling with whole-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 |
| 11 | Phylogeny Estimation by Integration over Isolation with Migration Models. <i>Molecular Biology and Evolution</i> , 2018, 35, 2805-2818. | 8.9 | 89 |
| 12 | 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 |
| 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 | Influence of forest fragmentation on an endangered large-bodied lemur in northwestern Madagascar. <i>Biological Conservation</i> , 2009, 142, 2862-2871. | 4.1 | 59 |
| 15 | Ancient admixture from an extinct ape lineage into bonobos. <i>Nature Ecology and Evolution</i> , 2019, 3, 957-965. | 7.8 | 59 |
| 16 | Identifying Loci Under Selection Against Gene Flow in Isolation-with-Migration Models. <i>Genetics</i> , 2013, 194, 211-233. | 2.9 | 58 |
| 17 | Approximate Bayesian Computation Without Summary Statistics: The Case of Admixture. <i>Genetics</i> , 2009, 181, 1507-1519. | 2.9 | 56 |
| 18 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Admixture between old lineages facilitated contemporary ecological speciation in Lake Constance stickleback. <i>Nature Communications</i> , 2019, 10, 4240. | 12.8 | 49 |
| 20 | On the nonidentifiability of migration time estimates in isolation with migration models. <i>Molecular Ecology</i> , 2011, 20, 3956-3962. | 3.9 | 47 |
| 21 | 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 |
| 22 | Population divergence with or without admixture: selecting models using an ABC approach. <i>Heredity</i> , 2012, 108, 521-530. | 2.6 | 44 |
| 23 | The genomic history of the Aegean palatial civilizations. <i>Cell</i> , 2021, 184, 2565-2586.e21. | 28.9 | 43 |
| 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 | 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 |
| 26 | Long-Distance Dispersal Shaped Patterns of Human Genetic Diversity in Eurasia. <i>Molecular Biology and Evolution</i> , 2016, 33, 946-958. | 8.9 | 36 |
| 27 | Different Genomic Changes Underlie Adaptive Evolution in Populations of Contrasting History. <i>Molecular Biology and Evolution</i> , 2018, 35, 549-563. | 8.9 | 32 |
| 28 | 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 |
| 29 | 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 |
| 30 | Genomic signatures of introgression between commercial and native bumblebees, <i>Bombus terrestris</i> , in western Iberian Peninsula—Implications for conservation and trade regulation. <i>Evolutionary Applications</i> , 2019, 12, 679-691. | 3.1 | 24 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | 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 |
| 35 | Faster haplodiploid evolution under divergence with gene flow: Simulations and empirical data from pine-feeding hymenopterans. <i>Molecular Ecology</i> , 2022, 31, 2348-2366. | 3.9 | 9 |
| 36 | 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 |

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|----|--|------|-----------|
| 37 | Whole-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 |
| 38 | Adaptation and convergence in circadian-related genes in Iberian freshwater fish. <i>Bmc Ecology and Evolution</i> , 2021, 21, 38. | 1.6 | 3 |
| 39 | Reply to "Re-evaluating the evidence for facilitation of stickleback speciation by admixture in the Lake Constance basin". <i>Nature Communications</i> , 2021, 12, 2807. | 12.8 | 3 |
| 40 | 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 |