OctÃ;vio S Paulo

List of Publications by Year in descending order

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91 papers 2,953 citations

218381 26 h-index 197535 49 g-index

93 all docs 93
docs citations

93 times ranked 4947 citing authors

#	Article	IF	CITATIONS
1	The era of reference genomes in conservation genomics. Trends in Ecology and Evolution, 2022, 37, 197-202.	4.2	138
2	Global urban environmental change drives adaptation in white clover. Science, 2022, 375, 1275-1281.	6.0	62
3	Worldwide Population Structure of the Coffee Rust Fungus <i>Hemileia vastatrix</i> Is Strongly Shaped by Local Adaptation and Breeding History. Phytopathology, 2022, 112, 1998-2011.	1.1	5
4	Using gradient Forest to predict climate response and adaptation in Cork oak. Journal of Evolutionary Biology, 2021, 34, 910-923.	0.8	25
5	A Transcriptomic Approach to Understanding the Combined Impacts of Supra-Optimal Temperatures and CO2 Revealed Different Responses in the Polyploid Coffea arabica and Its Diploid Progenitor C. canephora. International Journal of Molecular Sciences, 2021, 22, 3125.	1.8	16
6	Population structure, adaptation and divergence of the meadow spittlebug, <i>Philaenus spumarius</i> (Hemiptera, Aphrophoridae), revealed by genomic and morphological data. PeerJ, 2021, 9, e11425.	0.9	9
7	Habitat filtering and inferred dispersal ability condition acrossâ€scale species turnover and rarity in Macaronesian island spider assemblages. Journal of Biogeography, 2021, 48, 3131-3144.	1.4	5
8	Understanding the Impact of Drought in Coffea Genotypes: Transcriptomic Analysis Supports a Common High Resilience to Moderate Water Deficit but a Genotype Dependent Sensitivity to Severe Water Deficit. Agronomy, 2021, 11, 2255.	1.3	18
9	Genetic Diversity and Population Structure of Wild Beets (Beta spp.) from the Western Iberian Peninsula and the Azores and Madeira Islands. Diversity, 2021, 13, 593.	0.7	3
10	Chemical and Genetic Relationships of Cynara cardunculus L. (Cardoon) in Southern Portugal. , 2021, 11, .		1
11	Genetic variability on worldwide populations of the scale insect Pulvinariella mesembryanthemi. Biological Invasions, 2020, 22, 735-748.	1.2	2
12	Population genomics of Bombus terrestris reveals high but unstructured genetic diversity in a potential glacial refugium. Biological Journal of the Linnean Society, 2020, 129, 259-272.	0.7	10
13	Ancient divergence, a crisis of salt and another of ice shaped the evolution of the west Mediterranean butterfly <i>Euchloe tagis</i> . Biological Journal of the Linnean Society, 2020, 131, 487-504.	0.7	2
14	Building a Robust, Densely-Sampled Spider Tree of Life for Ecosystem Research. Diversity, 2020, 12, 288.	0.7	14
15	Transcriptomic Leaf Profiling Reveals Differential Responses of the Two Most Traded Coffee Species to Elevated [CO2]. International Journal of Molecular Sciences, 2020, 21, 9211.	1.8	11
16	Highly regional population structure of Spondyliosoma cantharus depicted by nuclear and mitochondrial DNA data. Scientific Reports, 2020, 10, 4063.	1.6	4
17	Standardised inventories of spiders (Arachnida, Araneae) of Macaronesia II: The native forests and dry habitats of Madeira archipelago (Madeira and Porto Santo islands). Biodiversity Data Journal, 2020, 8, e47502.	0.4	11
18	Genome-Wide Signatures of Selection in Colletotrichum kahawae Reveal Candidate Genes Potentially Involved in Pathogenicity and Aggressiveness. Frontiers in Microbiology, 2019, 10, 1374.	1.5	13

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19	Shortcomings of Phylogenetic Studies on Recent Radiated Insular Groups: A Meta-Analysis Using Cabo Verde Biodiversity. International Journal of Molecular Sciences, 2019, 20, 2782.	1.8	10
20	New insights into adaptation and population structure of cork oak using genotyping by sequencing. Global Change Biology, 2019, 25, 337-350.	4.2	48
21	Genomic signatures of introgression between commercial and native bumblebees, ⟨i⟩Bombus terrestris⟨i⟩, in western Iberian Peninsulaâ€"Implications for conservation and trade regulation. Evolutionary Applications, 2019, 12, 679-691.	1.5	24
22	Population genomic footprints of host adaptation, introgression and recombination in coffee leaf rust. Molecular Plant Pathology, 2018, 19, 1742-1753.	2.0	35
23	New data on polymorphism of the meadow spittlebug Philaenus spumarius (L.) (Hemiptera:) Tj ETQq1 1 0.784314	ł rgBT /Ov	erlock 10 T
24	Genetic and Genomic Tools to Asssist Sugar Beet Improvement: The Value of the Crop Wild Relatives. Frontiers in Plant Science, 2018, 9, 74.	1.7	46
25	Novel insights on colonization routes and evolutionary potential of <i>Colletotrichum kahawae</i> , a severe pathogen of <i>Coffea arabica</i> . Molecular Plant Pathology, 2018, 19, 2488-2501.	2.0	22
26	Morphology, songs and genetics identify two new cicada species from Morocco: Tettigettalna afroamissa sp. nov. and Berberigetta dimelodica gen. nov. & amp; sp. nov. (Hemiptera: Cicadettini). Zootaxa, 2017, 4237, 517.	0.2	4
27	<i>Structure_threader</i> : An improved method for automation and parallelization of programs <scp>structure</scp> , <scp> fastStructure</scp> and <i>MavericK</i> on multicore <scp>CPU</scp> systems. Molecular Ecology Resources, 2017, 17, e268-e274.	2.2	95
28	Deep analysis of wild Vitis flower transcriptome reveals unexplored genome regions associated with sex specification. Plant Molecular Biology, 2017, 93, 151-170.	2.0	19
29	Phylogeny of the most species-rich freshwater bivalve family (Bivalvia: Unionida: Unionidae): Defining modern subfamilies and tribes. Molecular Phylogenetics and Evolution, 2017, 106, 174-191.	1.2	133
30	Age estimates of (i) Frullania (i) (Frullaniaceae, Porellales) main lineages: another example of rapid and recent diversification in liverwort evolution. Systematics and Biodiversity, 2017, 15, 156-165.	0.5	13
31	Evolutionary and Biogeographic Insights on the Macaronesian Beta-Patellifolia Species (Amaranthaceae) from a Time-Scaled Molecular Phylogeny. PLoS ONE, 2016, 11, e0152456.	1.1	35
32	Genetic Diversity and Physiological Performance of Portuguese Wild Beet (Beta vulgaris spp. maritima) from Three Contrasting Habitats. Frontiers in Plant Science, 2016, 7, 1293.	1.7	29
33	Revisiting Vitis vinifera Subtilase Gene Family: A Possible Role in Grapevine Resistance against Plasmopara viticola. Frontiers in Plant Science, 2016, 7, 1783.	1.7	31
34	Assessing genotype-phenotype associations in three dorsal colour morphs in the meadow spittlebug Philaenus spumarius (L.) (Hemiptera: Aphrophoridae) using genomic and transcriptomic resources. BMC Genetics, 2016, 17, 144.	2.7	14
35	Shared and divergent pathways for flower abscission are triggered by gibberellic acid and carbon starvation in seedless Vitis vinifera L. BMC Plant Biology, 2016, 16, 38.	1.6	27
36	NCBI Mass Sequence Downloader–Large dataset downloading made easy. SoftwareX, 2016, 5, 80-83.	1.2	6

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37	Molecular candidates for early-stage flower-to-fruit transition in stenospermocarpic table grape (Vitis vinifera L.) inflorescences ascribed by differential transcriptome and metabolome profiles. Plant Science, 2016, 244, 40-56.	1.7	18
38	4Pipe4 $\hat{a}\in$ A 454 data analysis pipeline for SNP detection in datasets with no reference sequence or strain information. BMC Bioinformatics, 2016, 17, 41.	1.2	2
39	Phylogeography and modes of reproduction in diploid and tetraploid halophytes of <i>Limonium </i> species (Plumbaginaceae): evidence for a pattern of geographical parthenogenesis. Annals of Botany, 2016, 117, 37-50.	1.4	22
40	Comparative Validation of Conventional and RNA-Seq Data-Derived Reference Genes for qPCR Expression Studies of Colletotrichum kahawae. PLoS ONE, 2016, 11, e0150651.	1.1	14
41	Genetic and Morphological Variation of the Forkbeard, Phycis phycis (Pisces, Phycidae): Evidence of Panmixia and Recent Population Expansion along Its Distribution Area. PLoS ONE, 2016, 11, e0167045.	1.1	14
42	Differential survival and reproduction in colour forms of <i><i><scp>P</scp>hilaenus spumarius</i>give new insights to the study of its balanced polymorphism. Ecological Entomology, 2015, 40, 759-766.</i>	1.1	11
43	Genomic Patterns of Positive Selection at the Origin of Rust Fungi. PLoS ONE, 2015, 10, e0143959.	1.1	20
44	p53 gene discriminates two ecologically divergent sister species of pine voles. Heredity, 2015, 115, 444-451.	1.2	3
45	Phylogeographical patterns inCoenosia attenuata(Diptera: Muscidae): a widespread predator of insect species associated with greenhouse crops. Biological Journal of the Linnean Society, 2015, 114, 308-326.	0.7	12
46	Microsatellite loci isolated from Chamaeleo chamaeleon. Journal of Genetics, 2015, 94, 144-147.	0.4	0
47	New Mitochondrial and Nuclear Evidences Support Recent Demographic Expansion and an Atypical Phylogeographic Pattern in the Spittlebug Philaenus spumarius (Hemiptera, Aphrophoridae). PLoS ONE, 2014, 9, e98375.	1.1	31
48	Overview of the functional virulent genome of the coffee leaf rust pathogen Hemileia vastatrix with an emphasis on early stages of infection. Frontiers in Plant Science, 2014, 5, 88.	1.7	25
49	Isolation and characterization of fifteen polymorphic microsatellite loci for the citrus mealybug, Planococcus citri (Hemiptera: Pseudococcidae), and cross-amplification in two other mealybug species. Journal of Genetics, 2014, 93, 75-78.	0.4	6
50	Phylogenetic origin of the endemic pigeons from Madeira (Columba trocaz) and Azores Islands (Columba palumbus azorica). Journal of Ornithology, 2014, 155, 71-82.	0.5	7
51	Conflicting patterns of <scp>DNA</scp> barcoding and taxonomy in the cicada genus <i><scp>T</scp>ettigettalna</i> from southern <scp>E</scp> urope (<scp>H</scp> emiptera:) Tj ETQq1 1 0.784	31 4.2 gBT	/O ve rlock 10
52	Identifying signatures of natural selection in cork oak (Quercus suber L.) genes through SNP analysis. Tree Genetics and Genomes, 2014, 10, 1645-1660.	0.6	29
53	A comprehensive assessment of the transcriptome of cork oak (Quercus suber) through EST sequencing. BMC Genomics, 2014, 15, 371.	1.2	53
54	Oak Root Response to Ectomycorrhizal Symbiosis Establishment: RNA-Seq Derived Transcript Identification and Expression Profiling. PLoS ONE, 2014, 9, e98376.	1.1	45

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55	Tettigettalna josei (Boulard, 1982) (Hemiptera: Cicadoidea): first record in Spain, with notes on the distribution, genetic variation and behaviour of the species. Biodiversity Data Journal, 2014, 2, e1045.	0.4	2
56	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	3.3	582
57	Genetic and morphological variation in two littorinid gastropods: evidence for recent population expansions along the East African coast. Biological Journal of the Linnean Society, 2013, 108, 494-508.	0.7	21
58	Genetic analysis of a contact zone between two lineages of the ocellated lizard (<i>Lacerta) Tj ETQq0 0 0 rgBT /O Zoological Systematics and Evolutionary Research, 2013, 51, 45-54.</i>	verlock 10 0.6) Tf 50 627 T 21
59	Molecular Evidence of Polyandry in the Citrus Mealybug, Planococcus citri (Hemiptera:) Tj ETQq1 1 0.784314 rgB	T <u>/</u> Qverlock	R
60	Challenges and pitfalls in the characterization of anonymous outlier AFLP markers in non-model species: lessons from an ocellated lizard genome scan. Heredity, 2012, 109, 340-348.	1.2	12
61	Application of the <i>Apn2/MAT</i> locus to improve the systematics of the <i>Colletotrichum gloeosporioides</i> complex: an example from coffee (<i>Coffea</i> spp.) hosts. Mycologia, 2012, 104, 396-409.	0.8	152
62	Expression profiling of genes involved in the biotrophic colonisation of Coffea arabica leaves by Hemileia vastatrix. European Journal of Plant Pathology, 2012, 133, 261-277.	0.8	14
63	Numts help to reconstruct the demographic history of the ocellated lizard (<i>Lacerta lepida</i>) in a secondary contact zone. Molecular Ecology, 2012, 21, 1005-1018.	2.0	26
64	Hostâ€jump drives rapid and recent ecological speciation of the emergent fungal pathogen <i>Colletotrichum kahawae</i> . Molecular Ecology, 2012, 21, 2655-2670.	2.0	72
65	Isolation and characterization of fifteen polymorphic microsatellite loci for the citrus mealybug, Planococcus citri (Hemiptera: Pseudococcidae), and cross-amplification in two other mealybug species. Journal of Genetics, 2012, 91, e75-8.	0.4	3
66	Validation of RT-qPCR reference genes for in planta expression studies in Hemileia vastatrix, the causal agent of coffee leaf rust. Fungal Biology, 2011, 115, 891-901.	1.1	36
67	Origin and diversification of the genus <i>Echium</i> (Boraginaceae) in the Cape Verde archipelago. Taxon, 2011, 60, 1375-1385.	0.4	20
68	Association of Mc1r variants with ecologically relevant phenotypes in the European ocellated lizard, Lacerta lepida. Journal of Evolutionary Biology, 2011, 24, 2289-2298.	0.8	27
69	Multiple approaches to detect outliers in a genome scan for selection in ocellated lizards (Lacerta) Tj ETQq1 1 0.7	84314 rgE	3T ₄₄ Overlock
70	Genetic divergence in Cork Oak based on cpDNA sequence data. BMC Proceedings, 2011, 5, .	1.8	5
71	Phylogeography and demographic history of Lacerta lepida in the Iberian Peninsula: multiple refugia, range expansions and secondary contact zones. BMC Evolutionary Biology, 2011, 11, 170.	3.2	62

Molecular phylogeny and DNA barcoding in the meadow-spittlebug Philaenus spumarius (Hemiptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf

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73	Conus pennaceus: a phylogenetic analysis of the Mozambican molluscan complex. African Journal of Marine Science, 2010, 32, 591-599.	0.4	5
74	Systematic and phylogeographical assessment of the Acanthodactylus erythrurus group (Reptilia:) Tj ETQq0 0 0 rg Phylogenetics and Evolution, 2009, 51, 131-142.	gBT /Overlo 1.2	ock 10 Tf 50 53
75	The role of vicariance vs. dispersal in shaping genetic patterns in ocellated lizard species in the western Mediterranean. Molecular Ecology, 2008, 17, 1535-1551.	2.0	75
76	<scp>concatenator</scp> : sequence data matrices handling made easy. Molecular Ecology Resources, 2008, 8, 1254-1255.	2.2	47
77	THE EVOLUTION OF CICADA SONGS CONTRASTED WITH THE RELATIONSHIPS INFERRED FROM MITOCHONDRIAL DNA (INSECTA, HEMIPTERA). Bioacoustics, 2008, 18, 17-34.	0.7	10
78	Copulatory plugs do not assure high first male fertilisation success: sperm displacement in a lizard. Behavioral Ecology and Sociobiology, 2007, 62, 281-288.	0.6	16
79	NOTE: DISTRIBUTION AND CONSERVATION OF THE COMMON CHAMAELEO CHAMAELEON, IN ALGARVE, SOUTHERN PORTUGAL. Israel Journal of Zoology, 2005, 51, 157-164.	0.2	5
80	Using nested clade analysis to assess the history of colonization and the persistence of populations of an Iberian Lizard. Molecular Ecology, 2002, 11, 809-819.	2.0	48
81	The double origin of Iberian peninsular chameleons. Biological Journal of the Linnean Society, 2002, 75, 1-7.	0.7	43
82	Genetic differentiation of populations of Iberian rock-lizards Iberolacerta (Iberolacerta) sensuArribas (1999). Journal of Zoological Systematics and Evolutionary Research, 2002, 40, 57-64.	0.6	8
83	The persistence of Pliocene populations through the Pleistocene climatic cycles: evidence from the phylogeography of an Iberian lizard. Proceedings of the Royal Society B: Biological Sciences, 2001, 268, 1625-1630.	1.2	95
84	Trace element status (Se, Cu, Zn) and serum lipid profile in Portuguese subjects of San Miguel Island from Azores'archipelago. Journal of Trace Elements in Medicine and Biology, 2000, 14, 1-5.	1.5	32
85	Modelling wildlife distributions: Logistic Multiple Regression vs Overlap Analysis. Ecography, 1999, 22, 251-260.	2.1	88
86	Management strategies for conservation of the lizard Lacerta schreiberi in Portugal. Biological Conservation, 1999, 89, 311-319.	1.9	14
87	Morphological distinction of Iberian midwife toads: Alytes obstetricans may have two metacarpal tubercles. Amphibia - Reptilia, 1996, 17, 67-70.	0.1	O
88	Distribution of alien tetrapods in the Iberian Peninsula. NeoBiota, 0, 64, 1-21.	1.0	7
89	Revision of the morphology, phylogenetic relationships, behaviour and diversity of the Iberian and Italian ant-like Tachydromia Meigen, 1803 (Diptera: Hybotidae). European Journal of Taxonomy, 0, 732, 1-56.	0.6	4
90	PCR-based detection of prey DNA in the gut contents of the tiger-fly, Coenosia attenuata (Diptera:) Tj ETQq0 0 0 r Entomology, 0, 118, 335-343.	gBT /Over 1.2	lock 10 Tf 50 2

Entomology, 0, 118, 335-343.

OCTáVIO S PAULO

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91	Population structure in <i>Quercus suber</i> L. revealed by nuclear microsatellite markers. PeerJ, 0, 10, e13565.	0.9	4