OctÃ;vio S Paulo

List of Publications by Year in descending order

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ΟςτÃινμο S Ρλιμο

#	Article	IF	CITATIONS
1	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	3.3	582
2	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
3	The era of reference genomes in conservation genomics. Trends in Ecology and Evolution, 2022, 37, 197-202.	4.2	138
4	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
5	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
6	<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
7	Modelling wildlife distributions: Logistic Multiple Regression vs Overlap Analysis. Ecography, 1999, 22, 251-260.	2.1	88
8	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
9	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
10	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
11	Global urban environmental change drives adaptation in white clover. Science, 2022, 375, 1275-1281.	6.0	62
12	Systematic and phylogeographical assessment of the Acanthodactylus erythrurus group (Reptilia:) Tj ETQq0 0 0 Phylogenetics and Evolution, 2009, 51, 131-142.	rgBT /Ove 1.2	rlock 10 Tf 50 53
13	A comprehensive assessment of the transcriptome of cork oak (Quercus suber) through EST sequencing. BMC Genomics, 2014, 15, 371.	1.2	53
14	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
15	New insights into adaptation and population structure of cork oak using genotyping by sequencing. Global Change Biology, 2019, 25, 337-350.	4.2	48
16	<scp>concatenator</scp> : sequence data matrices handling made easy. Molecular Ecology Resources, 2008, 8, 1254-1255.	2.2	47
17	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
18	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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19	Multiple approaches to detect outliers in a genome scan for selection in ocellated lizards (Lacerta) Tj ETQq2	L 1 0.784314 rg	BT_/Overloci
20	The double origin of Iberian peninsular chameleons. Biological Journal of the Linnean Society, 2002, 75, 1-7.	0.7	43
21	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
22	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
23	Population genomic footprints of host adaptation, introgression and recombination in coffee leaf rust. Molecular Plant Pathology, 2018, 19, 1742-1753.	2.0	35
24	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
25	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
26	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
27	ldentifying 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
28	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
29	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
30	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
31	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
32	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
33	Using gradient Forest to predict climate response and adaptation in Cork oak. Journal of Evolutionary Biology, 2021, 34, 910-923.	0.8	25
34	Genomic signatures of introgression between commercial and native bumblebees, <i>Bombus terrestris</i> , in western Iberian Peninsula—Implications for conservation and trade regulation. Evolutionary Applications, 2019, 12, 679-691.	1.5	24
35	Molecular phylogeny and DNA barcoding in the meadow-spittlebug Philaenus spumarius (Hemiptera,) Tj ETG	Qq1 1 0.784314 1.2	4 rgBT /Over
36	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

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37	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
38	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
39	Genetic analysis of a contact zone between two lineages of the ocellated lizard (<i>Lacerta) Tj ETQq1 1 0.784314 Zoological Systematics and Evolutionary Research, 2013, 51, 45-54.</i>	4 rgBT 0.6	/Overlock 10 21
40	Origin and diversification of the genus <i>Echium</i> (Boraginaceae) in the Cape Verde archipelago. Taxon, 2011, 60, 1375-1385.	0.4	20
41	Genomic Patterns of Positive Selection at the Origin of Rust Fungi. PLoS ONE, 2015, 10, e0143959.	1.1	20
42	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
43	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
44	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
45	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
46	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
47	Management strategies for conservation of the lizard Lacerta schreiberi in Portugal. Biological Conservation, 1999, 89, 311-319.	1.9	14
48	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
49	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 0.7843	31 4.2 g	BT /O ve rlock 10
50	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
51	Building a Robust, Densely-Sampled Spider Tree of Life for Ecosystem Research. Diversity, 2020, 12, 288.	0.7	14
52	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
53	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
54	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

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55	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
56	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
57	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
58	Differential survival and reproduction in colour forms of <i><scp>P</scp>hilaenus spumarius</i> give new insights to the study of its balanced polymorphism. Ecological Entomology, 2015, 40, 759-766.	1.1	11
59	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
60	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
61	THE EVOLUTION OF CICADA SONGS CONTRASTED WITH THE RELATIONSHIPS INFERRED FROM MITOCHONDRIAL DNA (INSECTA, HEMIPTERA). Bioacoustics, 2008, 18, 17-34.	0.7	10
62	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
63	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
64	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
65	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
66	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
67	Distribution of alien tetrapods in the Iberian Peninsula. NeoBiota, 0, 64, 1-21.	1.0	7
68	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
69	NCBI Mass Sequence Downloader–Large dataset downloading made easy. SoftwareX, 2016, 5, 80-83.	1.2	6
70	NOTE: DISTRIBUTION AND CONSERVATION OF THE COMMON CHAMAELEO CHAMAELEON, IN ALGARVE, SOUTHERN PORTUGAL. Israel Journal of Zoology, 2005, 51, 157-164.	0.2	5
71	Conus pennaceus: a phylogenetic analysis of the Mozambican molluscan complex. African Journal of Marine Science, 2010, 32, 591-599.	0.4	5
72	Genetic divergence in Cork Oak based on cpDNA sequence data. BMC Proceedings, 2011, 5, .	1.8	5

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73	Molecular Evidence of Polyandry in the Citrus Mealybug, Planococcus citri (Hemiptera:) Tj ETQq1 1 0.784314 rgBT	/Overlock 1.1	10 Tf 50 7
74	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
75	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
76	Morphology, songs and genetics identify two new cicada species from Morocco: Tettigettalna afroamissa sp. nov. and Berberigetta dimelodica gen. nov. & sp. nov. (Hemiptera: Cicadettini). Zootaxa, 2017, 4237, 517.	0.2	4
77	New data on polymorphism of the meadow spittlebug Philaenus spumarius (L.) (Hemiptera:) Tj ETQq1 1 0.784314	rgBT /Ove	erlock 10 Tf
78	Highly regional population structure of Spondyliosoma cantharus depicted by nuclear and mitochondrial DNA data. Scientific Reports, 2020, 10, 4063.	1.6	4
79	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
80	Population structure in <i>Quercus suber</i> L. revealed by nuclear microsatellite markers. PeerJ, 0, 10, e13565.	0.9	4
81	p53 gene discriminates two ecologically divergent sister species of pine voles. Heredity, 2015, 115, 444-451.	1.2	3
82	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
83	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
84	4Pipe4 – 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
85	Genetic variability on worldwide populations of the scale insect Pulvinariella mesembryanthemi. Biological Invasions, 2020, 22, 735-748.	1.2	2
86	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
87	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
88	PCR-based detection of prey DNA in the gut contents of the tiger-fly, Coenosia attenuata (Diptera:) Tj ETQqO 0 0 r Entomology, 0, 118, 335-343.	gBT /Overl 1.2	ock 10 Tf 5 2
89	Chemical and Genetic Relationships of Cynara cardunculus L. (Cardoon) in Southern Portugal. , 2021, 11, .		1
90	Morphological distinction of Iberian midwife toads: Alytes obstetricans may have two metacarpal tubercles. Amphibia - Reptilia, 1996, 17, 67-70.	0.1	0

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91	Microsatellite loci isolated from Chamaeleo chamaeleon. Journal of Genetics, 2015, 94, 144-147.	0.4	0