

# Pedro Talhinhas

## List of Publications by Year in descending order

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54  
papers

1,990  
citations

304743

22  
h-index

254184

43  
g-index

54  
all docs

54  
docs citations

54  
times ranked

1978  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Analysis of Partial Sequences of the Flavonone 3 Hydroxylase Gene in <i>Lupinus mutabilis</i> Reveals Differential Expression of Two Paralogues Potentially Related to Seed Coat Colour. <i>Agronomy</i> , 2022, 12, 450.	3.0	1
2	Best practices in plant cytometry. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2021, 99, 311-317.	1.5	16
3	Diversification of <i>Aeonium</i> Species Across Macaronesian Archipelagos: Correlations Between Genome-Size Variation and Their Conservation Status. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	2.2	4
4	Metabarcoding reveals southern hemisphere fungal endophytes within wood of cultivated Proteaceae in Portugal. <i>European Journal of Plant Pathology</i> , 2021, 160, 173-184.	1.7	7
5	The use of flow cytometry for fungal nuclear DNA quantification. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2021, 99, 343-347.	1.5	4
6	Olive Oils from Fruits Infected with Different Anthracnose Pathogens Show Sensory Defects Earlier Than Chemical Degradation. <i>Agronomy</i> , 2021, 11, 1041.	3.0	14
7	Exploring physicochemical and cytogenomic diversity of African cowpea and common bean. <i>Scientific Reports</i> , 2021, 11, 12838.	3.3	7
8	Diversity and Cytogenomic Characterization of Wild Carrots in the Macaronesian Islands. <i>Plants</i> , 2021, 10, 1954.	3.5	3
9	<i>Colletotrichum</i> species and complexes: geographic distribution, host range and conservation status. <i>Fungal Diversity</i> , 2021, 110, 109-198.	12.3	79
10	Genetic and Genomic Diversity in a Tarwi ( <i>Lupinus mutabilis</i> Sweet) Germplasm Collection and Adaptability to Mediterranean Climate Conditions. <i>Agronomy</i> , 2020, 10, 21.	3.0	23
11	State and Progress of Andean Lupin Cultivation in Europe: A Review. <i>Agronomy</i> , 2020, 10, 1038.	3.0	20
12	The genetic legacy of fragmentation and overexploitation in the threatened medicinal African pepper-bark tree, <i>Warburgia salutaris</i> . <i>Scientific Reports</i> , 2020, 10, 19725.	3.3	10
13	Genetic Diversity among Cowpea ( <i>Vigna unguiculata</i> (L.) Walp.) Landraces Suggests Central Mozambique as an Important Hotspot of Variation. <i>Agronomy</i> , 2020, 10, 1893.	3.0	11
14	Urban and rural household energy consumption and deforestation patterns in Zaire province, Northern Angola: A landscape approach. <i>Applied Geography</i> , 2020, 119, 102207.	3.7	23
15	Response to Anthracnose in a Tarwi ( <i>Lupinus mutabilis</i> ) Collection Is Influenced by Anthocyanin Pigmentation. <i>Plants</i> , 2020, 9, 583.	3.5	11
16	Pathological and Epidemiological Characterization of First Outbreak of Daylily Rust in Europe and Evaluation of <i>Puccinia hemerocallidis</i> Resistance in <i>Hemerocallis</i> Cultivars. <i>Plants</i> , 2020, 9, 427.	3.5	3
17	Pathological, Morphological, Cytogenomic, Biochemical and Molecular Data Support the Distinction between <i>Colletotrichum cigarro</i> comb. et stat. nov. and <i>Colletotrichum kahawae</i> . <i>Plants</i> , 2020, 9, 502.	3.5	21
18	Petro-Landscapes: Urban Expansion and Energy Consumption in Mbanza Kongo City, Northern Angola. <i>Human Ecology</i> , 2019, 47, 565-575.	1.4	5

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19	Dynamics of change in a "female farming system"™, Mbanza Kongo/Northern Angola. <i>Journal of Peasant Studies</i> , 2019, 46, 258-275.	4.5	3
20	Olive anthracnose: a yield and oil quality degrading disease caused by several species of <i>Colletotrichum</i> that differ in virulence, host preference and geographical distribution. <i>Molecular Plant Pathology</i> , 2018, 19, 1797-1807.	4.2	48
21	Validation of standards suitable for genome size estimation of fungi. <i>Journal of Microbiological Methods</i> , 2017, 142, 76-78.	1.6	13
22	The coffee leaf rust pathogen <i>Hemileia vastatrix</i> : one and a half centuries around the tropics. <i>Molecular Plant Pathology</i> , 2017, 18, 1039-1051.	4.2	157
23	The <i>Colletotrichum acutatum</i> Species Complex as a Model System to Study Evolution and Host Specialization in Plant Pathogens. <i>Frontiers in Microbiology</i> , 2017, 8, 2001.	3.5	61
24	Characterization of <i>Colletotrichum gloeosporioides</i> , as the main causal agent of citrus anthracnose, and <i>C. karstii</i> as species preferentially associated with lemon twig dieback in Portugal. <i>Phytoparasitica</i> , 2016, 44, 549-561.	1.2	34
25	Legitimacy and Implications of Reducing <i>Colletotrichum kahawae</i> to Subspecies in Plant Pathology. <i>Frontiers in Plant Science</i> , 2016, 7, 2051.	3.6	35
26	First Report of <i>Puccinia hemerocallidis</i> Causing Daylily Rust in Europe. <i>Plant Disease</i> , 2016, 100, 2163.	1.4	5
27	First Report of <i>Puccinia thaliae</i> Causing Rust on <i>Canna</i> spp. in Europe. <i>Plant Disease</i> , 2016, 100, 1242-1242.	1.4	5
28	Comparative Validation of Conventional and RNA-Seq Data-Derived Reference Genes for qPCR Expression Studies of <i>Colletotrichum kahawae</i> . <i>PLoS ONE</i> , 2016, 11, e0150651.	2.5	14
29	Yield and seed chemical composition of <i>Lupinus mutabilis</i> in Portugal. <i>Revista De Ciências Agrárias</i> , 2016, 39, 518-525.	0.2	13
30	Avaliação da resistência à antracnose em germoplasma de <i>Lupinus</i> spp.. <i>Revista De Ciências Agrárias</i> , 2016, 39, 550-570.	0.2	2
31	Genomic Patterns of Positive Selection at the Origin of Rust Fungi. <i>PLoS ONE</i> , 2015, 10, e0143959.	2.5	20
32	A method for obtaining RNA from <i>Hemileia vastatrix</i> appressoria produced in planta, suitable for transcriptomic analyses. <i>Fungal Biology</i> , 2015, 119, 1093-1099.	2.5	7
33	Virulence diversity of anthracnose pathogens ( <i>Colletotrichum acutatum</i> and <i>C. gloeosporioides</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock <i>Pathology</i> , 2015, 142, 73-83.	1.7	38
34	Flow cytometry reveals that the rust fungus, <i>Uromyces bidentis</i> ( <i>Pucciniales</i> ), possesses the largest fungal genome reported (2489 Mb). <i>Molecular Plant Pathology</i> , 2015, 16, 1006-1010.	4.2	24
35	Genome size analyses of <i>Pucciniales</i> reveal the largest fungal genomes. <i>Frontiers in Plant Science</i> , 2014, 5, 422.	3.6	86
36	Overview of the functional virulent genome of the coffee leaf rust pathogen <i>Hemileia vastatrix</i> with an emphasis on early stages of infection. <i>Frontiers in Plant Science</i> , 2014, 5, 88.	3.6	25

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37	12 Rust Fungi: Achievements and Future Challenges on Genomics and Host-Parasite Interactions. , 2013, 315-341.		1
38	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. <i>Mycologia</i> , 2012, 104, 396-409.	1.9	152
39	Expression profiling of genes involved in the biotrophic colonisation of <i>Coffea arabica</i> leaves by <i>Hemileia vastatrix</i> . <i>European Journal of Plant Pathology</i> , 2012, 133, 261-277.	1.7	14
40	Cellular and molecular analyses of coffee resistance to <i>Hemileia vastatrix</i> and nonhost resistance to <i>Uromyces vignae</i> in the resistance-donor genotype HDT832/2. <i>European Journal of Plant Pathology</i> , 2012, 133, 141-157.	1.7	32
41	454-pyrosequencing of <i>Coffea arabica</i> leaves infected by the rust fungus <i>Hemileia vastatrix</i> reveals in planta-expressed pathogen-secreted proteins and plant functions in a late compatible plant-rust interaction. <i>Molecular Plant Pathology</i> , 2012, 13, 17-37.	4.2	81
42	Host-jump drives rapid and recent ecological speciation of the emergent fungal pathogen <i>Colletotrichum kahawae</i> . <i>Molecular Ecology</i> , 2012, 21, 2655-2670.	3.9	72
43	<i>Magnaporthe oryzae</i> Populations Adapted to Finger Millet and Rice Exhibit Distinctive Patterns of Genetic Diversity, Sexuality and Host Interaction. <i>Molecular Biotechnology</i> , 2012, 50, 145-158.	2.4	72
44	Validation of RT-qPCR reference genes for in planta expression studies in <i>Hemileia vastatrix</i> , the causal agent of coffee leaf rust. <i>Fungal Biology</i> , 2011, 115, 891-901.	2.5	36
45	Epidemiology, histopathology and aetiology of olive anthracnose caused by <i>Colletotrichum acutatum</i> and <i>C. gloeosporioides</i> in Portugal. <i>Plant Pathology</i> , 2011, 60, 483-495.	2.4	69
46	Characterization of <i>Colletotrichum kahawae</i> Isolates Causing Coffee Berry Disease in Angola. <i>Journal of Phytopathology</i> , 2010, 158, 310-313.	1.0	15
47	Non-host resistance responses of <i>Arabidopsis thaliana</i> to the coffee leaf rust fungus ( <i>Hemileia vastatrix</i> ). <i>Botany</i> , 2010, 88, 621-629.	1.0	22
48	The distinctive population structure of <i>Colletotrichum</i> species associated with olive anthracnose in the Algarve region of Portugal reflects a host-pathogen diversity hot spot. <i>FEMS Microbiology Letters</i> , 2009, 296, 31-38.	1.8	42
49	<i>Agrobacterium</i> -Mediated Transformation and Insertional Mutagenesis in <i>Colletotrichum acutatum</i> for Investigating Varied Pathogenicity Lifestyles. <i>Molecular Biotechnology</i> , 2008, 39, 57-67.	2.4	53
50	Collection of <i>Lupinus angustifolius</i> L. Germplasm and Characterisation of Morphological and Molecular Diversity. <i>Genetic Resources and Crop Evolution</i> , 2006, 53, 563-578.	1.6	20
51	Genotypic and phenotypic diversity in <i>Colletotrichum acutatum</i> , a cosmopolitan pathogen causing anthracnose on a wide range of hosts. <i>Molecular Plant Pathology</i> , 2005, 6, 361-378.	4.2	144
52	Molecular and Phenotypic Analyses Reveal Association of Diverse <i>Colletotrichum acutatum</i> Groups and a Low Level of <i>C. gloeosporioides</i> with Olive Anthracnose. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2987-2998.	3.1	156
53	AFLP, ISSR and RAPD markers reveal high levels of genetic diversity among <i>Lupinus</i> spp.. <i>Plant Breeding</i> , 2003, 122, 507-510.	1.9	32
54	Genetic and Morphological Characterization of <i>Colletotrichum acutatum</i> Causing Anthracnose of Lupins. <i>Phytopathology</i> , 2002, 92, 986-996.	2.2	125