Francesco Paolocci

List of Publications by Year
in descending order

75 papers	3,456 citations	126907 33 h-index	149698 56 g-index
75 all docs	75 docs citations	75 times ranked	2960 citing authors

#	Article	IF	Citations
1	PÃ©rigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. Nature, 2010, 464, 1033-1038.	27.8	641
2	Reevaluation of the Life Cycle of Tuber magnatum. Applied and Environmental Microbiology, 2006, 72, 2390-2393.	3.1	129
3	Isolation and characterization of MAT genes in the symbiotic ascomycete Tuber melanosporum. New Phytologist, 2011, 189, 710-722.	7.3	108
4	Tuber melanosporum: mating type distribution in a natural plantation and dynamics of strains of different mating types on the roots of nurseryâ€inoculated host plants. New Phytologist, 2011, 189, 723-735.	7.3	104
5	Rapid molecular approach for a reliable identification of Tuber spp. ectomycorrhizae. FEMS Microbiology Ecology, 1999, 28, 23-30.	2.7	103
6	Tuber melanosporum outcrosses: analysis of the genetic diversity within and among its natural populations under this new scenario. New Phytologist, 2008, 180, 466-478.	7.3	98
7	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. Nature Ecology and Evolution, 2018, 2, 1956-1965.	7.8	95
8	Molecular cytogenetics and DNA sequence analysis of an apomixis-linked BAC in Paspalum simplex reveal a non pericentromere location and partial microcolinearity with rice. Theoretical and Applied Genetics, 2006, 112, 1179-1191.	3.6	90
9	Ectopic Expression of a Basic Helix-Loop-Helix Gene Transactivates Parallel Pathways of Proanthocyanidin Biosynthesis. Structure, Expression Analysis, and Genetic Control of Leucoanthocyanidin 4-Reductase and Anthocyanidin Reductase Genes in Lotus corniculatus Â. Plant Physiology, 2007, 143, 504-516.	4.8	90
10	Genetic and Phylogeographic Structures of the Symbiotic Fungus Tuber magnatum. Applied and Environmental Microbiology, 2005, 71, 6584-6589.	3.1	84
11	Gene expression profiles of O3-treated Arabidopsis plants. Plant, Cell and Environment, 2006, 29, 1686-1702.	5.7	84
12	Fineâ€scale spatial genetic structure of the black truffle (Tuber melanosporum) investigated with neutral microsatellites and functional mating type genes. New Phytologist, 2013, 199, 176-187.	7.3	83
13	Typing Tuber melanosporum and Chinese black truffle species by molecular markers. FEMS Microbiology Letters, 2006, 153, 255-260.	1.8	82
14	The strawberry transcription factor FaMYB1 inhibits the biosynthesis of proanthocyanidins in Lotus corniculatus leaves. Journal of Experimental Botany, 2011, 62, 1189-1200.	4.8	82
15	Sn, a maize bHLH gene, modulates anthocyanin and condensed tannin pathways in Lotus corniculatus. Journal of Experimental Botany, 2003, 54, 239-248.	4.8	70
16	The Arabidopsis thaliana cysteine-rich receptor-like kinase CRK20 modulates host responses to Pseudomonas syringae pv. tomato DC3000 infection. Journal of Plant Physiology, 2011, 168, 1784-1794.	3.5	68
17	Distribution and localization of microsatellites in the Perigord black truffle genome and identification of new molecular markers. Fungal Genetics and Biology, 2011, 48, 592-601.	2.1	67
18	Single step molecular characterization of morphologically similar black truffle species. FEMS Microbiology Letters, 1998, 164, 7-12.	1.8	64

#	Article	IF	Citations
19	Isolation and characterization of some mycelia inhabiting Tuber ascomata. Mycological Research, 2007, 111, 1450-1460.	2.5	61
20	Certainties and uncertainties about the life cycle of the PÃ©rigord black truffle (Tuber melanosporum) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.6	61
21	The volatile organic compounds from the mycelium of Tuber borchii Vitt.. Phytochemistry, 2000, 55, 983-985.	2.9	55
22	The overexpression of an alternative oxidase gene triggers ozone sensitivity in tobacco plants. Plant, Cell and Environment, 2007, 30, 1545-1556.	5.7	54
23	An apomixis-linkedORC3-like pseudogene is associated with silencing of its functional homolog in apomicticPaspalum simplex. Journal of Experimental Botany, 2016, 67, 1965-1978.	4.8	53
24	Comparison of ectomycorrhizal communities in natural and cultivated Tuber melanosporum truffle grounds. FEMS Microbiology Ecology, 2012, 81, 547-561.	2.7	47
25	Tuber aestivumandTuber uncinatum: two morphotypes or two species?. FEMS Microbiology Letters, 2004, 235, 109-115.	1.8	45
26	Light and an exogenous transcription factor qualitatively and quantitatively affect the biosynthetic pathway of condensed tannins in Lotus corniculatus leaves. Journal of Experimental Botany, 2005, 56, 1093-1103.	4.8	45
27	Morphological and molecular analyses of ectomycorrhizal diversity in a man-made T. melanosporum plantation: description of novel truffle-like morphotypes. Mycorrhiza, 2006, 16, 475-484.	2.8	44
28	Impact of the competition between mating types on the cultivation of Tuber melanosporum: Romeo and Juliet and the matter of space and time. Mycorrhiza, 2014, 24, 19-27.	2.8	41
29	Identification ofTuber spp and corresponding ectomycorrhizae through molecular markers. Journal of the Science of Food and Agriculture, 1995, 69, 511-517.	3.5	40
30	The R2R3MYB VvMYBPA1 from grape reprograms the phenylpropanoid pathway in tobacco flowers. Planta, 2017, 246, 185-199.	3.2	38
31	Isolation and characterization of polymorphic microsatellite loci in white truffle (Tuber magnatum). Molecular Ecology Notes, 2004, 4, 116-118.	1.7	37
32	Troubles with truffles: unveiling more of their biology. New Phytologist, 2007, 174, 256-259.	7.3	36
33	Assessment of inter- and intra-specific variability in the main species ofBoletus eduliscomplex by ITS analysis. FEMS Microbiology Letters, 2005, 243, 411-416.	1.8	35
34	Self/nonself recognition in Tuber melanosporum is not mediated by a heterokaryon incompatibility system. Fungal Biology, 2012, 116, 261-275.	2.5	34
35	Morphological characterization of molecular-typed Tuber magnatum ectomycorrhizae. Mycorrhiza, 2001, 11, 179-185.	2.8	32
36	Orchard Conditions and Fruiting Body Characteristics Drive the Microbiome of the Black Truffle Tuber aestivum. Frontiers in Microbiology, 2019, 10, 1437.	3.5	31

#	Article	IF	Citations
37	Expression of the Neuron-Specific FE65 Gene Marks the Development of Embryo Ganglionic Derivatives. Developmental Neuroscience, 1994, 16, 53-60.	2.0	30
38	Lotus tenuis x L. corniculatus interspecific hybridization as a means to breed bloat-safe pastures and gain insight into the genetic control of proanthocyanidin biosynthesis in legumes. BMC Plant Biology, 2014, 14, 40.	3.6	27
39	The maize transcription factor Sn alters proanthocyanidin synthesis in transgenic Lotus corniculatus plants. Functional Plant Biology, 1999, 26, 159.	2.1	26
40	Mating Type Locus of Chinese Black Truffles Reveals Heterothallism and the Presence of Cryptic Species within the T. indicum Species Complex. PLoS ONE, 2013, 8, e82353.	2.5	26
41	Isolation and Characterization of the Flavonol Regulator CcMYB12 From the Globe Artichoke [Cynara cardunculus var. scolymus (L.) Fiori]. Frontiers in Plant Science, 2018, 9, 941.	3.6	25
42	The R2R3-MYB TT2b and the bHLH TT8 genes are the major regulators of proanthocyanidin biosynthesis in the leaves of Lotus species. Planta, 2017, 246, 243-261.	3.2	24
43	Early Responses to Severe Drought Stress in the Arabidopsis thaliana Cell Suspension Culture Proteome. Proteomes, 2018, 6, 38.	3.5	24
44	Characterization of the reproductive mode and life cycle of the whitish truffle T. borchii. Mycorrhiza, 2016, 26, 515-527.	2.8	23
45	A maize anthocyanin transactivator induces pigmentation in hairy roots of dicotyledonous species. Plant Cell Reports, 1998, 17, 339-344.	5.6	22
46	Tuber aestivum and Tuber uncinatum: two morphotypes or two species?. FEMS Microbiology Letters, 2004, 235, 109-115.	1.8	21
47	Cloning and characterization of two repeated sequences in the symbiotic fungus Tuber melanosporum Vitt.. FEMS Microbiology Ecology, 2000, 34, 139-146.	2.7	20
48	The AD-type ectomycorrhizas, one of the most common morphotypes present in truffle fields, result from fungi belonging to the Trichophaea woolhopeia species complex. Mycorrhiza, 2011, 21, 17-25.	2.8	19
49	Tuber magnatum: The Special One. What Makes It so Different from the Other Tuber spp.?. Soil Biology, 2016, , 87-103.	0.8	19
50	Desert truffle genomes reveal their reproductive modes and new insights into plantâ€“fungal interaction and ectendomycorrhizal lifestyle. New Phytologist, 2021, 229, 2917-2932.	7.3	19
51	Introduction of hygromycin resistance inLotus spp. throughAgrobacterium rhizogenes transformation. Transgenic Research, 1993, 2, 330-335.	2.4	18
52	Expression patterns of endothelial and inducible nitric oxide synthase isoforms in corpora lutea of pseudopregnant rabbits at different luteal stages. Journal of Endocrinology, 2002, 173, 285-296.	2.6	17
53	SSR-based identification of genetic groups within European populations of Tuber aestivum Vittad. Mycorrhiza, 2016, 26, 99-110.	2.8	17
54	Tmt1: the first LTR-retrotransposon from a Tuber spp.. Current Genetics, 2008, 53, 23-34.	1.7	13

#	Article	IF	Citations
55	Genetic Structure and Phylogeography of Tuber magnatum Populations. Diversity, 2020, 12, 44.	1.7	13
56	A repetitive and species-specific sequence as a tool for detecting the genome contribution in somatic hybrids of the genus Medicago. Theoretical and Applied Genetics, 1997, 95, 734-740.	3.6	12
57	Transcription of a maize cDNA in Lotus corniculatus is regulated by T-DNA methylation and transgene copy number. Theoretical and Applied Genetics, 1999, 98, 257-264.	3.6	12
58	Novel morphological and genetic tools to discriminate species among the family Plumatellidae (Phylactolaemata, Bryozoa). Hydrobiologia, 2011, 664, 81-93.	2.0	12
59	The Headspace Volatiles of the Asian TruffleTuber indicumCooke et Mass. Journal of Essential Oil Research, 2002, 14, 3-5.	2.7	10
60	Genomics of Tuber melanosporum: New Knowledge Concerning Reproductive Biology, Symbiosis, and Aroma Production. Soil Biology, 2012, , 57-72.	0.8	10
61	Ribosomal DNA polymorphisms reveal genetic structure and a phylogeographic pattern in the Burgundy truffleTuber aestivumVittad.. Mycologia, 2019, 111, 26-39.	1.9	10
62	Whole-Transcriptome Analysis Unveils the Synchronized Activities of Genes for Fructans in Developing Tubers of the Jerusalem Artichoke. Frontiers in Plant Science, 2020, 11, 101.	3.6	10
63	Rapid molecular approach for a reliable identification of Tuber spp. ectomycorrhizae. FEMS Microbiology Ecology, 1999, 28, 23-30.	2.7	7
64	Light and Temperature Shape the Phenylpropanoid Profile of Azolla filiculoides Fronds. Frontiers in Plant Science, 2021, 12, 727667.	3.6	6
65	Exposure to different light intensities affects emission of volatiles and accumulations of both pigments and phenolics in Azolla filiculoides. Physiologia Plantarum, 2022, 174, e13619.	5.2	6
66	Drought stress induces a biphasic NO accumulation in Arabidopsis thaliana. Plant Signaling and Behavior, 2019, 14, e1573098.	2.4	5
67	Birdsfoot Trefoil: A Model for Studying the Synthesis of Condensed Tannins. , 1999, 66, 343-356.		5
68	Functional Characterization of MtrGSTF7, a Glutathione S-Transferase Essential for Anthocyanin Accumulation in Medicago truncatula. Plants, 2022, 11, 1318.	3.5	5
69	Molecular phylogenetic analyses show that Amanita ovoidea and Amanita proxima are distinct species and suggest their assignment to Roanokenses section. Mycological Progress, 2019, 18, 1275-1283.	1.4	4
70	Agronomic and molecular analysis of heterosis in alfalfa. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 288-290.	0.8	3
71	Single step molecular characterization of morphologically similar black truffle species. FEMS Microbiology Letters, 1998, 164, 7-12.	1.8	3
72	Cloning and characterization of two repeated sequences in the symbiotic fungus Tuber melanosporum Vitt.. FEMS Microbiology Ecology, 2000, 34, 139-146.	2.7	1

#	Article	IF	Citations
73	Genetic Transformation of Lotus Species. , 2008, , 301-315.		1
74	Sn-Transgenic Lotus corniculatus Lines: A Potential Source of Differentially Expressed Genes Involved in Condensed Tannins Biosynthesis. , 2003, , 525-528.		0
75	Proanthocyanidin Biosynthesis in Forage Legumes with Especial Reference to the Regulatory Role of R2R3MYB Transcription Factors and Their Analysis in Lotus japonicus. , 2009, , 125-132.		0