

Massimo Delledonne

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5793888/massimo-delledonne-publications-by-citations.pdf>

Version: 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

208
papers

18,370
citations

62
h-index

134
g-index

218
ext. papers

21,581
ext. citations

6.5
avg, IF

6.19
L-index

#	Paper	IF	Citations
208	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. <i>Nature</i> , 2007 , 449, 463-7	50.4	2675
207	International network of cancer genome projects. <i>Nature</i> , 2010 , 464, 993-8	50.4	1613
206	Nitric oxide functions as a signal in plant disease resistance. <i>Nature</i> , 1998 , 394, 585-8	50.4	1543
205	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016 , 13, 1050-1054	21.6	1015
204	Signal interactions between nitric oxide and reactive oxygen intermediates in the plant hypersensitive disease resistance response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 13454-9	11.5	874
203	The involvement of cysteine proteases and protease inhibitor genes in the regulation of programmed cell death in plants. <i>Plant Cell</i> , 1999 , 11, 431-44	11.6	619
202	NO news is good news for plants. <i>Current Opinion in Plant Biology</i> , 2005 , 8, 390-6	9.9	395
201	Arabidopsis nonsymbiotic hemoglobin AHb1 modulates nitric oxide bioactivity. <i>Plant Cell</i> , 2004 , 16, 2785-2796	9.9	297
200	Characterization of transcriptional complexity during berry development in <i>Vitis vinifera</i> using RNA-Seq. <i>Plant Physiology</i> , 2010 , 152, 1787-95	6.6	294
199	S-nitrosylation of peroxiredoxin II E promotes peroxynitrite-mediated tyrosine nitration. <i>Plant Cell</i> , 2007 , 19, 4120-30	11.6	283
198	Genome analysis of <i>Bifidobacterium bifidum</i> PRL2010 reveals metabolic pathways for host-derived glycan foraging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 19514-9	11.5	266
197	The grapevine expression atlas reveals a deep transcriptome shift driving the entire plant into a maturation program. <i>Plant Cell</i> , 2012 , 24, 3489-505	11.6	252
196	Proteomic analysis of S-nitrosylated proteins in <i>Arabidopsis thaliana</i> undergoing hypersensitive response. <i>Proteomics</i> , 2008 , 8, 1459-69	4.8	243
195	NO signals in the haze: nitric oxide signalling in plant defence. <i>Current Opinion in Plant Biology</i> , 2009 , 12, 451-8	9.9	218
194	Decreased epigenetic age of PBMCs from Italian semi-supercentenarians and their offspring. <i>Aging</i> , 2015 , 7, 1159-70	5.6	211
193	Nitric oxide signalling functions in plant-pathogen interactions. <i>Cellular Microbiology</i> , 2004 , 6, 795-803	3.9	204
192	Insight into the evolution of the Solanaceae from the parental genomes of <i>Petunia hybrida</i> . <i>Nature Plants</i> , 2016 , 2, 16074	11.5	198

191	MYO1E mutations and childhood familial focal segmental glomerulosclerosis. <i>New England Journal of Medicine</i> , 2011 , 365, 295-306	59.2	195
190	Annotating genomes with massive-scale RNA sequencing. <i>Genome Biology</i> , 2008 , 9, R175	18.3	186
189	Metacaspase activity of <i>Arabidopsis thaliana</i> is regulated by S-nitrosylation of a critical cysteine residue. <i>Journal of Biological Chemistry</i> , 2007 , 282, 1352-8	5.4	182
188	Role of sortase-dependent pili of <i>Bifidobacterium bifidum</i> PRL2010 in modulating bacterium-host interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 11151-6	11.5	172
187	Nitric oxide- and hydrogen peroxide-responsive gene regulation during cell death induction in tobacco. <i>Plant Physiology</i> , 2006 , 141, 404-11	6.6	166
186	Nitric oxide-mediated transcriptional changes in <i>Arabidopsis thaliana</i> . <i>Molecular Plant-Microbe Interactions</i> , 2003 , 16, 1094-105	3.6	165
185	Cross talk between reactive nitrogen and oxygen species during the hypersensitive disease resistance response. <i>Plant Physiology</i> , 2006 , 141, 379-83	6.6	164
184	Genetic elucidation of nitric oxide signaling in incompatible plant-pathogen interactions. <i>Plant Physiology</i> , 2004 , 136, 2875-86	6.6	157
183	AtCYS1, a cystatin from <i>Arabidopsis thaliana</i> , suppresses hypersensitive cell death. <i>FEBS Journal</i> , 2003 , 270, 2593-604		154
182	Nitric oxide as a mediator for defense responses. <i>Molecular Plant-Microbe Interactions</i> , 2013 , 26, 271-7	3.6	149
181	Nitric oxide mediates iron-induced ferritin accumulation in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2002 , 30, 521-8	6.9	149
180	General and species-specific transcriptional responses to downy mildew infection in a susceptible (<i>Vitis vinifera</i>) and a resistant (<i>V. riparia</i>) grapevine species. <i>BMC Genomics</i> , 2010 , 11, 117	4.5	127
179	Identification of putative stage-specific grapevine berry biomarkers and omics data integration into networks. <i>Plant Physiology</i> , 2010 , 154, 1439-59	6.6	123
178	S-nitrosylation of ascorbate peroxidase is part of programmed cell death signaling in tobacco Bright Yellow-2 cells. <i>Plant Physiology</i> , 2013 , 163, 1766-75	6.6	122
177	Glutathione synthesis is regulated by nitric oxide in <i>Medicago truncatula</i> roots. <i>Planta</i> , 2007 , 225, 1597-607	6.7	121
176	The <i>Bifidobacterium dentium</i> Bd1 genome sequence reflects its genetic adaptation to the human oral cavity. <i>PLoS Genetics</i> , 2009 , 5, e1000785	6	120
175	The plasticity of the grapevine berry transcriptome. <i>Genome Biology</i> , 2013 , 14, r54	18.3	119
174	Peroxynitrite formation and function in plants. <i>Plant Science</i> , 2011 , 181, 534-9	5.3	119

173	The <i>Solanum commersonii</i> Genome Sequence Provides Insights into Adaptation to Stress Conditions and Genome Evolution of Wild Potato Relatives. <i>Plant Cell</i> , 2015 , 27, 954-68	11.6	112
172	Downy mildew resistance induced by <i>Trichoderma harzianum</i> T39 in susceptible grapevines partially mimics transcriptional changes of resistant genotypes. <i>BMC Genomics</i> , 2012 , 13, 660	4.5	108
171	Deciphering bifidobacterial-mediated metabolic interactions and their impact on gut microbiota by a multi-omics approach. <i>ISME Journal</i> , 2016 , 10, 1656-68	11.9	107
170	Protein nitration during defense response in <i>Arabidopsis thaliana</i> . <i>Electrophoresis</i> , 2009 , 30, 2460-8	3.6	103
169	Modulation of nitric oxide bioactivity by plant haemoglobins. <i>Journal of Experimental Botany</i> , 2006 , 57, 479-88	7	103
168	Comparative effects of various nitric oxide donors on ferritin regulation, programmed cell death, and cell redox state in plant cells. <i>Journal of Plant Physiology</i> , 2004 , 161, 777-83	3.6	101
167	<i>Bifidobacterium asteroides</i> PRL2011 genome analysis reveals clues for colonization of the insect gut. <i>PLoS ONE</i> , 2012 , 7, e44229	3.7	91
166	Auxin induces redox regulation of ascorbate peroxidase 1 activity by S-nitrosylation/denitrosylation balance resulting in changes of root growth pattern in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2013 , 64, 3339-49	7	89
165	The high polyphenol content of grapevine cultivar tannat berries is conferred primarily by genes that are not shared with the reference genome. <i>Plant Cell</i> , 2013 , 25, 4777-88	11.6	88
164	Functional genomic analysis of constitutive and inducible defense responses to <i>Fusarium verticillioides</i> infection in maize genotypes with contrasting ear rot resistance. <i>BMC Genomics</i> , 2014 , 15, 710	4.5	87
163	Expression of <i>Medicago truncatula</i> genes responsive to nitric oxide in pathogenic and symbiotic conditions. <i>Molecular Plant-Microbe Interactions</i> , 2008 , 21, 781-90	3.6	84
162	Sequence analysis of the cloned glossy8 gene of maize suggests that it may code for a beta-ketoacyl reductase required for the biosynthesis of cuticular waxes. <i>Plant Physiology</i> , 1997 , 115, 501-10	6.6	83
161	De novo transcriptome characterization of <i>Vitis vinifera</i> cv. Corvina unveils varietal diversity. <i>BMC Genomics</i> , 2013 , 14, 41	4.5	82
160	Metabolite and transcript profiling of berry skin during fruit development elucidates differential regulation between Cabernet Sauvignon and Shiraz cultivars at branching points in the polyphenol pathway. <i>BMC Plant Biology</i> , 2014 , 14, 188	5.3	80
159	Reactive oxygen intermediates modulate nitric oxide signaling in the plant hypersensitive disease-resistance response. <i>Plant Physiology and Biochemistry</i> , 2002 , 40, 605-610	5.4	80
158	Decreased Nucleotide and Expression Diversity and Modified Coexpression Patterns Characterize Domestication in the Common Bean. <i>Plant Cell</i> , 2014 , 26, 1901-1912	11.6	76
157	Resistance to <i>Plasmopara viticola</i> in a grapevine segregating population is associated with stilbenoid accumulation and with specific host transcriptional responses. <i>BMC Plant Biology</i> , 2011 , 11, 114	5.3	74
156	A chromosome-anchored eggplant genome sequence reveals key events in Solanaceae evolution. <i>Scientific Reports</i> , 2019 , 9, 11769	4.9	73

155	Expression dynamics of the Medicago truncatula transcriptome during the symbiotic interaction with Sinorhizobium meliloti: which role for nitric oxide?. <i>Plant Physiology</i> , 2013 , 161, 425-39	6.6	73
154	Molecular analysis of post-harvest withering in grape by AFLP transcriptional profiling. <i>Journal of Experimental Botany</i> , 2008 , 59, 4145-59	7	73
153	The sulfated laminarin triggers a stress transcriptome before priming the SA- and ROS-dependent defenses during grapevine's induced resistance against Plasmopara viticola. <i>PLoS ONE</i> , 2014 , 9, e88145	3.7	70
152	Transcriptomic analysis of the late stages of grapevine (Vitis vinifera cv. Cabernet Sauvignon) berry ripening reveals significant induction of ethylene signaling and flavor pathways in the skin. <i>BMC Plant Biology</i> , 2014 , 14, 370	5.3	68
151	Transformation of white poplar (Populus alba L.) with a novel Arabidopsis thaliana cysteine proteinase inhibitor and analysis of insect pest resistance. <i>Molecular Breeding</i> , 2001 , 7, 35-42	3.4	67
150	DNA methylation and gene expression profiles show novel regulatory pathways in hepatocellular carcinoma. <i>Clinical Epigenetics</i> , 2015 , 7, 43	7.7	64
149	Combining next-generation pyrosequencing with microarray for large scale expression analysis in non-model species. <i>BMC Genomics</i> , 2009 , 10, 555	4.5	64
148	Flavo-haemoglobin HmpX from Erwinia chrysanthemi confers nitrosative stress tolerance and affects the plant hypersensitive reaction by intercepting nitric oxide produced by the host. <i>Plant Journal</i> , 2005 , 43, 226-37	6.9	64
147	Molecular basis of autotrophic vs mixotrophic growth in Chlorella sorokiniana. <i>Scientific Reports</i> , 2018 , 8, 6465	4.9	62
146	On site DNA barcoding by nanopore sequencing. <i>PLoS ONE</i> , 2017 , 12, e0184741	3.7	62
145	Optimized pipeline of MuTect and GATK tools to improve the detection of somatic single nucleotide polymorphisms in whole-exome sequencing data. <i>BMC Bioinformatics</i> , 2016 , 17, 341	3.6	60
144	Characterization of the serpin-encoding gene of Bifidobacterium breve 210B. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 3206-19	4.8	58
143	The functions of nitric oxide-mediated signaling and changes in gene expression during the hypersensitive response. <i>Antioxidants and Redox Signaling</i> , 2003 , 5, 33-41	8.4	58
142	Transformation of elite white poplar (Populus alba L.) cv. 'Villafranca' and evaluation of herbicide resistance. <i>Plant Cell Reports</i> , 2000 , 19, 978-982	5.1	54
141	High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in Vitis vinifera. <i>BMC Genomics</i> , 2009 , 10, 558	4.5	52
140	Soybean Kunitz, C-II and PI-IV inhibitor genes confer different levels of insect resistance to tobacco and potato transgenic plants. <i>Theoretical and Applied Genetics</i> , 2000 , 101, 519-526	6	52
139	Detection of peroxynitrite accumulation in Arabidopsis thaliana during the hypersensitive defense response. <i>Nitric Oxide - Biology and Chemistry</i> , 2011 , 25, 222-8	5	51
138	Centenarians as super-controls to assess the biological relevance of genetic risk factors for common age-related diseases: a proof of principle on type 2 diabetes. <i>Aging</i> , 2013 , 5, 373-85	5.6	51

137	Intronic ATTTC repeat expansions in STARD7 in familial adult myoclonic epilepsy linked to chromosome 2. <i>Nature Communications</i> , 2019 , 10, 4920	17.4	48
136	Transcriptome analysis of <i>Medicago truncatula</i> leaf senescence: similarities and differences in metabolic and transcriptional regulations as compared with <i>Arabidopsis</i> , nodule senescence and nitric oxide signalling. <i>New Phytologist</i> , 2009 , 181, 563-75	9.8	47
135	The genetic basis of sex determination in grapes. <i>Nature Communications</i> , 2020 , 11, 2902	17.4	46
134	Toward clinical genomics in everyday medicine: perspectives and recommendations. <i>Expert Review of Molecular Diagnostics</i> , 2016 , 16, 521-32	3.8	46
133	Correction: High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , 2010 , 11, 109	4.5	44
132	Whole-genome sequencing and SNV genotyping of 'Nebbiolo' (<i>Vitis vinifera</i> L.) clones. <i>Scientific Reports</i> , 2017 , 7, 17294	4.9	42
131	The <i>Arabidopsis</i> Class III Peroxidase AtPRX71 Negatively Regulates Growth under Physiological Conditions and in Response to Cell Wall Damage. <i>Plant Physiology</i> , 2015 , 169, 2513-25	6.6	40
130	Ability of <i>Bifidobacterium breve</i> to grow on different types of milk: exploring the metabolism of milk through genome analysis. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 7408-17	4.8	38
129	A Rapid and Accurate MinION-Based Workflow for Tracking Species Biodiversity in the Field. <i>Genes</i> , 2019 , 10,	4.2	37
128	Grapevine Grafting: Scion Transcript Profiling and Defense-Related Metabolites Induced by Rootstocks. <i>Frontiers in Plant Science</i> , 2017 , 8, 654	6.2	37
127	Unraveling the complexity of transcriptomic, metabolomic and quality environmental response of tomato fruit. <i>BMC Plant Biology</i> , 2017 , 17, 66	5.3	36
126	Nitric oxide signaling in plant-pathogen interactions. <i>IUBMB Life</i> , 2003 , 55, 579-83	4.7	35
125	Apple fruit superficial scald resistance mediated by ethylene inhibition is associated with diverse metabolic processes. <i>Plant Journal</i> , 2018 , 93, 270-285	6.9	34
124	Bellerophonotes: an RNA-Seq data analysis framework for chimeric transcripts discovery based on accurate fusion model. <i>Bioinformatics</i> , 2012 , 28, 2114-21	7.2	33
123	Regeneration of <i>Populus nigra</i> transgenic plants expressing a Kunitz proteinase inhibitor (KTI3) gene. <i>Molecular Breeding</i> , 1998 , 4, 137-145	3.4	33
122	Interference with ethylene perception at receptor level sheds light on auxin and transcriptional circuits associated with the climacteric ripening of apple fruit (<i>Malus x domestica</i> Borkh.). <i>Plant Journal</i> , 2016 , 88, 963-975	6.9	32
121	Symbiotic competence in <i>Lotus japonicus</i> is affected by plant nitrogen status: transcriptomic identification of genes affected by a new signalling pathway. <i>New Phytologist</i> , 2009 , 183, 380-394	9.8	32
120	Revealing impaired pathways in the an11 mutant by high-throughput characterization of <i>Petunia axillaris</i> and <i>Petunia inflata</i> transcriptomes. <i>Plant Journal</i> , 2011 , 68, 11-27	6.9	31

119	Genomic dissection of pod shattering in common bean: mutations at non-orthologous loci at the basis of convergent phenotypic evolution under domestication of leguminous species. <i>Plant Journal</i> , 2019 , 97, 693-714	6.9	30
118	Patchwork sequencing of tomato San Marzano and Vesuviano varieties highlights genome-wide variations. <i>BMC Genomics</i> , 2014 , 15, 138	4.5	29
117	Distinct colonization patterns and cDNA-AFLP transcriptome profiles in compatible and incompatible interactions between melon and different races of <i>Fusarium oxysporum</i> f. sp. <i>melonis</i> . <i>BMC Genomics</i> , 2011 , 12, 122	4.5	29
116	Transcriptome analysis of <i>Bacillus thuringiensis</i> spore life, germination and cell outgrowth in a vegetable-based food model. <i>Food Microbiology</i> , 2016 , 55, 73-85	6	27
115	RNA-Seq profile of flavescence dorée phytoplasma in grapevine. <i>BMC Genomics</i> , 2014 , 15, 1088	4.5	27
114	RNA-Seq analysis discloses early senescence and nucleolar dysfunction triggered by Tdp1 β depletion in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2013 , 64, 1941-51	7	27
113	Detection and function of nitric oxide during the hypersensitive response in <i>Arabidopsis thaliana</i> : where there's a will there's a way. <i>Nitric Oxide - Biology and Chemistry</i> , 2014 , 43, 81-8	5	26
112	Centenarians as extreme phenotypes: An ecological perspective to get insight into the relationship between the genetics of longevity and age-associated diseases. <i>Mechanisms of Ageing and Development</i> , 2017 , 165, 195-201	5.6	25
111	Identification of new BMP6 pro-peptide mutations in patients with iron overload. <i>American Journal of Hematology</i> , 2017 , 92, 562-568	7.1	25
110	Transcriptomic Profiling Discloses Molecular and Cellular Events Related to Neuronal Differentiation in SH-SY5Y Neuroblastoma Cells. <i>Cellular and Molecular Neurobiology</i> , 2017 , 37, 665-682	4.6	24
109	Global genome transcription profiling of <i>Bifidobacterium bifidum</i> PRL2010 under in vitro conditions and identification of reference genes for quantitative real-time PCR. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 8578-87	4.8	24
108	Not Just a Pathogen? Description of a Plant-Beneficial Strain. <i>Frontiers in Microbiology</i> , 2019 , 10, 1409	5.7	23
107	Early transcriptional changes in <i>Beta vulgaris</i> in response to low temperature. <i>Planta</i> , 2015 , 242, 187-201	4.7	21
106	De novo genome assembly of the soil-borne fungus and tomato pathogen <i>Pyrenochaeta lycopersici</i> . <i>BMC Genomics</i> , 2014 , 15, 313	4.5	20
105	Investigating topic models' capabilities in expression microarray data classification. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 1831-6	3	20
104	A mutation in the FZL gene of <i>Arabidopsis</i> causing alteration in chloroplast morphology results in a lesion mimic phenotype. <i>Journal of Experimental Botany</i> , 2013 , 64, 4313-28	7	20
103	IDH2 somatic mutations in chronic myeloid leukemia patients in blast crisis. <i>Leukemia</i> , 2011 , 25, 178-81	10.7	20
102	<i>Chlorella vulgaris</i> genome assembly and annotation reveals the molecular basis for metabolic acclimation to high light conditions. <i>Plant Journal</i> , 2019 , 100, 1289-1305	6.9	18

101	Histological and molecular analysis of Rdg2a barley resistance to leaf stripe. <i>Molecular Plant Pathology</i> , 2008 , 9, 463-78	5.7	18
100	Genomic history of the Italian population recapitulates key evolutionary dynamics of both Continental and Southern Europeans. <i>BMC Biology</i> , 2020 , 18, 51	7.3	18
99	Host-Mediated -Nitrosylation Disarms the Bacterial Effector HopAI1 to Reestablish Immunity. <i>Plant Cell</i> , 2017 , 29, 2871-2881	11.6	17
98	SETD2 and histone H3 lysine 36 methylation deficiency in advanced systemic mastocytosis. <i>Leukemia</i> , 2018 , 32, 139-148	10.7	17
97	A molecular signature associated with prolonged survival in glioblastoma patients treated with regorafenib. <i>Neuro-Oncology</i> , 2021 , 23, 264-276	1	17
96	Slug/Ectenin-dependent proinflammatory phenotype in hypoxic breast cancer stem cells. <i>American Journal of Pathology</i> , 2013 , 183, 1688-1697	5.8	16
95	The three genetics (nuclear DNA, mitochondrial DNA, and gut microbiome) of longevity in humans considered as metaorganisms. <i>BioMed Research International</i> , 2014 , 2014, 560340	3	16
94	Phased Diploid Genome Assembly with Single Molecule Real-Time Sequencing		16
93	Transcriptional Reprogramming of the Mycoparasitic Fungus <i>Ampelomyces quisqualis</i> During the Powdery Mildew Host-Induced Germination. <i>Phytopathology</i> , 2015 , 105, 199-209	3.8	15
92	Transcriptomic and biochemical investigations support the role of rootstock-scion interaction in grapevine berry quality. <i>BMC Genomics</i> , 2020 , 21, 468	4.5	15
91	Exploration of the genomic diversity and core genome of the <i>Bifidobacterium adolescentis</i> phylogenetic group by means of a polyphasic approach. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 336-46	4.8	15
90	Biclustering of Expression Microarray Data with Topic Models 2010 ,		15
89	Methods for nitric oxide detection during plant-pathogen interactions. <i>Methods in Enzymology</i> , 2008 , 437, 575-94	1.7	15
88	Identification of novel mutations in hemochromatosis genes by targeted next generation sequencing in Italian patients with unexplained iron overload. <i>American Journal of Hematology</i> , 2016 , 91, 420-5	7.1	15
87	Small supernumerary marker chromosomes: A legacy of trisomy rescue?. <i>Human Mutation</i> , 2019 , 40, 193-200	4.9	15
86	Molecular response of <i>Sargassum vulgare</i> to acidification at volcanic CO vents: insights from de novo transcriptomic analysis. <i>Molecular Ecology</i> , 2017 , 26, 2276-2290	5.7	14
85	Functional Transcriptome Analysis in ARSACS KO Cell Model Reveals a Role of Sacsin in Autophagy. <i>Scientific Reports</i> , 2019 , 9, 11878	4.9	14
84	Physical Activity and Nutrition Influences In ageing (PANINI): consortium mission statement. <i>Aging Clinical and Experimental Research</i> , 2018 , 30, 685-692	4.8	13

83	SOX2: Not always eye malformations. Severe genital but no major ocular anomalies in a female patient with the recurrent c.70del20 variant. <i>European Journal of Medical Genetics</i> , 2018 , 61, 335-340	2.6	12
82	Physiological and Biochemical Analyses Shed Light on the Response of to Ocean Acidification at Different Time Scales. <i>Frontiers in Plant Science</i> , 2017 , 8, 570	6.2	12
81	The Networks of Genes Encoding Palmitoylated Proteins in Axonal and Synaptic Compartments Are Affected in PPT1 Overexpressing Neuronal-Like Cells. <i>Frontiers in Molecular Neuroscience</i> , 2017 , 10, 266	6.1	12
80	The Involvement of Cysteine Proteases and Protease Inhibitor Genes in the Regulation of Programmed Cell Death in Plants. <i>Plant Cell</i> , 1999 , 11, 431	11.6	11
79	Nucleotide sequence of the nodG gene of <i>Azospirillum brasilense</i> . <i>Nucleic Acids Research</i> , 1990 , 18, 6435-6440	20.1	11
78	Whole-genome sequencing analysis of semi-supercentenarians. <i>ELife</i> , 2021 , 10,	8.9	11
77	Chromothripsis and ring chromosome 22: a paradigm of genomic complexity in the Phelan-McDermid syndrome (22q13 deletion syndrome). <i>Journal of Medical Genetics</i> , 2018 , 55, 269-277	5.8	10
76	<i>Curtobacterium</i> sp. Genome Sequencing Underlines Plant Growth Promotion-Related Traits. <i>Genome Announcements</i> , 2014 , 2,		10
75	The Use of Non-Variant Sites to Improve the Clinical Assessment of Whole-Genome Sequence Data. <i>PLoS ONE</i> , 2015 , 10, e0132180	3.7	10
74	Investigation of the transcriptomic and metabolic changes associated with superficial scald physiology impaired by lovastatin and 1-methylcyclopropene in pear fruit (cv. "Blanquilla"). <i>Horticulture Research</i> , 2020 , 7, 49	7.7	9
73	The genome assembly of the fungal pathogen <i>Pyrenochaeta lycopersici</i> from Single-Molecule Real-Time sequencing sheds new light on its biological complexity. <i>PLoS ONE</i> , 2018 , 13, e0200217	3.7	9
72	Physical Mapping of Bread Wheat Chromosome 5A: An Integrated Approach. <i>Plant Genome</i> , 2015 , 8, eplantgenome2015.03.0011	4.4	9
71	Hybrid genome assembly and annotation of <i>Paenibacillus pasadenensis</i> strain R16 reveals insights on endophytic life style and antifungal activity. <i>PLoS ONE</i> , 2018 , 13, e0189993	3.7	9
70	Nitric Oxide Signaling during the Hypersensitive Disease Resistance Response. <i>Advances in Botanical Research</i> , 2016 , 77, 219-243	2.2	8
69	Investigation of orthologous pathogen recognition gene-rich regions in solanaceous species. <i>Genome</i> , 2017 , 60, 850-859	2.4	8
68	Characterization of a new B-ALL cell line with constitutional defect of the Notch signaling pathway. <i>Oncotarget</i> , 2018 , 9, 18341-18350	3.3	8
67	Insertional translocation involving an additional nonchromothriptic chromosome in constitutional chromothripsis: Rule or exception?. <i>Molecular Genetics & Genomic Medicine</i> , 2019 , 7, e00496	2.3	8
66	Improved lipid productivity in in nitrogen-replete conditions by selection of pale green mutants. <i>Biotechnology for Biofuels</i> , 2020 , 13, 78	7.8	7

65	Application of the whole-transcriptome shotgun sequencing approach to the study of Philadelphia-positive acute lymphoblastic leukemia. <i>Blood Cancer Journal</i> , 2012 , 2, e61	7	7
64	Detection of a rare mutation in the ferroportin gene through targeted next generation sequencing. <i>Blood Transfusion</i> , 2016 , 14, 531-534	3.6	7
63	A Transcriptomic Analysis of Sensitive and Tolerant Citrus Rootstocks under Natural Iron Deficiency Conditions. <i>Journal of the American Society for Horticultural Science</i> , 2013 , 138, 487-498	2.3	7
62	Depletion of tyrosyl-DNA phosphodiesterase 1 affects transposon expression in <i>Medicago truncatula</i> . <i>Journal of Integrative Plant Biology</i> , 2016 , 58, 618-22	8.3	7
61	Wide transcriptional investigation unravel novel insights of the on-tree maturation and postharvest ripening of 'Abate Fetel' pear fruit. <i>Horticulture Research</i> , 2019 , 6, 32	7.7	7
60	Centrosome Linker-induced Tetraploid Segregation Errors Link Rhabdoid Phenotypes and Lethal Colorectal Cancers. <i>Molecular Cancer Research</i> , 2018 , 16, 1385-1395	6.6	7
59	Whole-Transcriptome Analysis Unveils the Synchronized Activities of Genes for Fructans in Developing Tubers of the Jerusalem Artichoke. <i>Frontiers in Plant Science</i> , 2020 , 11, 101	6.2	6
58	A patient with PMP22-related hereditary neuropathy and DBH-gene-related dysautonomia. <i>Journal of Neurology</i> , 2015 , 262, 2373-81	5.5	6
57	Apoptosis-like DNA fragmentation in leaves and floral organs precedes their developmental senescence. <i>Plant Biosystems</i> , 2001 , 135, 183-189	1.6	6
56	A geroscience approach for Parkinson's disease: Conceptual framework and design of PROPAG-AGEING project. <i>Mechanisms of Ageing and Development</i> , 2021 , 194, 111426	5.6	6
55	Exosomes from Plasma of Neuroblastoma Patients Contain Doublestranded DNA Reflecting the Mutational Status of Parental Tumor Cells. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	6
54	Phenotype and gene expression analyses of the Rfo-sa1 resistant aubergine interaction with <i>Fusarium oxysporum</i> f. sp. <i>melongenae</i> and <i>Verticillium dahliae</i> . <i>Plant Pathology</i> , 2016 , 65, 1297-1309	2.8	6
53	Characterization of <i>Lysinibacillus fusiformis</i> strain S4C11: In vitro, in planta, and in silico analyses reveal a plant-beneficial microbe. <i>Microbiological Research</i> , 2021 , 244, 126665	5.3	6
52	Symbiotic plant-fungi interactions stripped down to the root. <i>Nature Genetics</i> , 2015 , 47, 309-10	36.3	5
51	Distinct Metabolic Signals Underlie Clone by Environment Interplay in "Nebbiolo" Grapes Over Ripening. <i>Frontiers in Plant Science</i> , 2019 , 10, 1575	6.2	5
50	Role of phage ϕ 1 in two strains of <i>Salmonella</i> Rissen, sensitive and resistant to phage ϕ 1. <i>BMC Microbiology</i> , 2018 , 18, 208	4.5	5
49	The INCREASE project: Intelligent Collections of food-legume genetic resources for European agrofood systems. <i>Plant Journal</i> , 2021 , 108, 646-660	6.9	5
48	Shedding light on dark genes: enhanced targeted resequencing by optimizing the combination of enrichment technology and DNA fragment length. <i>Scientific Reports</i> , 2020 , 10, 9424	4.9	4

47	The genetic basis of sex determination in grapevines (<i>Vitis</i> spp.)		4
46	Pod indehiscence in common bean is associated to the fine regulation of PvMYB26 and a non-functional abscission layer		4
45	ACoRE: Accurate SARS-CoV-2 genome reconstruction for the characterization of intra-host and inter-host viral diversity in clinical samples and for the evaluation of re-infections. <i>Genomics</i> , 2021 , 113, 1628-1638	4.3	4
44	Bringing the lab to the field: a new lowland <i>Microparmarion</i> semi-slug (Gastropoda: Ariophantidae) described and DNA-barcoded in the forest. <i>Journal of Molluscan Studies</i> , 2019 , 85, 35-40	1.1	4
43	MtTdp1 Δ depleted <i>Medicago truncatula</i> plants show reduced cuticle permeability and altered expression of defense genes. <i>Biologia Plantarum</i> , 2017 , 61, 192-196	2.1	3
42	EFFECT OF COOL STORAGE DURATION ON RIPENING INITIATION OF 'ANGELYS' PEAR FRUIT. <i>Acta Horticulturae</i> , 2015 , 129-136	0.3	3
41	Whole-Transcriptome Sequencing In Chronic Myeloid Leukemia Reveals Novel Gene Mutations That May Be Associated with Disease Pathogenesis and Progression. <i>Blood</i> , 2010 , 116, 885-885	2.2	3
40	Pod indehiscence in common bean is associated with the fine regulation of PvMYB26. <i>Journal of Experimental Botany</i> , 2021 , 72, 1617-1633	7	3
39	A rapid and accurate MinION-based workflow for tracking species biodiversity in the field		3
38	A Long-Read Sequencing Approach for Direct Haplotype Phasing in Clinical Settings. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	3
37	Real-Time On-Site Diagnosis of Quarantine Pathogens in Plant Tissues by Nanopore-Based Sequencing.. <i>Pathogens</i> , 2022 , 11,	4.5	2
36	METABOLIC AND TRANSCRIPTIONAL CHANGES IN RESISTANT AND SUSCEPTIBLE GENOTYPES OF A GRAPEVINE POPULATION SEGREGATING FOR THE RESISTANCE TO PLASMOPARA VITICOLA. <i>Acta Horticulturae</i> , 2009 , 635-640	0.3	2
35	A transcriptional analysis reveals an extensive range of genes responsible for increasing the tolerance of Carrizo citrange to oxygen deficiency. <i>Tree Genetics and Genomes</i> , 2019 , 15, 1	2.1	2
34	The Tannat genome: Unravelling its unique characteristics. <i>BIO Web of Conferences</i> , 2019 , 12, 01016	0.4	1
33	Detection of Peroxynitrite in Plants Exposed to Bacterial Infection. <i>Methods in Molecular Biology</i> , 2016 , 1424, 191-200	1.4	1
32	Palmoplantar keratoderma and Charcot-Marie-Tooth disease: combination of two independent genetic diseases? Identification of two point mutations in the MPZ and KRT1 genes by whole-exome sequencing. <i>British Journal of Dermatology</i> , 2017 , 177, 284-286	4	1
31	Nitric Oxide-Mediated Signaling Functions During the Plant Hypersensitive Response. <i>Plant Cell Monographs</i> , 2006 , 207-222	0.6	1
30	Metabolite and lipoprotein profiles reveal sex-related oxidative stress imbalance in de novo drug-naive Parkinson's disease patients.. <i>Npj Parkinson's Disease</i> , 2022 , 8, 14	9.7	1

29	Aggressive Aneuploid Acute Myeloid Leukemia Is Dependent on Alterations of P53, Gain of APC and PLK1 and Loss of RAD50. <i>Blood</i> , 2016 , 128, 1702-1702	2.2	1
28	Genomic structural variation in Nebbiolo grapevines at the individual, clonal and cultivar levels		1
27	Enhanced targeted resequencing by optimizing the combination of enrichment technology and DNA fragment length		1
26	Nitric Oxide Involvement in Incompatible Plant-Pathogen Interactions 2006 , 111-121		1
25	The Genomic and Transcriptomic Landscape of Systemic Mastocytosis. <i>Blood</i> , 2016 , 128, 3136-3136	2.2	1
24	Whole Transcriptome Sequencing of a Philadelphia-Positive Acute Lymphoblastic Leukemia (ALL) with Next Generation Sequencing Technology Revealed Novel Point Mutations Associated with Disease-Progression.. <i>Blood</i> , 2009 , 114, 3074-3074	2.2	1
23	Genome-wide DNA methylation and gene expression profiles analysis show novel regulatory pathways in alcohol-related hepatocellular carcinoma. <i>FASEB Journal</i> , 2013 , 27, 248.4	0.9	1
22	Genome wide association studies and whole transcriptomic survey decipher the fruit texture regulation in apple towards the selection of novel superior accessions. <i>Acta Horticulturae</i> , 2019 , 441-446 ^{0.3}		1
21	'Nebbiolo' genome assembly allows surveying the occurrence and functional implications of genomic structural variations in grapevines (<i>Vitis vinifera</i> L.).. <i>BMC Genomics</i> , 2022 , 23, 159	4.5	1
20	The interference of the ethylene perception machinery leads to a re-programming of the fruit quality-related transcriptome and induces a cross-talk circuit with auxin in apple. <i>Acta Horticulturae</i> , 2018 , 69-74	0.3	0
19	Whole-exome sequencing of the mummified remains of Cangrande della Scala (1291-1329 CE) indicates the first known case of late-onset Pompe disease. <i>Scientific Reports</i> , 2021 , 11, 21070	4.9	0
18	Genomic Analysis Of Notch Mutations In a Case Of Alagille Syndrome With Acute Lymphoblastic Leukemia. <i>Blood</i> , 2013 , 122, 4992-4992	2.2	0
17	Characterization of Repeat Expansion and Intragenic Variants by Indirect Sequence Capture. <i>Frontiers in Genetics</i> , 2021 , 12, 743230	4.5	0
16	Heterogeneity of prodromal Parkinson symptoms in siblings of Parkinson disease patients. <i>Npj Parkinsons Disease</i> , 2021 , 7, 78	9.7	0
15	The Physical Activity and Nutritional Influences in Ageing (PANINI) Toolkit: A Standardized Approach towards Physical Activity and Nutritional Assessment of Older Adults. <i>Healthcare (Switzerland)</i> , 2022 , 10, 1017	3.4	0
14	Next Generation Sequencing for Next Generation Diagnostics and Therapy 2017 , 87-102		
13	'OMICS' AND CHEMICAL APPROACHES USED TO MONITOR IRON-DEFICIENCY IN CITRUS ROOTSTOCKS. <i>Acta Horticulturae</i> , 2015 , 1293-1301	0.3	
12	TRANSCRIPTIONAL REPROGRAMMING DURING BERRY RIPENING AND WITHERING IN VITIS VINIFERA 'CORVINA'. <i>Acta Horticulturae</i> , 2009 , 351-354	0.3	

- 11 A multidisciplinary approach reveals new aspects of superficial scald aetiology and cold resistance mechanism in Granny Smith Apples. *Acta Horticulturae*, **2019**, 447-454 0.3
- 10 Inoculation of genetically modified strains of *Azospirillum*: monitoring of population dynamic **1995**, 515-521
- 9 Nitric oxide signalling in the plant hypersensitive disease resistance response. *Developments in Plant Breeding*, **1999**, 127-133
- 8 SIRPB1 Is a Strong Predictor Biomarker of Response to 5-Azacytidine Therapy in MDS and AML Patients. *Blood*, **2014**, 124, 1030-1030 2.2
- 7 Alterations of BRCA1 and PALB2 Define a Novel Class of Complex-Karyotype AML with a Very Bad Prognosis. *Blood*, **2016**, 128, 1677-1677 2.2
- 6 Identification of New BMP6 Pro-Peptide Mutations in Patients with Unexplained Iron-Overload. *Blood*, **2016**, 128, 264-264 2.2
- 5 Whole-Transcriptome Sequencing of a Chronic Myeloid Leukemia (CML) Patient at Diagnosis and at the Time of Progression to Blast Crisis (BC).. *Blood*, **2009**, 114, 4259-4259 2.2
- 4 Whole Transcriptome Resequencing of Paired Diagnosis-Relapse BCR-ABL1-Positive Acute Lymphoblastic Leukemia (ALL) Samples Reveals the Loss of Cell Cycle Regulation as the Main Mechanism Responsible for Leukemia Progression.. *Blood*, **2010**, 116, 1024-1024 2.2
- 3 Generation of a large catalog of unique transcripts for whole-genome expression analysis in nonmodel species. *Methods in Molecular Biology*, **2011**, 729, 257-69 1.4
- 2 TP53 Alterations Including Missense Mutations, Aberrant Exon-Junctions and Internal Intron Retentions Are Frequent and May Contribute to MDM2 Antagonist-Resistance in B-Acute Lymphoblastic leukemia. *Blood*, **2011**, 118, 1484-1484 2.2
- 1 Nitric Oxide Involvement in Incompatible Plant-Pathogen Interactions 111-121