Massimo Delledonne

List of Publications by Year in Descending Order

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	Real-Time On-Site Diagnosis of Quarantine Pathogens in Plant Tissues by Nanopore-Based Sequencing.. *Pathogens*, **2022**, 11,	4.5	2
207	Metabolite and lipoprotein profiles reveal sex-related oxidative stress imbalance in de novo drug-naive Parkinson's disease patients.. *Npj Parkinsonis Disease*, **2022**, 8, 14	9.7	1
206	'Nebbiolo' genome assembly allows surveying the occurrence and functional implications of genomic structural variations in grapevines (Vitis vinifera L.).. *BMC Genomics*, **2022**, 23, 159	4.5	1
205	The Physical Activity and Nutritional INfluences in Ageing (PANINI) Toolkit: A Standardized Approach towards Physical Activity and Nutritional Assessment of Older Adults. *Healthcare (Switzerland)*, **2022**, 10, 1017	3.4	0
204	Whole-exome sequencing of the mummified remains of Cangrande della Scala (1291-1329 CE) indicates the first known case of late-onset Pompe disease. *Scientific Reports*, **2021**, 11, 21070	4.9	0
203	Pod indehiscence in common bean is associated with the fine regulation of PvMYB26. *Journal of Experimental Botany*, **2021**, 72, 1617-1633	7	3
202	A geroscience approach for Parkinson's disease: Conceptual framework and design of PROPAG-AGEING project. *Mechanisms of Ageing and Development*, **2021**, 194, 111426	5.6	6
201	Exosomes from Plasma of Neuroblastoma Patients Contain Doublestranded DNA Reflecting the Mutational Status of Parental Tumor Cells. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	6
200	Whole-genome sequencing analysis of semi-supercentenarians. *ELife*, **2021**, 10,	8.9	11
199	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. *Genomics*, **2021**, 113, 1628-1638	4.3	4
198	A molecular signature associated with prolonged survival in glioblastoma patients treated with regorafenib. *Neuro-Oncology*, **2021**, 23, 264-276	1	17
197	Characterization of Lysinibacillus fusiformis strain S4C11: In vitro, in planta, and in silico analyses reveal a plant-beneficial microbe. *Microbiological Research*, **2021**, 244, 126665	5.3	6
196	Characterization of Repeat Expansion and Intragenic Variants by Indirect Sequence Capture. *Frontiers in Genetics*, **2021**, 12, 743230	4.5	0
195	The INCREASE project: Intelligent Collections of food-legume genetic resources for European agrofood systems. *Plant Journal*, **2021**, 108, 646-660	6.9	5
194	Heterogeneity of prodromal Parkinson symptoms in siblings of Parkinson disease patients. *Npj Parkinsonis Disease*, **2021**, 7, 78	9.7	0
193	The genetic basis of sex determination in grapes. *Nature Communications*, **2020**, 11, 2902	17.4	46
192	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	6.2	6

191	Shedding light on dark genes: enhanced targeted resequencing by optimizing the combination of enrichment technology and DNA fragment length. *Scientific Reports*, **2020**, 10, 9424	4.9	4
190	Transcriptomic and biochemical investigations support the role of rootstock-scion interaction in grapevine berry quality. *BMC Genomics*, **2020**, 21, 468	4.5	15
189	Investigation of the transcriptomic and metabolic changes associated with superficial scald physiology impaired by lovastatin and 1-methylcyclopropene in pear fruit (cv. "Blanquilla"). *Horticulture Research*, **2020**, 7, 49	7.7	9
188	Improved lipid productivity in in nitrogen-replete conditions by selection of pale green mutants. *Biotechnology for Biofuels*, **2020**, 13, 78	7.8	7
187	Genomic history of the Italian population recapitulates key evolutionary dynamics of both Continental and Southern Europeans. *BMC Biology*, **2020**, 18, 51	7.3	18
186	A Long-Read Sequencing Approach for Direct Haplotype Phasing in Clinical Settings. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	3
185	The Tannat genome: Unravelling its unique characteristics. *BIO Web of Conferences*, **2019**, 12, 01016	0.4	1
184	Not Just a Pathogen? Description of a Plant-Beneficial Strain. *Frontiers in Microbiology*, **2019**, 10, 1409	5.7	23
183	A chromosome-anchored eggplant genome sequence reveals key events in Solanaceae evolution. *Scientific Reports*, **2019**, 9, 11769	4.9	73
182	Functional Transcriptome Analysis in ARSACS KO Cell Model Reveals a Role of Sacsin in Autophagy. *Scientific Reports*, **2019**, 9, 11878	4.9	14
181	Chlorella vulgaris genome assembly and annotation reveals the molecular basis for metabolic acclimation to high light conditions. *Plant Journal*, **2019**, 100, 1289-1305	6.9	18
180	A Rapid and Accurate MinION-Based Workflow for Tracking Species Biodiversity in the Field. *Genes*, **2019**, 10,	4.2	37
179	Intronic ATTTC repeat expansions in STARD7 in familial adult myoclonic epilepsy linked to chromosome 2. *Nature Communications*, **2019**, 10, 4920	17.4	48
178	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	
177	Wide transcriptional investigation unravel novel insights of the on-tree maturation and postharvest ripening of 'Abate Fetel' pear fruit. *Horticulture Research*, **2019**, 6, 32	7.7	7
176	A transcriptional analysis reveals an extensive range of genes responsible for increasing the tolerance of Carrizo citrange to oxygen deficiency. *Tree Genetics and Genomes*, **2019**, 15, 1	2.1	2
175	Genome wide association studies and whole transcriptomic survey decipher the fruit texture regulation in apple towards the selection of novel superior accessions. *Acta Horticulturae*, **2019**, 441-446	0.3	1
174	Distinct Metabolic Signals Underlie Clone by Environment Interplay in "Nebbiolo" Grapes Over Ripening. *Frontiers in Plant Science*, **2019**, 10, 1575	6.2	5

173	Bringing the lab to the field: a new lowland Microparmarion semi-slug (Gastropoda: Ariophantidae) described and DNA-barcoded in the forest. *Journal of Molluscan Studies*, **2019**, 85, 35-40	1.1	4
172	Insertional translocation involving an additional nonchromothriptic chromosome in constitutional chromothripsis: Rule or exception?. *Molecular Genetics & Genomic Medicine*, **2019**, 7, e00496	2.3	8
171	Small supernumerary marker chromosomes: A legacy of trisomy rescue?. *Human Mutation*, **2019**, 40, 193-200	4.7	15
170	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. *Plant Journal*, **2019**, 97, 693-714	6.9	30
169	Chromothripsis and ring chromosome 22: a paradigm of genomic complexity in the Phelan-McDermid syndrome (22q13 deletion syndrome). *Journal of Medical Genetics*, **2018**, 55, 269-277	5.8	10
168	SETD2 and histone H3 lysine 36 methylation deficiency in advanced systemic mastocytosis. *Leukemia*, **2018**, 32, 139-148	10.7	17
167	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. *Acta Horticulturae*, **2018**, 69-74	0.3	0
166	The genome assembly of the fungal pathogen Pyrenochaeta lycopersici from Single-Molecule Real-Time sequencing sheds new light on its biological complexity. *PLoS ONE*, **2018**, 13, e0200217	3.7	9
165	Molecular basis of autotrophic vs mixotrophic growth in Chlorella sorokiniana. *Scientific Reports*, **2018**, 8, 6465	4.9	62
164	Physical Activity and Nutrition INfluences In ageing (PANINI): consortium mission statement. *Aging Clinical and Experimental Research*, **2018**, 30, 685-692	4.8	13
163	SOX2: Not always eye malformations. Severe genital but no major ocular anomalies in a female patient with the recurrent c.70del20 variant. *European Journal of Medical Genetics*, **2018**, 61, 335-340	2.6	12
162	Hybrid genome assembly and annotation of Paenibacillus pasadenensis strain R16 reveals insights on endophytic life style and antifungal activity. *PLoS ONE*, **2018**, 13, e0189993	3.7	9
161	Characterization of a new B-ALL cell line with constitutional defect of the Notch signaling pathway. *Oncotarget*, **2018**, 9, 18341-18350	3.3	8
160	Apple fruit superficial scald resistance mediated by ethylene inhibition is associated with diverse metabolic processes. *Plant Journal*, **2018**, 93, 270-285	6.9	34
159	Role of phage ?1 in two strains of Salmonella Rissen, sensitive and resistant to phage ?1. *BMC Microbiology*, **2018**, 18, 208	4.5	5
158	Centrosome Linker-induced Tetraploid Segregation Errors Link Rhabdoid Phenotypes and Lethal Colorectal Cancers. *Molecular Cancer Research*, **2018**, 16, 1385-1395	6.6	7
157	Molecular response of Sargassum vulgare to acidification at volcanic CO vents: insights from de novo transcriptomic analysis. *Molecular Ecology*, **2017**, 26, 2276-2290	5.7	14
156	Centenarians as extreme phenotypes: An ecological perspective to get insight into the relationship between the genetics of longevity and age-associated diseases. *Mechanisms of Ageing and Development*, **2017**, 165, 195-201	5.6	25

155	Unraveling the complexity of transcriptomic, metabolomic and quality environmental response of tomato fruit. *BMC Plant Biology*, **2017**, 17, 66	5.3	36
154	Identification of new BMP6 pro-peptide mutations in patients with iron overload. *American Journal of Hematology*, **2017**, 92, 562-568	7.1	25
153	MtTdp1-depleted Medicago truncatula plants show reduced cuticle permeability and altered expression of defense genes. *Biologia Plantarum*, **2017**, 61, 192-196	2.1	3
152	Host-Mediated -Nitrosylation Disarms the Bacterial Effector HopAI1 to Reestablish Immunity. *Plant Cell*, **2017**, 29, 2871-2881	11.6	17
151	Investigation of orthologous pathogen recognition gene-rich regions in solanaceous species. *Genome*, **2017**, 60, 850-859	2.4	8
150	Next Generation Sequencing for Next Generation Diagnostics and Therapy **2017**, 87-102		
149	Transcriptomic Profiling Discloses Molecular and Cellular Events Related to Neuronal Differentiation in SH-SY5Y Neuroblastoma Cells. *Cellular and Molecular Neurobiology*, **2017**, 37, 665-682	4.6	24
148	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. *British Journal of Dermatology*, **2017**, 177, 284-286	4	1
147	Whole-genome sequencing and SNV genotyping of 'Nebbiolo' (Vitis vinifera L.) clones. *Scientific Reports*, **2017**, 7, 17294	4.9	42
146	Physiological and Biochemical Analyses Shed Light on the Response of to Ocean Acidification at Different Time Scales. *Frontiers in Plant Science*, **2017**, 8, 570	6.2	12
145	Grapevine Grafting: Scion Transcript Profiling and Defense-Related Metabolites Induced by Rootstocks. *Frontiers in Plant Science*, **2017**, 8, 654	6.2	37
144	The Networks of Genes Encoding Palmitoylated Proteins in Axonal and Synaptic Compartments Are Affected in PPT1 Overexpressing Neuronal-Like Cells. *Frontiers in Molecular Neuroscience*, **2017**, 10, 266	6.1	12
143	On site DNA barcoding by nanopore sequencing. *PLoS ONE*, **2017**, 12, e0184741	3.7	62
142	Interference with ethylene perception at receptor level sheds light on auxin and transcriptional circuits associated with the climacteric ripening of apple fruit (Malus x domestica Borkh.). *Plant Journal*, **2016**, 88, 963-975	6.9	32
141	Phased diploid genome assembly with single-molecule real-time sequencing. *Nature Methods*, **2016**, 13, 1050-1054	21.6	1015
140	Insight into the evolution of the Solanaceae from the parental genomes of Petunia hybrida. *Nature Plants*, **2016**, 2, 16074	11.5	198
139	Detection of Peroxynitrite in Plants Exposed to Bacterial Infection. *Methods in Molecular Biology*, **2016**, 1424, 191-200	1.4	1
138	Toward clinical genomics in everyday medicine: perspectives and recommendations. *Expert Review of Molecular Diagnostics*, **2016**, 16, 521-32	3.8	46

137	Nitric Oxide Signaling during the Hypersensitive Disease Resistance Response. *Advances in Botanical Research*, **2016**, 77, 219-243	2.2	8
136	Deciphering bifidobacterial-mediated metabolic interactions and their impact on gut microbiota by a multi-omics approach. *ISME Journal*, **2016**, 10, 1656-68	11.9	107
135	Transcriptome analysis of Bacillus thuringiensis spore life, germination and cell outgrowth in a vegetable-based food model. *Food Microbiology*, **2016**, 55, 73-85	6	27
134	Aggressive Aneuploid Acute Myeloid Leukemia Is Dependent on Alterations of P53, Gain of APC and PLK1 and Loss of RAD50. *Blood*, **2016**, 128, 1702-1702	2.2	1
133	Detection of a rare mutation in the ferroportin gene through targeted next generation sequencing. *Blood Transfusion*, **2016**, 14, 531-534	3.6	7
132	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	
131	Identification of New BMP6 Pro-Peptide Mutations in Patients with Unexplained Iron-Overload. *Blood*, **2016**, 128, 264-264	2.2	
130	The Genomic and Transcriptomic Landscape of Systemic Mastocytosis. *Blood*, **2016**, 128, 3136-3136	2.2	1
129	Identification of novel mutations in hemochromatosis genes by targeted next generation sequencing in Italian patients with unexplained iron overload. *American Journal of Hematology*, **2016**, 91, 420-5	7.1	15
128	Phenotype and gene expression analyses of the Rfo-sa1 resistant aubergine interaction with Fusarium oxysporum f.˙sp. melongenae and Verticillium dahliae. *Plant Pathology*, **2016**, 65, 1297-1309	2.8	6
127	Depletion of tyrosyl-DNA phosphodiesterase 1 (MtTdp1) affects transposon expression in Medicago truncatula. *Journal of Integrative Plant Biology*, **2016**, 58, 618-22	8.3	7
126	Optimized pipeline of MuTect and GATK tools to improve the detection of somatic single nucleotide polymorphisms in whole-exome sequencing data. *BMC Bioinformatics*, **2016**, 17, 341	3.6	60
125	Early transcriptional changes in Beta vulgaris in response to low temperature. *Planta*, **2015**, 242, 187-201	4.7	21
124	The Solanum commersonii Genome Sequence Provides Insights into Adaptation to Stress Conditions and Genome Evolution of Wild Potato Relatives. *Plant Cell*, **2015**, 27, 954-68	11.6	112
123	Symbiotic plant-fungi interactions stripped down to the root. *Nature Genetics*, **2015**, 47, 309-10	36.3	5
122	Transcriptional Reprogramming of the Mycoparasitic Fungus Ampelomyces quisqualis During the Powdery Mildew Host-Induced Germination. *Phytopathology*, **2015**, 105, 199-209	3.8	15
121	EFFECT OF COOL STORAGE DURATION ON RIPENING INITIATION OF 'ANGELYS' PEAR FRUIT. *Acta Horticulturae*, **2015**, 129-136	0.3	3
120	'OMICS' AND CHEMICAL APPROACHES USED TO MONITOR IRON-DEFICIENCY IN CITRUS ROOTSTOCKS. *Acta Horticulturae*, **2015**, 1293-1301	0.3	

119	A patient with PMP22-related hereditary neuropathy and DBH-gene-related dysautonomia. *Journal of Neurology*, **2015**, 262, 2373-81	5.5	6
118	The Arabidopsis Class III Peroxidase AtPRX71 Negatively Regulates Growth under Physiological Conditions and in Response to Cell Wall Damage. *Plant Physiology*, **2015**, 169, 2513-25	6.6	40
117	Physical Mapping of Bread Wheat Chromosome 5A: An Integrated Approach. *Plant Genome*, **2015**, 8, eplantgenome2015.03.0011	4.4	9
116	DNA methylation and gene expression profiles show novel regulatory pathways in hepatocellular carcinoma. *Clinical Epigenetics*, **2015**, 7, 43	7.7	64
115	The Use of Non-Variant Sites to Improve the Clinical Assessment of Whole-Genome Sequence Data. *PLoS ONE*, **2015**, 10, e0132180	3.7	10
114	Decreased epigenetic age of PBMCs from Italian semi-supercentenarians and their offspring. *Aging*, **2015**, 7, 1159-70	5.6	211
113	Patchwork sequencing of tomato San Marzano and Vesuviano varieties highlights genome-wide variations. *BMC Genomics*, **2014**, 15, 138	4.5	29
112	Detection and function of nitric oxide during the hypersensitive response in Arabidopsis thaliana: where there's a will there's a way. *Nitric Oxide - Biology and Chemistry*, **2014**, 43, 81-8	5	26
111	Functional genomic analysis of constitutive and inducible defense responses to Fusarium verticillioides infection in maize genotypes with contrasting ear rot resistance. *BMC Genomics*, **2014** , 15, 710	4.5	87
110	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. *BMC Plant Biology*, **2014**, 14, 188	5.3	80
109	De novo genome assembly of the soil-borne fungus and tomato pathogen Pyrenochaeta lycopersici. *BMC Genomics*, **2014**, 15, 313	4.5	20
108	The sulfated laminarin triggers a stress transcriptome before priming the SA- and ROS-dependent defenses during grapevine's induced resistance against Plasmopara viticola. *PLoS ONE*, **2014**, 9, e88145	3.7	70
107	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. *BMC Plant Biology*, **2014**, 14, 370	5.3	68
106	Decreased Nucleotide and Expression Diversity and Modified Coexpression Patterns Characterize Domestication in the Common Bean. *Plant Cell*, **2014**, 26, 1901-1912	11.6	76
105	The three genetics (nuclear DNA, mitochondrial DNA, and gut microbiome) of longevity in humans considered as metaorganisms. *BioMed Research International*, **2014**, 2014, 560340	3	16
104	Curtobacterium sp. Genome Sequencing Underlines Plant Growth Promotion-Related Traits. *Genome Announcements*, **2014**, 2,		10
103	RNA-Seq profile of flavescence dorée phytoplasma in grapevine. *BMC Genomics*, **2014**, 15, 1088	4.5	27
102	SIRPB1 Is a Strong Predictor Biomarker of Response to 5-Azacitidine Therapy in MDS and AML Patients. *Blood*, **2014**, 124, 1030-1030	2.2	

101	The plasticity of the grapevine berry transcriptome. *Genome Biology*, **2013**, 14, r54	18.3	119
100	Role of sortase-dependent pili of Bifidobacterium bifidum PRL2010 in modulating bacterium-host interactions. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 11151-6	11.5	172
99	The high polyphenol content of grapevine cultivar tannat berries is conferred primarily by genes that are not shared with the reference genome. *Plant Cell*, **2013**, 25, 4777-88	11.6	88
98	Auxin induces redox regulation of ascorbate peroxidase 1 activity by S-nitrosylation/denitrosylation balance resulting in changes of root growth pattern in Arabidopsis. *Journal of Experimental Botany*, **2013**, 64, 3339-49	7	89
97	Slug/Ecatenin-dependent proinflammatory phenotype in hypoxic breast cancer stem cells. *American Journal of Pathology*, **2013**, 183, 1688-1697	5.8	16
96	Exploration of the genomic diversity and core genome of the Bifidobacterium adolescentis phylogenetic group by means of a polyphasic approach. *Applied and Environmental Microbiology*, **2013**, 79, 336-46	4.8	15
95	Nitric oxide as a mediator for defense responses. *Molecular Plant-Microbe Interactions*, **2013**, 26, 271-7	3.6	149
94	De novo transcriptome characterization of Vitis vinifera cv. Corvina unveils varietal diversity. *BMC Genomics*, **2013**, 14, 41	4.5	82
93	S-nitrosylation of ascorbate peroxidase is part of programmed cell death signaling in tobacco Bright Yellow-2 cells. *Plant Physiology*, **2013**, 163, 1766-75	6.6	122
92	A mutation in the FZL gene of Arabidopsis causing alteration in chloroplast morphology results in a lesion mimic phenotype. *Journal of Experimental Botany*, **2013**, 64, 4313-28	7	20
91	RNA-Seq analysis discloses early senescence and nucleolar dysfunction triggered by Tdp1 depletion in Medicago truncatula. *Journal of Experimental Botany*, **2013**, 64, 1941-51	7	27
90	Expression dynamics of the Medicago truncatula transcriptome during the symbiotic interaction with Sinorhizobium meliloti: which role for nitric oxide?. *Plant Physiology*, **2013**, 161, 425-39	6.6	73
89	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. *Aging*, **2013**, 5, 373-85	5.6	51
88	A Transcriptomic Analysis of Sensitive and Tolerant Citrus Rootstocks under Natural Iron Deficiency Conditions. *Journal of the American Society for Horticultural Science*, **2013**, 138, 487-498	2.3	7
87	Genome-wide DNA methylation and gene expression profiles analysis show novel regulatory pathways in alcohol-related hepatocellular carcinoma. *FASEB Journal*, **2013**, 27, 248.4	0.9	1
86	Genomic Analysis Of Notch Mutations In a Case Of Alagille Syndrome With Acute Lymphoblastic Leukemia. *Blood*, **2013**, 122, 4992-4992	2.2	0
85	Investigating topic models' capabilities in expression microarray data classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2012**, 9, 1831-6	3	20
84	Downy mildew resistance induced by Trichoderma harzianum T39 in susceptible grapevines partially mimics transcriptional changes of resistant genotypes. *BMC Genomics*, **2012**, 13, 660	4.5	108

83	Bellerophontes: an RNA-Seq data analysis framework for chimeric transcripts discovery based on accurate fusion model. *Bioinformatics*, **2012**, 28, 2114-21	7.2	33
82	The grapevine expression atlas reveals a deep transcriptome shift driving the entire plant into a maturation program. *Plant Cell*, **2012**, 24, 3489-505	11.6	252
81	Application of the whole-transcriptome shotgun sequencing approach to the study of Philadelphia-positive acute lymphoblastic leukemia. *Blood Cancer Journal*, **2012**, 2, e61	7	7
80	Bifidobacterium asteroides PRL2011 genome analysis reveals clues for colonization of the insect gut. *PLoS ONE*, **2012**, 7, e44229	3.7	91
79	Peroxynitrite formation and function in plants. *Plant Science*, **2011**, 181, 534-9	5.3	119
78	Detection of peroxynitrite accumulation in Arabidopsis thaliana during the hypersensitive defense response. *Nitric Oxide - Biology and Chemistry*, **2011**, 25, 222-8	5	51
77	Revealing impaired pathways in the an11 mutant by high-throughput characterization of Petunia axillaris and Petunia inflata transcriptomes. *Plant Journal*, **2011**, 68, 11-27	6.9	31
76	IDH2 somatic mutations in chronic myeloid leukemia patients in blast crisis. *Leukemia*, **2011**, 25, 178-81	10.7	20
75	Resistance to Plasmopara viticola in a grapevine segregating population is associated with stilbenoid accumulation and with specific host transcriptional responses. *BMC Plant Biology*, **2011**, 11, 114	5.3	74
74	Distinct colonization patterns and cDNA-AFLP transcriptome profiles in compatible and incompatible interactions between melon and different races of Fusarium oxysporum f. sp. melonis. *BMC Genomics*, **2011**, 12, 122	4.5	29
73	MYO1E mutations and childhood familial focal segmental glomerulosclerosis. *New England Journal of Medicine*, **2011**, 365, 295-306	59.2	195
72	Global genome transcription profiling of Bifidobacterium bifidum PRL2010 under in vitro conditions and identification of reference genes for quantitative real-time PCR. *Applied and Environmental Microbiology*, **2011**, 77, 8578-87	4.8	24
71	Ability of Bifidobacterium breve to grow on different types of milk: exploring the metabolism of milk through genome analysis. *Applied and Environmental Microbiology*, **2011**, 77, 7408-17	4.8	38
70	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	
69	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	
68	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
67	Identification of putative stage-specific grapevine berry biomarkers and omics data integration into networks. *Plant Physiology*, **2010**, 154, 1439-59	6.6	123
66	Characterization of the serpin-encoding gene of Bifidobacterium breve 210B. *Applied and Environmental Microbiology*, **2010**, 76, 3206-19	4.8	58

65	Genome analysis of Bifidobacterium bifidum PRL2010 reveals metabolic pathways for host-derived glycan foraging. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 19514-9	11.5	266
64	Biclustering of Expression Microarray Data with Topic Models **2010**,		15
63	Characterization of transcriptional complexity during berry development in Vitis vinifera using RNA-Seq. *Plant Physiology*, **2010**, 152, 1787-95	6.6	294
62	Correction: High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in Vitis vinifera. *BMC Genomics*, **2010**, 11, 109	4.5	44
61	General and species-specific transcriptional responses to downy mildew infection in a susceptible (Vitis vinifera) and a resistant (V. riparia) grapevine species. *BMC Genomics*, **2010**, 11, 117	4.5	127
60	Whole-Transcriptome Sequencing In Chronic Myeloid Leukemia Reveals Novel Gene Mutations That May Be Associated with Disease Pathogenesis and Progression. *Blood*, **2010**, 116, 885-885	2.2	3
59	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	
58	NO signals in the haze: nitric oxide signalling in plant defence. *Current Opinion in Plant Biology*, **2009**, 12, 451-8	9.9	218
57	Combining next-generation pyrosequencing with microarray for large scale expression analysis in non-model species. *BMC Genomics*, **2009**, 10, 555	4.5	64
56	High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in Vitis vinifera. *BMC Genomics*, **2009**, 10, 558	4.5	52
55	Protein nitration during defense response in Arabidopsis thaliana. *Electrophoresis*, **2009**, 30, 2460-8	3.6	103
54	Transcriptome analysis of Medicago truncatula leaf senescence: similarities and differences in metabolic and transcriptional regulations as compared with Arabidopsis, nodule senescence and nitric oxide signalling. *New Phytologist*, **2009**, 181, 563-75	9.8	47
53	Symbiotic competence in Lotus japonicus is affected by plant nitrogen status: transcriptomic identification of genes affected by a new signalling pathway. *New Phytologist*, **2009**, 183, 380-394	9.8	32
52	The Bifidobacterium dentium Bd1 genome sequence reflects its genetic adaptation to the human oral cavity. *PLoS Genetics*, **2009**, 5, e1000785	6	120
51	TRANSCRIPTIONAL REPROGRAMMING DURING BERRY RIPENING AND WITHERING IN VITIS VINIFERA 'CORVINA'. *Acta Horticulturae*, **2009**, 351-354	0.3	
50	METABOLIC AND TRANSCRIPTIONAL CHANGES IN RESISTANT AND SUSCEPTIBLE GENOTYPES OF A GRAPEVINE POPULATION SEGREGATING FOR THE RESISTANCE TO PLASMOPARA VITICOLA. *Acta Horticulturae*, **2009**, 635-640	0.3	2
49	Whole Transcriptome Sequencing of a Philadelphia-Positive Acute Lymphoblastic Leukemia (ALL) with Next Generation Sequencing Technology Revealed Novel Point Mutations Associated with Disease-Progression.. *Blood*, **2009**, 114, 3074-3074	2.2	1
48	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	

47	Histological and molecular analysis of Rdg2a barley resistance to leaf stripe. *Molecular Plant Pathology*, **2008**, 9, 463-78	5.7	18
46	Annotating genomes with massive-scale RNA sequencing. *Genome Biology*, **2008**, 9, R175	18.3	186
45	Methods for nitric oxide detection during plant-pathogen interactions. *Methods in Enzymology*, **2008**, 437, 575-94	1.7	15
44	Molecular analysis of post-harvest withering in grape by AFLP transcriptional profiling. *Journal of Experimental Botany*, **2008**, 59, 4145-59	7	73
43	Expression of Medicago truncatula genes responsive to nitric oxide in pathogenic and symbiotic conditions. *Molecular Plant-Microbe Interactions*, **2008**, 21, 781-90	3.6	84
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6	Enhanced targeted resequencing by optimizing the combination of enrichment technology and DNA fragment length		1
5	Phased Diploid Genome Assembly with Single Molecule Real-Time Sequencing		16
4	The genetic basis of sex determination in grapevines (Vitis spp.)		4
3	Pod indehiscence in common bean is associated to the fine regulation of PvMYB26 and a non-functional abscission layer		4
2	A rapid and accurate MinION-based workflow for tracking species biodiversity in the field		3
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