Riccardo Velasco

List of Publications by Year in Descending Order

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

167	11,368 citations	53	104
papers		h-index	g-index
180	13,564 ext. citations	5.3	5.65
ext. papers		avg, IF	L-index

#	Paper	IF	Citations
167	The hidden world within plants: metatranscriptomics unveils the complexity of wood microbiomes <i>Journal of Experimental Botany</i> , 2022 ,	7	2
166	Studi sui tratti di qualit[hegativa nelle nuove viti mediamente resistenti alle malattie fungine. <i>BIO Web of Conferences</i> , 2022 , 44, 04003	0.4	
165	Somatic Embryogenesis in Vitis for Genome Editing: Optimization of Protocols for Recalcitrant Genotypes. <i>Horticulturae</i> , 2021 , 7, 511	2.5	O
164	Construction of a high-density genetic map and detection of a major QTL of resistance to powdery mildew (Erysiphe necator Sch.) in Caucasian grapes (Vitis vinifera L.). <i>BMC Plant Biology</i> , 2021 , 21, 528	5.3	3
163	Novel and emerging biotechnological crop protection approaches. <i>Plant Biotechnology Journal</i> , 2021 , 19, 1495-1510	11.6	6
162	Unraveling the genetic origin of 'Glera', 'Ribolla Gialla' and other autochthonous grapevine varieties from Friuli Venezia Giulia (northeastern Italy). <i>Scientific Reports</i> , 2020 , 10, 7206	4.9	6
161	Mediated Defense Responses in Grapevine Offspring Resistant to. <i>Plants</i> , 2020 , 9,	4.5	10
160	NoPv1: a synthetic antimicrobial peptide aptamer targeting the causal agents of grapevine downy mildew and potato late blight. <i>Scientific Reports</i> , 2020 , 10, 17574	4.9	5
159	Marker-assisted breeding for Downy mildew, Powderey mildew and Phylloxera resistance at FEM. <i>BIO Web of Conferences</i> , 2019 , 13, 01002	0.4	1
158	Data mining for apple S-RNase alleles in resequencing datasets. <i>Acta Horticulturae</i> , 2019 , 135-152	0.3	
157	The Haplotype and Stilbenoid Induction Mediate Downy Mildew Resistance in a Grapevine Interspecific Population. <i>Frontiers in Plant Science</i> , 2019 , 10, 234	6.2	29
156	-Loci Arrangement Versus Downy and Powdery Mildew Resistance Level: A Hybrid Survey. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	31
155	The Fondazione Edmund Mach grapevine breeding program for downy and powdery mildew resistances: toward a green viticulture. <i>Acta Horticulturae</i> , 2019 , 109-114	0.3	4
154	A multidisciplinary approach reveals new aspects of superficial scald aetiology and cold resistance mechanism in G ranny Smith pples. <i>Acta Horticulturae</i> , 2019 , 447-454	0.3	
153	The Rpv3-3 haplotype and stilbenoid induction mediate downy mildew resistance in a grapevine interspecific population. <i>Acta Horticulturae</i> , 2019 , 581-586	0.3	
152	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 , 441-44	16 ^{0.3}	1
151	Pseudo-chromosome-length genome assembly of a double haploid "Bartlett" pear (Pyrus communis L.). <i>GigaScience</i> , 2019 , 8,	7.6	34

150	An integrated approach for increasing breeding efficiency in apple and peach in Europe. <i>Horticulture Research</i> , 2018 , 5, 11	7.7	52	
149	The genome sequence and transcriptome of Potentilla micrantha and their comparison to Fragaria vesca (the woodland strawberry). <i>GigaScience</i> , 2018 , 7, 1-14	7.6	29	
148	Development of a novel phenotyping method to assess downy mildew symptoms on grapevine inflorescences. <i>Scientia Horticulturae</i> , 2018 , 236, 79-89	4.1	12	
147	A study of gene expression changes at the Bp-2 locus associated with bitter pit symptom expression in apple (Malus pumila). <i>Molecular Breeding</i> , 2018 , 38, 1	3.4	4	
146	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	О	
145	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	
144	CRISPR-Cas9-mediated genome editing in apple and grapevine. <i>Nature Protocols</i> , 2018 , 13, 2844-2863	18.8	86	
143	Identification of a leucine-rich repeat receptor-like serine/threonine-protein kinase as a candidate gene for Rvi12 (Vb)-based apple scab resistance. <i>Molecular Breeding</i> , 2018 , 38, 1	3.4	6	
142	Characterization of 25 full-length S-RNase alleles, including flanking regions, from a pool of resequenced apple cultivars. <i>Plant Molecular Biology</i> , 2018 , 97, 279-296	4.6	11	
141	Breeding for grapevine downy mildew resistance: a review of bmicsbpproaches. <i>Euphytica</i> , 2017 , 213, 1	2.1	47	
140	Structural dynamics at the berry colour locus in Vitis vinifera L. somatic variants. <i>Acta Horticulturae</i> , 2017 , 27-32	0.3	3	
139	A new in vitro method for the assessment of Plasmopara viticola resistance on grapevine inflorescences. <i>Acta Horticulturae</i> , 2017 , 21-26	0.3		
138	Apple genes involved in the response to Venturia inaequalis and salicylic acid treatment. <i>Scientia Horticulturae</i> , 2017 , 226, 157-172	4.1	6	
137	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <i>Nature Genetics</i> , 2017 , 49, 1099-1106	36.3	421	
136	Genome-wide association study unravels the genetic control of the apple volatilome and its interplay with fruit texture. <i>Journal of Experimental Botany</i> , 2017 , 68, 1467-1478	7	36	
135	Grapevine downy mildew dual epidemics: a leaf and inflorescence transcriptomics study. <i>Acta Horticulturae</i> , 2017 , 265-270	0.3	2	
134	Genome wide association study of two phenology traits (flowering time and maturity date) in apple. <i>Acta Horticulturae</i> , 2017 , 411-418	0.3	1	
133	Genome-Wide Association Mapping of Flowering and Ripening Periods in Apple. <i>Frontiers in Plant Science</i> , 2017 , 8, 1923	6.2	51	

132	HaploSNP affinities and linkage map positions illuminate subgenome composition in the octoploid, cultivated strawberry (Fragaria Inanassa). <i>Plant Science</i> , 2016 , 242, 140-150	5.3	56
131	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.). <i>Plant Journal</i> , 2016 , 88, 963-975	6.9	32
130	A high-density, multi-parental SNP genetic map on apple validates a new mapping approach for outcrossing species. <i>Horticulture Research</i> , 2016 , 3, 16057	7.7	52
129	A QTL detected in an interspecific pear population confers stable fire blight resistance across different environments and genetic backgrounds. <i>Molecular Breeding</i> , 2016 , 36, 1	3.4	18
128	Genotyping-by-sequencing in an orphan plant species Physocarpus opulifolius helps identify the evolutionary origins of the genus Prunus. <i>BMC Research Notes</i> , 2016 , 9, 268	2.3	4
127	Development and validation of the Axiom(\square) Apple480K SNP genotyping array. Plant Journal, 2016 , 86, 62-74	6.9	111
126	Candidate gene expression profiling reveals a time specific activation among different harvesting dates in C olden Delicious A nd E uji A pple cultivars. <i>Euphytica</i> , 2016 , 208, 401-413	2.1	6
125	DNA-Free Genetically Edited Grapevine and Apple Protoplast Using CRISPR/Cas9 Ribonucleoproteins. <i>Frontiers in Plant Science</i> , 2016 , 7, 1904	6.2	351
124	Genome mapping of postzygotic hybrid necrosis in an interspecific pear population. <i>Horticulture Research</i> , 2016 , 3, 15064	7.7	11
123	Genome Sequencing, Transcriptomics, and Proteomics. Compendium of Plant Genomes, 2016, 141-161	0.8	8
122	Knockdown of MLO genes reduces susceptibility to powdery mildew in grapevine. <i>Horticulture Research</i> , 2016 , 3, 16016	7.7	94
121	The knock-down of the expression of MdMLO19 reduces susceptibility to powdery mildew (Podosphaera leucotricha) in apple (Malus domestica). <i>Plant Biotechnology Journal</i> , 2016 , 14, 2033-44	11.6	41
120	Fine-Tuning Next-Generation Genome Editing Tools. <i>Trends in Biotechnology</i> , 2016 , 34, 562-574	15.1	43
119	High frequency of chromosome deletions in regenerated and mutagenized apple (Malus I domestica Borkh.) seedlings. <i>Molecular Breeding</i> , 2015 , 35, 1	3.4	3
118	Regulation of flavonol content and composition in (Syrah P inot Noir) mature grapes: integration of transcriptional profiling and metabolic quantitative trait locus analyses. <i>Journal of Experimental Botany</i> , 2015 , 66, 4441-53	7	27
117	Grapevine breeding programs in Italy 2015 , 135-157		7
116	Non-GMO genetically edited crop plants. <i>Trends in Biotechnology</i> , 2015 , 33, 489-91	15.1	56
115	Genetic mapping of Cacopsylla pyri resistance in an interspecific pear (Pyrus spp.) population. <i>Tree Genetics and Genomes</i> , 2015 , 11, 1	2.1	14

114	ASSIST: an automatic SNP scoring tool for in- and outbreeding species. <i>Bioinformatics</i> , 2015 , 31, 3873-4	7.2	35
113	A major QTL controlling apple skin russeting maps on the linkage group 12 of 'Renetta Grigia di Torriana'. <i>BMC Plant Biology</i> , 2015 , 15, 150	5.3	32
112	Untargeted metabolomics investigation of volatile compounds involved in the development of apple superficial scald by PTR-ToFMS. <i>Metabolomics</i> , 2015 , 11, 341-349	4.7	26
111	Looking forward to genetically edited fruit crops. <i>Trends in Biotechnology</i> , 2015 , 33, 62-4	15.1	68
110	QTL Analysis Coupled with PTR-ToF-MS and Candidate Gene-Based Association Mapping Validate the Role of Md-AAT1 as a Major Gene in the Control of Flavor in Apple Fruit. <i>Plant Molecular Biology Reporter</i> , 2015 , 33, 239-252	1.7	13
109	Fine mapping of the Rvi5 (Vm) apple scab resistance locus in the Murray apple genotype. <i>Molecular Breeding</i> , 2015 , 35, 1	3.4	9
108	A FIRST PEDIGREE-BASED ANALYSIS (PBA) APPROACH FOR THE DISSECTION OF DISEASE RESISTANCE TRAITS IN GRAPEVINE HYBRIDS. <i>Acta Horticulturae</i> , 2015 , 113-121	0.3	3
107	Accuracy and responses of genomic selection on key traits in apple breeding. <i>Horticulture Research</i> , 2015 , 2, 15060	7.7	78
106	Exploration of alternative splicing events in ten different grapevine cultivars. <i>BMC Genomics</i> , 2015 , 16, 706	4.5	18
105	A JOINT LAIMBURG - FEM MOLECULAR MARKERS PROJECT FOR APPLE FRUIT QUALITY TRAITS USING THE PEDIGREE BASED ANALYSIS STRATEGY. <i>Acta Horticulturae</i> , 2015 , 91-94	0.3	
104	Identification and validation of a QTL influencing bitter pit symptoms in apple (Malus Idomestica). <i>Molecular Breeding</i> , 2015 , 35, 1	3.4	18
103	High-resolution genetic and physical map of the Rvi1 (Vg) apple scab resistance locus. <i>Molecular Breeding</i> , 2015 , 35, 1	3.4	11
102	Advances in QTL mapping for ethylene production in apple (Malus Idomestica Borkh.). <i>Postharvest Biology and Technology</i> , 2014 , 87, 126-132	6.2	24
101	Structural dynamics at the berry colour locus in Vitis vinifera L. somatic variants. <i>Australian Journal of Grape and Wine Research</i> , 2014 , 20, 485-495	2.4	26
100	Target metabolite and gene transcription profiling during the development of superficial scald in apple (Malus x domestica Borkh). <i>BMC Plant Biology</i> , 2014 , 14, 193	5.3	36
99	One-step reconstruction of multi-generation pedigree networks in apple (Malus domestica Borkh.) and the parentage of Golden Delicious. <i>Molecular Breeding</i> , 2014 , 34, 511-524	3.4	19
98	F1 hybrid of cultivated apple (Malus domestica) and European pear (Pyrus communis) with fertile F2 offspring. <i>Molecular Breeding</i> , 2014 , 34, 817-828	3.4	7
97	A genealogy of the citrus family. <i>Nature Biotechnology</i> , 2014 , 32, 640-2	44.5	37

96	Molecular genetics and genomics of the Rosoideae: state of the art and future perspectives. <i>Horticulture Research</i> , 2014 , 1, 1	7.7	58
95	Development and validation of a 20K single nucleotide polymorphism (SNP) whole genome genotyping array for apple (Malus domestica Borkh). <i>PLoS ONE</i> , 2014 , 9, e110377	3.7	144
94	Fine-mapping of the apple scab resistance locus Rvi12 (Vb) derived from ⊞ansen baccata #2□ <i>Molecular Breeding</i> , 2014 , 34, 2119-2129	3.4	15
93	Fast and cost-effective genetic mapping in apple using next-generation sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1681-7	3.2	85
92	The peculiar landscape of repetitive sequences in the olive (Olea europaea L.) genome. <i>Genome Biology and Evolution</i> , 2014 , 6, 776-91	3.9	51
91	Fine mapping of the gene Rvi18 (V25) for broad-spectrum resistance to apple scab, and development of a linked SSR marker suitable for marker-assisted breeding. <i>Molecular Breeding</i> , 2014 , 34, 2021-2032	3.4	12
90	Characterization of resistance gene analogues (RGAs) in apple (Malus domestica Borkh.) and their evolutionary history of the Rosaceae family. <i>PLoS ONE</i> , 2014 , 9, e83844	3.7	53
89	The draft genome sequence of European pear (Pyrus communis L. 'Bartlett'). PLoS ONE, 2014 , 9, e9264	43.7	186
88	Saturated linkage map construction in Rubus idaeus using genotyping by sequencing and genome-independent imputation. <i>BMC Genomics</i> , 2013 , 14, 2	4.5	132
87	A candidate gene based approach validates Md-PG1 as the main responsible for a QTL impacting fruit texture in apple (Malus x domestica Borkh). <i>BMC Plant Biology</i> , 2013 , 13, 37	5.3	54
86	Phylogenetic analysis of 47 chloroplast genomes clarifies the contribution of wild species to the domesticated apple maternal line. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1751-60	8.3	65
85	An evaluation of the PacBio RS platform for sequencing and de novo assembly of a chloroplast genome. <i>BMC Genomics</i> , 2013 , 14, 670	4.5	110
84	Genetic and physical characterisation of the locus controlling columnar habit in apple (Malus I domestica Borkh.). <i>Molecular Breeding</i> , 2013 , 31, 429-440	3.4	36
83	An ancient duplication of apple MYB transcription factors is responsible for novel red fruit-flesh phenotypes. <i>Plant Physiology</i> , 2013 , 161, 225-39	6.6	198
82	Evidence for regulation of columnar habit in apple by a putative 2OG-Fe(II) oxygenase. <i>New Phytologist</i> , 2013 , 200, 993-9	9.8	36
81	Evaluation of SNP Data from the Malus Infinium Array Identifies Challenges for Genetic Analysis of Complex Genomes of Polyploid Origin. <i>PLoS ONE</i> , 2013 , 8, e67407	3.7	15
80	Identification of Pyrus single nucleotide polymorphisms (SNPs) and evaluation for genetic mapping in European pear and interspecific Pyrus hybrids. <i>PLoS ONE</i> , 2013 , 8, e77022	3.7	50
79	A multidisciplinary approach providing new insight into fruit flesh browning physiology in apple (Malus x domestica Borkh.). <i>PLoS ONE</i> , 2013 , 8, e78004	3.7	46

(2011-2012)

78	Profiling and accurate quantification of trans-resveratrol, trans-piceid, trans-pterostilbene and 11 viniferins induced by Plasmopara viticola in partially resistant grapevine leaves. <i>Australian Journal of Grape and Wine Research</i> , 2012 , 18, 11-19	2.4	20
77	The mitochondrial genome of Malus domestica and the import-driven hypothesis of mitochondrial genome expansion in seed plants. <i>Plant Journal</i> , 2012 , 71, 615-26	6.9	48
76	Functional allelic diversity of the apple alcohol acyl-transferase gene MdAAT1 associated with fruit ester volatile contents in apple cultivars. <i>Molecular Breeding</i> , 2012 , 29, 609-625	3.4	51
75	Rosaceae conserved orthologous set (RosCOS) markers as a tool to assess genome synteny between Malus and Fragaria. <i>Tree Genetics and Genomes</i> , 2012 , 8, 643-658	2.1	13
74	Argot2: a large scale function prediction tool relying on semantic similarity of weighted Gene Ontology terms. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 4, S14	3.6	100
73	Whole genome comparisons of Fragaria, Prunus and Malus reveal different modes of evolution between Rosaceous subfamilies. <i>BMC Genomics</i> , 2012 , 13, 129	4.5	62
72	Development of a dense SNP-based linkage map of an apple rootstock progeny using the Malus Infinium whole genome genotyping array. <i>BMC Genomics</i> , 2012 , 13, 203	4.5	69
71	The genes and enzymes of the carotenoid metabolic pathway in Vitis vinifera L. <i>BMC Genomics</i> , 2012 , 13, 243	4.5	87
70	Downy mildew resistance induced by Trichoderma harzianum T39 in susceptible grapevines partially mimics transcriptional changes of resistant genotypes. <i>BMC Genomics</i> , 2012 , 13, 660	4.5	108
69	Comprehensive QTL mapping survey dissects the complex fruit texture physiology in apple (Malus x domestica Borkh.). <i>Journal of Experimental Botany</i> , 2012 , 63, 1107-21	7	80
68	Genome-wide SNP detection, validation, and development of an 8K SNP array for apple. <i>PLoS ONE</i> , 2012 , 7, e31745	3.7	216
67	Deconstruction of the (paleo)polyploid grapevine genome based on the analysis of transposition events involving NBS resistance genes. <i>PLoS ONE</i> , 2012 , 7, e29762	3.7	27
66	Genetic control of biennial bearing in apple. Journal of Experimental Botany, 2012, 63, 131-49	7	102
65	Genetic analysis of metabolites in apple fruits indicates an mQTL hotspot for phenolic compounds on linkage group 16. <i>Journal of Experimental Botany</i> , 2012 , 63, 2895-908	7	59
64	REVIEW OF FRUIT GENETICS AND BREEDING PROGRAMMES AND A NEW EUROPEAN INITIATIVE TO INCREASE FRUIT BREEDING EFFICIENCY. <i>Acta Horticulturae</i> , 2012 , 95-102	0.3	16
63	Pinot blanc and Pinot gris arose as independent somatic mutations of Pinot noir. <i>Journal of Experimental Botany</i> , 2012 , 63, 6359-69	7	55
62	Profiling of resveratrol oligomers, important stress metabolites, accumulating in the leaves of hybrid Vitis vinifera (Merzling lareroldego) genotypes infected with Plasmopara viticola. <i>Journal of Agricultural and Food Chemistry</i> , 2011 , 59, 5364-75	5.7	84
61	The genome of woodland strawberry (Fragaria vesca). <i>Nature Genetics</i> , 2011 , 43, 109-16	36.3	881

60	Assessment of apple (Malus Idomestica Borkh.) fruit texture by a combined acoustic-mechanical profiling strategy. <i>Postharvest Biology and Technology</i> , 2011 , 61, 21-28	6.2	104
59	Genetic linkage maps of two interspecific grape crosses (Vitis spp.) used to localize quantitative trait loci for downy mildew resistance. <i>Tree Genetics and Genomes</i> , 2011 , 7, 153-167	2.1	61
58	Genetic diversity of the genus Malus and implications for linkage mapping with SNPs. <i>Tree Genetics and Genomes</i> , 2011 , 7, 857-868	2.1	37
57	Resistance to Plasmopara viticola 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
56	Comparative analysis of rosaceous genomes and the reconstruction of a putative ancestral genome for the family. <i>BMC Evolutionary Biology</i> , 2011 , 11, 9	3	86
55	Signaling pathways mediating the induction of apple fruitlet abscission. <i>Plant Physiology</i> , 2011 , 155, 18	35 &6 8	132
54	On the evolutionary history of the domesticated apple. <i>Nature Genetics</i> , 2011 , 43, 1044-1045	36.3	11
53	The genome of the domesticated apple (Malus Idomestica Borkh.). <i>Nature Genetics</i> , 2010 , 42, 833-9	36.3	1524
52	Armillaria mellea induces a set of defense genes in grapevine roots and one of them codifies a protein with antifungal activity. <i>Molecular Plant-Microbe Interactions</i> , 2010 , 23, 485-96	3.6	12
51	ETHYLENE PRODUCTION DURING GRAPE BERRY DEVELOPMENT AND EXPRESSION OF GENES INVOLVED IN ETHYLENE BIOSYNTHESIS AND RESPONSE. <i>Acta Horticulturae</i> , 2010 , 73-80	0.3	8
50	Physical mapping in highly heterozygous genomes: a physical contig map of the Pinot Noir grapevine cultivar. <i>BMC Genomics</i> , 2010 , 11, 204	4.5	15
49	NOVEL POSSIBILITIES FOR MARKER-ASSISTED BREEDING EXPLOITING THE APPLE GENOME. <i>Acta Horticulturae</i> , 2010 , 357-360	0.3	2
48	Analysis of polymorphism based on SSCP markers in gamma-irradiated (Co60) grape (Vitis vinifera) varieties. <i>Genetics and Molecular Research</i> , 2010 , 9, 2357-63	1.2	5
47	Grapevine cell early activation of specific responses to DIMEB, a resveratrol elicitor. <i>BMC Genomics</i> , 2009 , 10, 363	4.5	46
46	Dominance induction of fruitlet shedding in Malus x domestica (L. Borkh): molecular changes associated with polar auxin transport. <i>BMC Plant Biology</i> , 2009 , 9, 139	5.3	35
45	Ontology-oriented retrieval of putative microRNAs in Vitis vinifera via GrapeMiRNA: a web database of de novo predicted grape microRNAs. <i>BMC Plant Biology</i> , 2009 , 9, 82	5.3	6
44	The 1-deoxy-D: -xylulose 5-phosphate synthase gene co-localizes with a major QTL affecting monoterpene content in grapevine. <i>Theoretical and Applied Genetics</i> , 2009 , 118, 653-69	6	104
43	Use of SSR markers to assess sexual vs. apomictic origin and ploidy level of breeding progeny derived from crosses of apple proliferation-resistant Malus sieboldii and its hybrids with Malus Idomestica cultivars. <i>Plant Breeding</i> , 2009 , 128, 507-513	2.4	16

(2007-2009)

42	of immature fruits reveals the involvement of a putative auxin hydrogen symporter in apple (Malus domestica L. Borkh). <i>Gene</i> , 2009 , 442, 26-36	3.8	35
41	Rosaceaous Genome Sequencing: Perspectives and Progress 2009 , 601-615		11
40	Mitochondrial DNA of Vitis vinifera and the issue of rampant horizontal gene transfer. <i>Molecular Biology and Evolution</i> , 2009 , 26, 99-110	8.3	187
39	Italian horticulture, fruitculture and floriculture may gain fundamental role by new opportunities offered by genetics and genomics. <i>Italian Journal of Agronomy</i> , 2009 , 4, 69	1.4	
38	Rapid annotation of anonymous sequences from genome projects using semantic similarities and a weighting scheme in gene ontology. <i>PLoS ONE</i> , 2009 , 4, e4619	3.7	29
37	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
36	SNP high-throughput screening in grapevine using the SNPlex genotyping system. <i>BMC Plant Biology</i> , 2008 , 8, 12	5.3	48
35	A SNP transferability survey within the genus Vitis. <i>BMC Plant Biology</i> , 2008 , 8, 128	5.3	38
34	A PCR-based diagnostic tool for distinguishing grape skin color mutants. <i>Plant Science</i> , 2008 , 175, 402-	40,93	15
33	Ripening and genotype control stilbene accumulation in healthy grapes. <i>Journal of Agricultural and Food Chemistry</i> , 2008 , 56, 11773-85	5.7	150
32	A grapevine (Vitis vinifera L.) genetic map integrating the position of 139 expressed genes. <i>Theoretical and Applied Genetics</i> , 2008 , 116, 1129-43	6	59
31	A reference integrated map for cultivated grapevine (Vitis vinifera L.) from three crosses, based on 283 SSR and 501 SNP-based markers. <i>Theoretical and Applied Genetics</i> , 2008 , 117, 499-511	6	82
30	Sequencing and assembly of highly heterozygous genome of Vitis vinifera L. cv Pinot Noir: problems and solutions. <i>Journal of Biotechnology</i> , 2008 , 136, 38-43	3.7	34
29	A high quality draft consensus sequence of the genome of a heterozygous grapevine variety. <i>PLoS ONE</i> , 2007 , 2, e1326	3.7	779
28	Genome-wide transcriptional analysis of grapevine berry ripening reveals a set of genes similarly modulated during three seasons and the occurrence of an oxidative burst at vitaison. <i>BMC Genomics</i> , 2007 , 8, 428	4.5	190
27	Genetic mapping in the presence of genotyping errors. <i>Genetics</i> , 2007 , 176, 2521-7	4	84
26	A dense single-nucleotide polymorphism-based genetic linkage map of grapevine (Vitis vinifera L.) anchoring Pinot Noir bacterial artificial chromosome contigs. <i>Genetics</i> , 2007 , 176, 2637-50	4	109
25	Microsatellite fingerprinting of homonymous grapevine (Vitis vinifera L.) varieties in neighboring regions of South-East Turkey. <i>Scientia Horticulturae</i> , 2007 , 114, 164-169	4.1	17

24	Low-night temperature increased the photoinhibition of photosynthesis in grapevine (Vitis vinifera L. cv. Riesling) leaves. <i>Environmental and Experimental Botany</i> , 2006 , 57, 25-31	5.9	47
23	Metabolite profiling of grape: Flavonols and anthocyanins. <i>Journal of Agricultural and Food Chemistry</i> , 2006 , 54, 7692-702	5.7	426
22	Construction and characterization of BAC libraries from major grapevine cultivars. <i>Theoretical and Applied Genetics</i> , 2005 , 110, 1363-71	6	43
21	Comparative analysis of expressed sequence tags from different organs of Vitis vinifera L. <i>Functional and Integrative Genomics</i> , 2005 , 5, 208-17	3.8	40
20	Genome diversity and gene haplotypes in the grapevine (Vitis vinifera L.), as revealed by single nucleotide polymorphisms. <i>Molecular Breeding</i> , 2005 , 14, 385-395	3.4	8
19	ZmMPK6, a novel maize MAP kinase that interacts with 14-3-3 proteins. <i>Plant Molecular Biology</i> , 2005 , 59, 713-22	4.6	32
18	GENE EXPRESSION PROFILING DURING GRAPE LEAF DEVELOPMENT AND SENESCENCE BY HIGH DENSITY FILTERS. <i>Acta Horticulturae</i> , 2005 , 441-446	0.3	
17	Cloning and characterization of GLOSSY1, a maize gene involved in cuticle membrane and wax production. <i>Plant Physiology</i> , 2005 , 138, 478-89	6.6	83
16	The SSEA server for protein secondary structure alignment. <i>Bioinformatics</i> , 2005 , 21, 393-5	7.2	31
15	Isolation of functional RNA from small amounts of different grape and apple tissues. <i>Molecular Biotechnology</i> , 2004 , 26, 95-100	3	40
14	Genome diversity and gene haplotypes in the grapevine (Vitis vinifera L.), as revealed by single nucleotide polymorphisms. <i>Molecular Breeding</i> , 2004 , 14, 385-395	3.4	62
13	Cloning and linkage mapping of resistance gene homologues in apple. <i>Theoretical and Applied Genetics</i> , 2004 , 109, 231-9	6	54
12	QTL MAPPING FOR DISEASE RESISTANCE AND FRUIT QUALITY IN GRAPE. Acta Horticulturae, 2003, 527-	-5333	14
11	Molecular linkage maps of Vitis vinifera L. and Vitis riparia Mchx. <i>Theoretical and Applied Genetics</i> , 2003 , 106, 1213-24	6	82
10	Alteration of GCN5 levels in maize reveals dynamic responses to manipulating histone acetylation. <i>Plant Journal</i> , 2003 , 33, 455-69	6.9	35
9	Development and mapping of SSR markers for maize. <i>Plant Molecular Biology</i> , 2002 , 48, 463-81	4.6	232
8	Gene structure and expression analysis of the drought- and abscisic acid-responsive CDeT11-24 gene family from the resurrection plant Craterostigma plantagineum Hochst. <i>Planta</i> , 1998 , 204, 459-71	4.7	34
7	Structural analysis of rDNA in the genus Nicotiana. <i>Plant Molecular Biology</i> , 1997 , 35, 655-60	4.6	43

LIST OF PUBLICATIONS

6	Dehydration and ABA increase mRNA levels and enzyme activity of cytosolic GAPDH in the resurrection plant Craterostigma plantagineum. <i>Plant Molecular Biology</i> , 1994 , 26, 541-6	4.6	87
5	Molecular analysis of desiccation tolerance in barley embryos and in the resurrection plant Craterostigma plantagineum. <i>Agronomy for Sustainable Development</i> , 1994 , 14, 161-167		6
4	The biologic activity of ACTH and related peptides on peripheral blood mononuclear cells is altered by the presence of dexamethasone. <i>Cellular Immunology</i> , 1993 , 151, 110-7	4.4	8
3	A New Synthesis of L-Ascorbic Acid (Vitamin C) from Protected Derivatives of D-Glucitol. <i>Synthetic Communications</i> , 1991 , 21, 1153-1161	1.7	2
2	Lipoprotein profiles and their relation to animal fat intake in healthy old people from four Spanish localities. <i>Archives of Gerontology and Geriatrics</i> , 1989 , 9, 97-105	4	0
1	Pseudo-chromosome length genome assembly of a double haploid B artlett[þear (Pyrus communis L.)		3