

# Alessandro Cestaro

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

5,374  
citations

236912

25  
h-index

361001

35  
g-index

38  
all docs

38  
docs citations

38  
times ranked

6383  
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of the domesticated apple ( <i>Malus Æ domestica</i> Borkh.). <i>Nature Genetics</i> , 2010, 42, 833-839.	21.4	1,891
2	A High Quality Draft Consensus Sequence of the Genome of a Heterozygous Grapevine Variety. <i>PLoS ONE</i> , 2007, 2, e1326.	2.5	945
3	Genome-Wide SNP Detection, Validation, and Development of an 8K SNP Array for Apple. <i>PLoS ONE</i> , 2012, 7, e31745.	2.5	249
4	The Draft Genome Sequence of European Pear ( <i>Pyrus communis</i> L. Æ BartlettÆ™). <i>PLoS ONE</i> , 2014, 9, e92644.	2.5	241
5	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 vÆraison. <i>BMC Genomics</i> , 2007, 8, 428.	2.8	216
6	Development and Validation of a 20K Single Nucleotide Polymorphism (SNP) Whole Genome Genotyping Array for Apple ( <i>Malus Æ domestica</i> Borkh.). <i>PLoS ONE</i> , 2014, 9, e110377.	2.5	200
7	Development and validation of the AxiomÆApple480K <scp>SNP</scp> genotyping array. <i>Plant Journal</i> , 2016, 86, 62-74.	5.7	156
8	An evaluation of the PacBio RS platform for sequencing and de novo assembly of a chloroplast genome. <i>BMC Genomics</i> , 2013, 14, 670.	2.8	146
9	Linking Genomics and Ecology to Investigate the Complex Evolution of an Invasive <i>Drosophila</i> Pest. <i>Genome Biology and Evolution</i> , 2013, 5, 745-757.	2.5	138
10	Computational reconstruction of the human skeletal muscle secretome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 776-792.	2.6	111
11	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.	3.6	103
12	Comparative analysis of rosaceous genomes and the reconstruction of a putative ancestral genome for the family. <i>BMC Evolutionary Biology</i> , 2011, 11, 9.	3.2	103
13	Microbiome of vineyard soils is shaped by geography and management. <i>Microbiome</i> , 2019, 7, 140.	11.1	94
14	Laterally transferred elements and high pressure adaptation in <i>Photobacterium profundum</i> strains. <i>BMC Genomics</i> , 2005, 6, 122.	2.8	91
15	Whole genome comparisons of <i>Fragaria</i> , <i>Prunus</i> and <i>Malus</i> reveal different modes of evolution between Rosaceous subfamilies. <i>BMC Genomics</i> , 2012, 13, 129.	2.8	77
16	Pseudo-chromosomeÆlength genome assembly of a double haploid ÆBartlettÆpear ( <i>Pyrus communis</i> L.). <i>GigaScience</i> , 2019, 8, .	6.4	76
17	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, 2895-2908.	4.8	74
18	Structural insights into the function of human caveolin 1. <i>Biochemical and Biophysical Research Communications</i> , 2005, 338, 1383-1390.	2.1	55

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19	Grapevine cell early activation of specific responses to DIMEB, a resveratrol elicitor. BMC Genomics, 2009, 10, 363.	2.8	54
20	Deconstruction of the (Paleo)Polyploid Grapevine Genome Based on the Analysis of Transposition Events Involving NBS Resistance Genes. PLoS ONE, 2012, 7, e29762.	2.5	38
21	Draft Genome Sequence of the <i>Wolbachia</i> Endosymbiont of <i>Drosophila suzukii</i> . Genome Announcements, 2013, 1, .	0.8	37
22	The genome sequence and transcriptome of <i>Potentilla micrantha</i> and their comparison to <i>Fragaria vesca</i> (the woodland strawberry). GigaScience, 2018, 7, 1-14.	6.4	37
23	Sequencing and assembly of highly heterozygous genome of <i>Vitis vinifera</i> L. cv Pinot Noir: Problems and solutions. Journal of Biotechnology, 2008, 136, 38-43.	3.8	34
24	Rapid Annotation of Anonymous Sequences from Genome Projects Using Semantic Similarities and a Weighting Scheme in Gene Ontology. PLoS ONE, 2009, 4, e4619.	2.5	33
25	MANIFOLD: protein fold recognition based on secondary structure, sequence similarity and enzyme classification. Protein Engineering, Design and Selection, 2003, 16, 785-789.	2.1	29
26	Two-omics data revealed commonalities and differences between Rpv12- and Rpv3-mediated resistance in grapevine. Scientific Reports, 2020, 10, 12193.	3.3	24
27	Exploration of alternative splicing events in ten different grapevine cultivars. BMC Genomics, 2015, 16, 706.	2.8	21
28	Evaluation of SNP Data from the Malus Infinium Array Identifies Challenges for Genetic Analysis of Complex Genomes of Polyploid Origin. PLoS ONE, 2013, 8, e67407.	2.5	17
29	Characterization of 25 full-length S-RNase alleles, including flanking regions, from a pool of resequenced apple cultivars. Plant Molecular Biology, 2018, 97, 279-296.	3.9	17
30	Induction of Terpene Biosynthesis in Berries of Microvine Transformed with VvDXS1 Alleles. Frontiers in Plant Science, 2017, 8, 2244.	3.6	15
31	High-resolution genetic and physical map of the Rvi1 (Vg) apple scab resistance locus. Molecular Breeding, 2015, 35, 1.	2.1	14
32	Wide transcriptional investigation unravel novel insights of the on-tree maturation and postharvest ripening of 'Abate Fetel' pear fruit. Horticulture Research, 2019, 6, 32.	6.3	14
33	Ontology-oriented retrieval of putative microRNAs in <i>Vitis vinifera</i> via GrapeMiRNA: a web database of de novo predicted grape microRNAs. BMC Plant Biology, 2009, 9, 82.	3.6	8
34	Distinct and Temporally Stable Assembly Mechanisms Shape Bacterial and Fungal Communities in Vineyard Soils. Microbial Ecology, 2023, 86, 337-349.	2.8	6
35	Unfoldome variation upon plant-pathogen interactions: strawberry infection by <i>Colletotrichum acutatum</i> . Plant Molecular Biology, 2015, 89, 49-65.	3.9	3