

Massimo Pindo

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

5,812
citations

136950

32
h-index

128289

60
g-index

64
all docs

64
docs citations

64
times ranked

7370
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of the domesticated apple (<i>Malus 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	The Draft Genome Sequence of European Pear (<i>Pyrus communis</i> L. "Bartlett™"). <i>PLoS ONE</i> , 2014, 9, e92644.	2.5	241
4	Habitat fragmentation is associated to gut microbiota diversity of an endangered primate: implications for conservation. <i>Scientific Reports</i> , 2015, 5, 14862.	3.3	170
5	Development and validation of the Axiom [®] Apple480K SNP genotyping array. <i>Plant Journal</i> , 2016, 86, 62-74.	5.7	156
6	Resilience of the Natural Phyllosphere Microbiota of the Grapevine to Chemical and Biological Pesticides. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3585-3596.	3.1	144
7	Cloning and characterization of small non-coding RNAs from grape. <i>Plant Journal</i> , 2009, 59, 750-763.	5.7	133
8	A Dense Single-Nucleotide Polymorphism-Based Genetic Linkage Map of Grapevine (<i>Vitis</i>). <i>PLoS ONE</i> , 2014, 9, e012763.	2.9	126
9	Bacterial Endophytic Communities in the Grapevine Depend on Pest Management. <i>PLoS ONE</i> , 2014, 9, e112763.	2.5	125
10	Altered gut microbiota in Rett syndrome. <i>Microbiome</i> , 2016, 4, 41.	11.1	120
11	QTL and candidate gene mapping for polyphenolic composition in apple fruit. <i>BMC Plant Biology</i> , 2012, 12, 12.	3.6	117
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	Reduced fire blight susceptibility in apple cultivars using a high-efficiency CRISPR/Cas9-based gene editing system. <i>Plant Biotechnology Journal</i> , 2020, 18, 845-858.	8.3	98
14	Microbiome of vineyard soils is shaped by geography and management. <i>Microbiome</i> , 2019, 7, 140.	11.1	94
15	A MITE Transposon Insertion Is Associated with Differential Methylation at the Maize Flowering Time QTL. <i>Genes, Genomes, Genetics</i> , 2014, 4, 805-812.	1.8	93
16	Diversity and Cyclical Seasonal Transitions in the Bacterial Community in a Large and Deep Perialpine Lake. <i>Microbial Ecology</i> , 2018, 76, 125-143.	2.8	81
17	The Peculiar Landscape of Repetitive Sequences in the Olive (<i>Olea europaea</i> L.) Genome. <i>Genome Biology and Evolution</i> , 2014, 6, 776-791.	2.5	77
18	Legal immigrants: invasion of alien microbial communities during winter occurring desert dust storms. <i>Microbiome</i> , 2017, 5, 32.	11.1	69

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19	Alteration of Fecal Microbiota Profiles in Juvenile Idiopathic Arthritis. Associations with HLA-B27 Allele and Disease Status. <i>Frontiers in Microbiology</i> , 2016, 7, 1703.	3.5	65
20	Fumigation with dazomet modifies soil microbiota in apple orchards affected by replant disease. <i>Applied Soil Ecology</i> , 2017, 113, 71-79.	4.3	62
21	Measuring the impact of olive pomace enriched biscuits on the gut microbiota and its metabolic activity in mildly hypercholesterolaemic subjects. <i>European Journal of Nutrition</i> , 2019, 58, 63-81.	3.9	59
22	SNP high-throughput screening in grapevine using the SNPlex [®] genotyping system. <i>BMC Plant Biology</i> , 2008, 8, 12.	3.6	52
23	Unique resistance traits against downy mildew from the center of origin of grapevine (<i>Vitis vinifera</i>). <i>Scientific Reports</i> , 2018, 8, 12523.	3.3	50
24	Isolation of Functional RNA From Small Amounts of Different Grape and Apple Tissues. <i>Molecular Biotechnology</i> , 2004, 26, 95-100.	2.4	47
25	The Root of Flowering Plants and Total Evidence. <i>Systematic Biology</i> , 2015, 64, 879-891.	5.6	46
26	Comparative analysis of expressed sequence tags from different organs of <i>Vitis vinifera</i> L.. <i>Functional and Integrative Genomics</i> , 2005, 5, 208-217.	3.5	44
27	Tissue age and plant genotype affect the microbiota of apple and pear bark. <i>Microbiological Research</i> , 2018, 211, 57-68.	5.3	44
28	Reduced diversity of gut microbiota in two <i>Aedes</i> mosquitoes species in areas of recent invasion. <i>Scientific Reports</i> , 2018, 8, 16091.	3.3	41
29	A SNP transferability survey within the genus <i>Vitis</i> . <i>BMC Plant Biology</i> , 2008, 8, 128.	3.6	40
30	Changes in Microbiota Across Developmental Stages of <i>Aedes koreicus</i> , an Invasive Mosquito Vector in Europe: Indications for Microbiota-Based Control Strategies. <i>Frontiers in Microbiology</i> , 2019, 10, 2832.	3.5	38
31	Novel Aspects on The Interaction Between Grapevine and <i>Plasmopara viticola</i> : Dual-RNA-Seq Analysis Highlights Gene Expression Dynamics in The Pathogen and The Plant During The Battle For Infection. <i>Genes</i> , 2020, 11, 261.	2.4	37
32	Sequencing and assembly of highly heterozygous genome of <i>Vitis vinifera</i> L. cv Pinot Noir: Problems and solutions. <i>Journal of Biotechnology</i> , 2008, 136, 38-43.	3.8	34
33	Global change-driven use of onshore habitat impacts polar bear faecal microbiota. <i>ISME Journal</i> , 2019, 13, 2916-2926.	9.8	33
34	Nod2 Deficiency in mice is Associated with Microbiota Variation Favouring the Expansion of mucosal CD4 ⁺ LAP ⁺ Regulatory Cells. <i>Scientific Reports</i> , 2018, 8, 14241.	3.3	25
35	Alpine headwaters emerging from glaciers and rock glaciers host different bacterial communities: Ecological implications for the future. <i>Science of the Total Environment</i> , 2020, 717, 137101.	8.0	25
36	Two-omics data revealed commonalities and differences between Rpv12- and Rpv3-mediated resistance in grapevine. <i>Scientific Reports</i> , 2020, 10, 12193.	3.3	24

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37	One-step reconstruction of multi-generation pedigree networks in apple (<i>Malus domestica</i> Borkh.) and the parentage of Golden Delicious. <i>Molecular Breeding</i> , 2014, 34, 511-524.	2.1	21
38	Fine-tuning of the flavonoid and monolignol pathways during apple early fruit development. <i>Planta</i> , 2017, 245, 1021-1035.	3.2	21
39	Leaf Treatments with a Protein-Based Resistance Inducer Partially Modify Phyllosphere Microbial Communities of Grapevine. <i>Frontiers in Plant Science</i> , 2016, 7, 1053.	3.6	20
40	Initial pH influences microbial communities composition in dark fermentation of scotta permeate. <i>International Journal of Hydrogen Energy</i> , 2018, 43, 8707-8717.	7.1	20
41	Unraveling the Diversity of Eukaryotic Microplankton in a Large and Deep Perialpine Lake Using a High Throughput Sequencing Approach. <i>Frontiers in Microbiology</i> , 2020, 11, 789.	3.5	20
42	Influence of essential oils in diet and life-stage on gut microbiota and fillet quality of rainbow trout (<i>Oncorhynchus mykiss</i>). <i>International Journal of Food Sciences and Nutrition</i> , 2018, 69, 318-333.	2.8	19
43	DNA sequence and taxonomic gap analyses to quantify the coverage of aquatic cyanobacteria and eukaryotic microalgae in reference databases: Results of a survey in the Alpine region. <i>Science of the Total Environment</i> , 2022, 834, 155175.	8.0	18
44	Physical mapping in highly heterozygous genomes: a physical contig map of the Pinot Noir grapevine cultivar. <i>BMC Genomics</i> , 2010, 11, 204.	2.8	15
45	Raw milk and fecal microbiota of commercial Alpine dairy cows varies with herd, fat content and diet. <i>PLoS ONE</i> , 2020, 15, e0237262.	2.5	13
46	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.	3.3	13
47	Temporal variability of bacterioplankton is habitat driven. <i>Molecular Ecology</i> , 2018, 27, 4322-4335.	3.9	11
48	A pilot study of eDNA metabarcoding to estimate plant biodiversity by an alpine glacier core (Adamello) Tj ETQqO 0,0,rgBT /Overlock 10	3.3	11
49	A multi-kingdom metabarcoding study on cattle grazing Alpine pastures discloses intra-seasonal shifts in plant selection and faecal microbiota. <i>Scientific Reports</i> , 2021, 11, 889.	3.3	9
50	Kinase domain-targeted isolation of defense-related receptor-like kinases (RLK/Pelle) in <i>Platanus acerifolia</i> : phylogenetic and structural analysis. <i>BMC Research Notes</i> , 2014, 7, 884.	1.4	7
51	Multifaceted aspects of synchrony between freshwater prokaryotes and protists. <i>Molecular Ecology</i> , 2019, 28, 4500-4512.	3.9	6
52	Grapevine (<i>Vitis vinifera</i> L.) varietal assortment and evolution in the Marche region (central Italy). <i>Oeno One</i> , 2021, 55, .	1.4	6
53	Distinct and Temporally Stable Assembly Mechanisms Shape Bacterial and Fungal Communities in Vineyard Soils. <i>Microbial Ecology</i> , 2023, 86, 337-349.	2.8	6
54	Responses of cucumber (<i>Cucumis sativus</i> L.) rhizosphere microbial community to some agronomic management practices. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	4

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55	Effect of a Wood-Based Carrier of <i>Trichoderma atroviride</i> SC1 on the Microorganisms of the Soil. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 751.	3.5	4
56	Do inferences about freshwater phytoplankton communities change when based on microscopy or high-throughput sequencing data?. <i>Freshwater Biology</i> , 2021, 66, 640-655.	2.4	4
57	Diet-driven mercury contamination is associated with polar bear gut microbiota. <i>Scientific Reports</i> , 2021, 11, 23372.	3.3	4
58	Soil Communities: Who Responds and How Quickly to a Change in Agricultural System?. <i>Sustainability</i> , 2022, 14, 383.	3.2	3
59	Genome sequencing provides new insights on the distribution of <i>Erwinia amylovora</i> lineages in northern Italy. <i>Environmental Microbiology Reports</i> , 2022, 14, 584-590.	2.4	3
60	Dissecting the susceptibility/resistance mechanism of <i>Vitis vinifera</i> for the future control of downy mildew. <i>BIO Web of Conferences</i> , 2022, 44, 04002.	0.2	2
61	On the Origin and Propagation of the COVID-19 Outbreak in the Italian Province of Trento, a Tourist Region of Northern Italy. <i>Viruses</i> , 2022, 14, 580.	3.3	1