

Fabio Marroni

List of Publications by Year in descending order

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Version: 2024-02-01

77
papers

8,396
citations

159573

30
h-index

76898

74
g-index

82
all docs

82
docs citations

82
times ranked

15626
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation of sensitivity and specificity in RNA-Seq-based detection of grapevine viral pathogens. <i>Journal of Virological Methods</i> , 2022, 300, 114383.	2.1	6
2	ddRAD-seq reveals the genetic structure and detects signals of selection in Italian brown trout. <i>Genetics Selection Evolution</i> , 2022, 54, 8.	3.0	8
3	Genetic and Phenotypic Characteristics of the <i>Salmo trutta</i> Complex in Italy. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 3219.	2.5	6
4	Infection by phloem-limited phytoplasma affects mineral nutrient homeostasis in tomato leaf tissues. <i>Journal of Plant Physiology</i> , 2022, 271, 153659.	3.5	9
5	Epidemiology of a major honey bee pathogen, deformed wing virus: potential worldwide replacement of genotype A by genotype B. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2022, 18, 157-171.	1.5	31
6	Environmental methane emissions from seagrass wrack and evaluation of salinity effect on microbial community composition. <i>Journal of Cleaner Production</i> , 2021, 285, 125426.	9.3	13
7	Testcrosses are an efficient strategy for identifying <i>cis</i> -regulatory variation: Bayesian analysis of allele-specific expression (BayesASE). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	3
8	Transcriptomic and metabolomic profiles of <i>Zea mays</i> fed with urea and ammonium. <i>Physiologia Plantarum</i> , 2021, 173, 935-953.	5.2	4
9	A forward genetics approach integrating genome-wide association study and expression quantitative trait locus mapping to dissect leaf development in maize (<i>Zea mays</i>). <i>Plant Journal</i> , 2021, 107, 1056-1071.	5.7	19
10	Open chromatin in grapevine marks candidate CREs and with other chromatin features correlates with gene expression. <i>Plant Journal</i> , 2021, 107, 1631-1647.	5.7	17
11	A Transcriptomic Approach Provides Insights on the Mycorrhizal Symbiosis of the Mediterranean Orchid <i>Limodorum abortivum</i> in Nature. <i>Plants</i> , 2021, 10, 251.	3.5	16
12	Power calculator for detecting allelic imbalance using hierarchical Bayesian model. <i>BMC Research Notes</i> , 2021, 14, 436.	1.4	1
13	The genomes of 204 <i>Vitis vinifera</i> accessions reveal the origin of European wine grapes. <i>Nature Communications</i> , 2021, 12, 7240.	12.8	39
14	Transcriptome Analysis of <i>Amyloodinium ocellatum</i> Tomonts Revealed Basic Information on the Major Potential Virulence Factors. <i>Genes</i> , 2020, 11, 1252.	2.4	6
15	A draft genome of sweet cherry (<i>Prunus avium</i> L.) reveals genome-wide and local effects of domestication. <i>Plant Journal</i> , 2020, 103, 1420-1432.	5.7	23
16	On the origin of European sheep as revealed by the diversity of the Balkan breeds and by optimizing population-genetic analysis tools. <i>Genetics Selection Evolution</i> , 2020, 52, 25.	3.0	58
17	Common and specific responses to iron and phosphorus deficiencies in roots of apple tree (<i>Malus × Tj ETQq1 1 0,784314 rgBT /Over</i>	3.9	15
18	â€ˆCandidatus <i>Phytoplasma solani</i> ™ interferes with the distribution and uptake of iron in tomato. <i>BMC Genomics</i> , 2019, 20, 703.	2.8	19

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19	Physiological and RNA sequencing data of white lupin plants grown under Fe and P deficiency. Data in Brief, 2019, 25, 104069.	1.0	5
20	Physiological and transcriptomic data highlight common features between iron and phosphorus acquisition mechanisms in white lupin roots. Plant Science, 2019, 285, 110-121.	3.6	22
21	Genetic, epigenetic and genomic effects on variation of gene expression among grape varieties. Plant Journal, 2019, 99, 895-909.	5.7	19
22	Single primer enrichment technology as a tool for massive genotyping: a benchmark on black poplar and maize. Annals of Botany, 2019, 124, 543-551.	2.9	46
23	Metagenomic profiles of different types of Italian high-moisture Mozzarella cheese. Food Microbiology, 2019, 79, 123-131.	4.2	65
24	Direct Testing for Allele-Specific Expression Differences Between Conditions. G3: Genes, Genomes, Genetics, 2018, 8, 447-460.	1.8	13
25	Do you cov me? Effect of coverage reduction on species identification and genome reconstruction in complex biological matrices by metagenome shotgun high-throughput sequencing. F1000Research, 2018, 7, 1767.	1.6	7
26	Do you cov me? Effect of coverage reduction on metagenome shotgun sequencing studies. F1000Research, 2018, 7, 1767.	1.6	16
27	Reduction of heterozygosity ($\langle scp \rangle ROH \langle /scp \rangle$) as a method to detect mosaic structural variation. Plant Biotechnology Journal, 2017, 15, 791-793.	8.3	11
28	Impact of an arbuscular mycorrhizal fungus versus a mixed microbial inoculum on the transcriptome reprogramming of grapevine roots. Mycorrhiza, 2017, 27, 417-430.	2.8	44
29	Characterization of the Poplar Pan-Genome by Genome-Wide Identification of Structural Variation. Molecular Biology and Evolution, 2016, 33, 2706-2719.	8.9	95
30	Genome-wide analysis of LTR-retrotransposon expression in leaves of <i>Populus trichocarpa</i> canadensis water-deprived plants. Tree Genetics and Genomes, 2016, 12, 1.	1.6	17
31	Merino and Merino-derived sheep breeds: a genome-wide intercontinental study. Genetics Selection Evolution, 2015, 47, 64.	3.0	97
32	First insights into the transcriptome and development of new genomic tools of a widespread circum-Mediterranean tree species, <i>Pinus halepensis</i> Mill. Molecular Ecology Resources, 2014, 14, 846-856.	4.8	61
33	Structural variation and genome complexity: is dispensable really dispensable?. Current Opinion in Plant Biology, 2014, 18, 31-36.	7.1	101
34	Fine-Mapping of Restless Legs Locus 4 (RLS4) Identifies a Haplotype over the SPATS2L and KCTD18 Genes. Journal of Molecular Neuroscience, 2013, 49, 600-605.	2.3	12
35	$\langle scp \rangle SNP \langle /scp \rangle$ Prioritization Using a $\langle scp \rangle B \langle /scp \rangle$ayesian Probability of Association. Genetic Epidemiology, 2013, 37, 214-221.	1.3	13
36	Importance of Different Types of Prior Knowledge in Selecting Genome-Wide Findings for Follow-Up. Genetic Epidemiology, 2013, 37, 205-213.	1.3	14

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37	The high-quality draft genome of peach (<i>Prunus persica</i>) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 2013, 45, 487-494.	21.4	1,031
38	Breeding with rare defective alleles (BRDA): a natural <i>Populus nigra</i> HCT mutant with modified lignin as a case study. <i>New Phytologist</i> , 2013, 198, 765-776.	7.3	92
39	The Quest for Rare Variants: Pooled Multiplexed Next Generation Sequencing in Plants. <i>Frontiers in Plant Science</i> , 2012, 3, 133.	3.6	31
40	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	3.5	419
41	The Endemic Paraganglioma Syndrome Type 1: Origin, Spread, and Clinical Expression. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2012, 97, E637-E641.	3.6	25
42	Large-scale detection of rare variants via pooled multiplexed next-generation sequencing: towards next-generation Ecotilling. <i>Plant Journal</i> , 2011, 67, 736-745.	5.7	81
43	Nucleotide diversity and linkage disequilibrium in <i>Populus nigra</i> cinnamyl alcohol dehydrogenase (CAD4) gene. <i>Tree Genetics and Genomes</i> , 2011, 7, 1011-1023.	1.6	138
44	Identification of a common variant in the TFR2 gene implicated in the physiological regulation of serum iron levels. <i>Human Molecular Genetics</i> , 2011, 20, 1232-1240.	2.9	67
45	Integrated analysis of unclassified variants in mismatch repair genes. <i>Genetics in Medicine</i> , 2011, 13, 115-124.	2.4	34
46	<i>Parkin</i> gene modifies the effect of <i>RLS4</i> on the age at onset of restless legs syndrome (RLS). <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2010, 153B, 350-355.	1.7	3
47	Drawing the history of the Hutterite population on a genetic landscape: inference from Y-chromosome and mtDNA genotypes. <i>European Journal of Human Genetics</i> , 2010, 18, 463-470.	2.8	26
48	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010, 466, 707-713.	27.8	3,249
49	Estimating <i>CDKN2A</i> Carrier Probability and Personalizing Cancer Risk Assessments in Hereditary Melanoma Using MelaPRO. <i>Cancer Research</i> , 2010, 70, 552-559.	0.9	41
50	Genome-wide association analysis identifies multiple loci related to resting heart rate. <i>Human Molecular Genetics</i> , 2010, 19, 3885-3894.	2.9	133
51	Linkage and Genome-wide Association Analysis of Obesity-related Phenotypes: Association of Weight With the <i>MGAT1</i> Gene. <i>Obesity</i> , 2010, 18, 803-808.	3.0	54
52	Genetic Determinants of Circulating Sphingolipid Concentrations in European Populations. <i>PLoS Genetics</i> , 2009, 5, e1000672.	3.5	184
53	Common variants in the <i>JAZF1</i> gene associated with height identified by linkage and genome-wide association analysis. <i>Human Molecular Genetics</i> , 2009, 18, 373-380.	2.9	88
54	A Genome-Wide Association Scan of RR and QT Interval Duration in 3 European Genetically Isolated Populations. <i>Circulation: Cardiovascular Genetics</i> , 2009, 2, 322-328.	5.1	67

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55	ParkScreen: A Low-Cost Rapid Linkage Marker Panel for Parkinson's Disease. <i>Journal of Molecular Neuroscience</i> , 2009, 39, 235-241.	2.3	0
56	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. <i>Nature Genetics</i> , 2009, 41, 47-55.	21.4	776
57	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. <i>Nature Genetics</i> , 2009, 41, 407-414.	21.4	356
58	Genome-wide linkage analysis of serum creatinine in three isolated European populations. <i>Kidney International</i> , 2009, 76, 297-306.	5.2	71
59	Reconstructing the Genealogy of a BRCA1 Founder Mutation by Phylogenetic Analysis. <i>Annals of Human Genetics</i> , 2008, 72, 310-318.	0.8	22
60	Estimates of Genetic and Environmental Contribution to 43 Quantitative Traits Support Sharing of a Homogeneous Environment in an Isolated Population from South Tyrol, Italy. <i>Human Heredity</i> , 2008, 65, 175-182.	0.8	30
61	ISOLATION AND MARRIAGE PATTERNS IN FOUR SOUTH TYROLEAN VILLAGES (ITALY) DURING THE NINETEENTH CENTURY. <i>Journal of Biosocial Science</i> , 2008, 40, 787-91.	1.2	7
62	The genetic study of three population microisolates in South Tyrol (MICROS): study design and epidemiological perspectives. <i>BMC Medical Genetics</i> , 2007, 8, 29.	2.1	56
63	Linkage Analysis Identifies a Novel Locus for Restless Legs Syndrome on Chromosome 2q in a South Tyrolean Population Isolate. <i>American Journal of Human Genetics</i> , 2006, 79, 716-723.	6.2	101
64	Y-chromosome haplotypes and male isonymy: Genetic and genealogical study in a small town of Tuscany (Buti, Italy). <i>International Congress Series</i> , 2006, 1288, 225-227.	0.2	0
65	Statistical analysis of individual assignment tests among four cattle breeds using fifteen STR loci. <i>Journal of Animal Science</i> , 2006, 84, 11-19.	0.5	38
66	A genetic model for determining MSH2 and MLH1 carrier probabilities based on family history and tumor microsatellite instability. <i>Clinical Genetics</i> , 2006, 69, 254-262.	2.0	20
67	Population Isolates in South Tyrol and Their Value for Genetic Dissection of Complex Diseases. <i>Annals of Human Genetics</i> , 2006, 70, 812-821.	0.8	15
68	Effect of UV-B Radiation on Ciliated Protozoa. , 2006, , 231-248.		1
69	Haplotypic structure of the X chromosome in the COGA population sample and the quality of its reconstruction by extant software packages. <i>BMC Genetics</i> , 2005, 6, S77.	2.7	8
70	Evaluation of widely used models for predicting BRCA1 and BRCA2 mutations. <i>Journal of Medical Genetics</i> , 2004, 41, 278-285.	3.2	55
71	Microgeographic variation of HLA-A, -B, and -DR haplotype frequencies in Tuscany, Italy: implications for recruitment of bone marrow donors. <i>Tissue Antigens</i> , 2004, 64, 478-485.	1.0	10
72	Penetrances of breast and ovarian cancer in a large series of families tested for BRCA1/2 mutations. <i>European Journal of Human Genetics</i> , 2004, 12, 899-906.	2.8	55

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73	The number of STR markers necessary to resolve relationships in deficiency paternity cases. International Congress Series, 2004, 1261, 541-543.	0.2	1
74	Assigning individuals to ethnic groups based on 13 STR loci. International Congress Series, 2004, 1261, 59-61.	0.2	6
75	Biological Weighting Function of the UV-Bâ€“induced Impairment of Phototaxis in the Freshwater Ciliate <i>Ophryoglena flava</i> Â¶. Photochemistry and Photobiology, 2004, 80, 408.	2.5	0
76	Different Expressivity of BRCA1 and BRCA2: Analysis of 179 Italian Pedigrees with Identified Mutation. Breast Cancer Research and Treatment, 2003, 81, 71-79.	2.5	22
77	Phototaxis in the ciliated protozoan <i>Ophryoglena flava</i> : doseâ€“effect curves and action spectrum determination. Journal of Photochemistry and Photobiology B: Biology, 2000, 57, 41-50.	3.8	16