Roberto Papa

List of Publications by Year
in descending order

102 papers	5,852 citations	57631 44 h-index	88477 70 g-index
106 all docs	106 docs citations	106 times ranked	5291 citing authors

#	Article	IF	Citations
1	Mesoamerican origin of the common bean (<i>Phaseolus vulgaris</i> L.) is revealed by sequence data. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E788-96.	3.3	327
2	Molecular analysis of the parallel domestication of the common bean (<i><scp>P</scp>haseolus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.5	240
3	Asymmetry of gene flow and differential geographical structure of molecular diversity in wild and domesticated common bean (Phaseolus vulgaris L.) from Mesoamerica. Theoretical and Applied Genetics, 2003, 106, 239-250.	1.8	209
4	Beans (Phaseolus ssp.) as a Model for Understanding Crop Evolution. Frontiers in Plant Science, 2017, 8, 722.	1.7	177
5	AFLP analysis of the phenetic organization and genetic diversity of Vigna unguiculata L. Walp. reveals extensive gene flow between wild and domesticated types. Theoretical and Applied Genetics, 2002, 104, 358-366.	1.8	155
6	Genetic diversity, structure and marker-trait associations in a collection of Italian tomato (Solanum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.8	150
7	The colours of durum wheat: a review. Crop and Pasture Science, 2014, 65, 1.	0.7	142
8	Linkage disequilibrium and population structure in wild and domesticated populations of <i>Phaseolus vulgaris</i> L.. Evolutionary Applications, 2009, 2, 504-522.	1.5	139
9	Genetic Diversity and Population Structure of Tetraploid Wheats (Triticum turgidum L.) Estimated by SSR, DArT and Pedigree Data. PLoS ONE, 2013, 8, e67280.	1.1	137
10	Possible effects of (trans)gene flow from crops on the genetic diversity from landraces and wild relatives. Environmental Biosafety Research, 2003, 2, 89-103.	1.1	129
11	Beans in Europe: origin and structure of the European landraces of Phaseolus vulgaris L.. Theoretical and Applied Genetics, 2010, 121, 829-843.	1.8	123
12	A high-density consensus map of A and B wheat genomes. Theoretical and Applied Genetics, 2012, 125, 1619-1638.	1.8	117
13	Decreased Nucleotide and Expression Diversity and Modified Coexpression Patterns Characterize Domestication in the Common Bean. Plant Cell, 2014, 26, 1901-1912.	3.1	103
14	A genome-wide analysis of differentiation between wild and domesticated Phaseolus vulgaris from Mesoamerica. Theoretical and Applied Genetics, 2005, 111, 1147-1158.	1.8	102
15	Biodiversity in Agricultural Landscapes: Saving Natural Capital without Losing Interest. Conservation Biology, 2006, 20, 263-264.	2.4	101
16	Syntenic relationships among legumes revealed using a gene-based genetic linkage map of common bean (Phaseolus vulgaris L.). Theoretical and Applied Genetics, 2010, 121, 1103-1116.	1.8	99
17	Demographic factors shaped diversity in the two gene pools of wild common bean Phaseolus vulgaris L.. Heredity, 2013, 110, 267-276.	1.2	99
18	Evolutionary Metabolomics Reveals Domestication-Associated Changes in Tetraploid Wheat Kernels. Molecular Biology and Evolution, 2016, 33, 1740-1753.	3.5	99

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19	Evolution of the Crop Rhizosphere: Impact of Domestication on Root Exudates in Tetraploid Wheat (Triticum turgidum L.). Frontiers in Plant Science, 2017, 8, 2124.	1.7	87
20	Landscape genetics, adaptive diversity and population structure in <i>Phaseolus vulgaris</i>. New Phytologist, 2016, 209, 1781-1794.	3.5	86
21	Population genetic structure of Pyrenophora teresDrechs. the causal agent of net blotch in Sardinian landraces of barley (Hordeum vulgare L.). Theoretical and Applied Genetics, 2003, 106, 947-959.	1.8	85
22	Tagging the Signatures of Domestication in Common Bean (Phaseolus vulgaris) by Means of Pooled DNA Samples. Annals of Botany, 2007, 100, 1039-1051.	1.4	84
23	Genetic basis of qualitative and quantitative resistance to powdery mildew in wheat: from consensus regions to candidate genes. BMC Genomics, 2013, 14, 562.	1.2	84
24	Genetic diversity of Phaseolus vulgaris L. and P. coccineus L. landraces in central Italy. Plant Breeding, 2005, 124, 464-472.	1.0	83
25	Genetic Variability in Anthocyanin Composition and Nutritional Properties of Blue, Purple, and Red Bread (<i>Triticum aestivum</i> L.) and Durum (<i>Triticum turgidum</i> L. ssp. <i>turgidum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	2.3	82
26	Investigation of the domestication of common bean (Phaseolus vulgaris) using multilocus sequence data. Functional Plant Biology, 2011, 38, 953.	1.1	75
27	Linkage Disequilibrium and Genome-Wide Association Mapping in Tetraploid Wheat (Triticum turgidum) Tj ETQq1 1 0.784314 rgBT /Ov	1.1	75
28	Adapting legume crops to climate change using genomic approaches. Plant, Cell and Environment, 2019, 42, 6-19.	2.8	74
29	Impact of domestication on the phenotypic architecture of durum wheat under contrasting nitrogen fertilization. Journal of Experimental Botany, 2015, 66, 5519-5530.	2.4	69
30	A dense durum wheatÂÃ—ÂT. dicoccum linkage map based on SNP markers for the study of seed morphology. Molecular Breeding, 2014, 34, 1579-1597.	1.0	67
31	Phylogeny and evolution of mating-type genes from Pyrenophora teres, the causal agent of barley â€œnet blotchâ€• disease. Current Genetics, 2007, 51, 377-392.	0.8	63
32	Analysis of the contribution of Mesoamerican and Andean gene pools to European common bean (Phaseolus vulgaris L.) germplasm and strategies to establish a core collection. Genetic Resources and Crop Evolution, 2007, 54, 1763-1779.	0.8	63
33	Effect of genotype, environment and genotype-by-environment interaction on metabolite profiling in durum wheat (Triticum durum Desf.) grain. Journal of Cereal Science, 2013, 57, 183-192.	1.8	63
34	Genotype by environment interactions in barley (Hordeum vulgare L.): different responses of landraces, recombinant inbred lines and varieties to Mediterranean environment. Euphytica, 2008, 163, 231-247.	0.6	61
35	Metabolomics and Food Processing: From Semolina to Pasta. Journal of Agricultural and Food Chemistry, 2011, 59, 9366-9377.	2.4	60
36	Genomics of Origin, Domestication and Evolution of Phaseolus vulgaris. , 2014, , 483-507.		60

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37	Domestication of Crop Metabolomes: Desired and Unintended Consequences. Trends in Plant Science, 2021, 26, 650-661.	4.3	60
38	Introgression from modern hybrid varieties into landrace populations of maize (<i>Zea mays</i> ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.0	55
39	Isolation and characterization of the mating-type locus of the barley pathogen<i>Pyrenophora teres</i>and frequencies of mating-type idiomorphs within and among fungal populations collected from barley landraces. Genome, 2005, 48, 855-869.	0.9	54
40	Genetic diversity and structure of a worldwide collection of Phaseolus coccineus L.. Theoretical and Applied Genetics, 2011, 122, 1281-1291.	1.8	54
41	Genomic dissection of pod shattering in common bean: mutations at nonâ€orthologous loci at the basis of convergent phenotypic evolution under domestication of leguminous species. Plant Journal, 2019, 97, 693-714.	2.8	54
42	Adaptation and diversity along an altitudinal gradient in Ethiopian barley (Hordeum vulgare L.) landraces revealed by molecular analysis. BMC Plant Biology, 2010, 10, 121.	1.6	51
43	Evidence for Introduction Bottleneck and Extensive Inter-Gene Pool (Mesoamerica x Andes) Hybridization in the European Common Bean (Phaseolus vulgaris L.) Germplasm. PLoS ONE, 2013, 8, e75974.	1.1	50
44	Mobilizing Crop Biodiversity. Molecular Plant, 2020, 13, 1341-1344.	3.9	50
45	Whole Genome Scan Reveals Molecular Signatures of Divergence and Selection Related to Important Traits in Durum Wheat Germplasm. Frontiers in Genetics, 2020, 11, 217.	1.1	50
46	Genetic diversity in landrace populations of Hordeum vulgare L. from Sardinia, Italy, as revealed by RAPDs, isozymes and morphophenological traits. Plant Breeding, 1998, 117, 523-530.	1.0	49
47	Assessment of Inter Simple Sequence Repeat Markers to Differentiate Sympatric Wild and Domesticated Populations of Common Bean. Crop Science, 2005, 45, 606-615.	0.8	48
48	Proteomic study of a tolerant genotype of durum wheat under salt-stress conditions. Analytical and Bioanalytical Chemistry, 2014, 406, 1423-1435.	1.9	48
49	A Comprehensive Phenotypic Investigation of the â€œPod-Shattering Syndromeâ€• in Common Bean. Frontiers in Plant Science, 2017, 8, 251.	1.7	47
50	Characterization of wheat DArT markers: genetic and functional features. Molecular Genetics and Genomics, 2012, 287, 741-753.	1.0	46
51	Insight into durum wheat Lpx-B1: a small gene family coding for the lipoxygenase responsible for carotenoid bleaching in mature grains. BMC Plant Biology, 2010, 10, 263.	1.6	45
52	Development and use of chloroplast microsatellites in <i>Phaseolus</i> spp. and other legumes. Plant Biology, 2009, 11, 598-612.	1.8	44
53	Structure of genetic diversity in Olea europaea L. cultivars from central Italy. Molecular Breeding, 2011, 27, 533-547.	1.0	44
54	Nucleotide diversity of a genomic sequence similar to SHATTERPROOF (PvSHP1) in domesticated and wild common bean (Phaseolus vulgaris L.). Theoretical and Applied Genetics, 2011, 123, 1341-1357.	1.8	44

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55	Analysis of metabolic and mineral changes in response to salt stress in durum wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Biochemistry, 2018, 133, 57-70.	2.8	43
56	Population Structure of Barley Landrace Populations and Gene-Flow with Modern Varieties. PLoS ONE, 2013, 8, e83891.	1.1	42
57	Plant growth and phenolic compounds in the rhizosphere soil of wild oat (Avena fatua L.). Frontiers in Plant Science, 2013, 4, 509.	1.7	41
58	Convergent Evolution of the Seed Shattering Trait. Genes, 2019, 10, 68.	1.0	41
59	Chloroplast Microsatellite Diversity in Phaseolus vulgaris. Frontiers in Plant Science, 2012, 3, 312.	1.7	37
60	Genetic diversity of barley (Hordeum vulgare L.) landraces from the central highlands of Ethiopia: comparison between the Belg and Meher growing seasons using morphological traits. Genetic Resources and Crop Evolution, 2009, 56, 1131-1148.	0.8	34
61	Multiâ€tissue integration of transcriptomic and specialized metabolite profiling provides tools for assessing the common bean (<i>Phaseolus vulgaris</i>) metabolome. Plant Journal, 2019, 97, 1132-1153.	2.8	33
62	European Phaseolus coccineus L. landraces: Population Structure and Adaptation, as Revealed by cpSSRs and Phenotypic Analyses. PLoS ONE, 2013, 8, e57337.	1.1	31
63	Durum wheat and allelopathy: toward wheat breeding for natural weed management. Frontiers in Plant Science, 2013, 4, 375.	1.7	30
64	Ancient genomes reveal early Andean farmers selected common beans while preserving diversity. Nature Plants, 2021, 7, 123-128.	4.7	29
65	The INCREASE project: Intelligent Collections of foodâ€legume genetic resources for European agrofood systems. Plant Journal, 2021, 108, 646-660.	2.8	29
66	Pod indehiscence in common bean is associated with the fine regulation of<i>PvMYB26</i>. Journal of Experimental Botany, 2021, 72, 1617-1633.	2.4	29
67	Molecular Phylogeny of Anthyllis spp.. Plant Biology, 2004, 6, 454-464.	1.8	28
68	Biodiversity studies in<i>Phaseolus</i>species by DNA barcoding. Genome, 2011, 54, 529-545.	0.9	27
69	Co-evolution in a landrace meta-population: two closely related pathogens interacting with the same host can lead to different adaptive outcomes. Scientific Reports, 2015, 5, 12834.	1.6	27
70	Nuclear and chloroplast microsatellite diversity in Phaseolus vulgaris L. from Sardinia (Italy). Molecular Breeding, 2009, 23, 413-429.	1.0	25
71	6. Evolution of Genetic Diversity in Phaseolus vulgaris L.. , 2006, , 121-142.		25
72	Varietal differences in sodium uptake in barley cultivars exposed to soil salinity or salt spray. Journal of Experimental Botany, 1994, 45, 895-901.	2.4	24

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73	Development of single nucleotide polymorphisms in Phaseolus vulgaris and related Phaseolus spp. Molecular Breeding, 2014, 33, 531-544.	1.0	23
74	Genetic structure and linkage disequilibrium in landrace populations of barley in Sardinia. Theoretical and Applied Genetics, 2012, 125, 171-184.	1.8	22
75	Adaptation to novel environments during crop diversification. Current Opinion in Plant Biology, 2020, 56, 203-217.	3.5	22
76	The genetic make-up of the European landraces of the common bean. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 197-201.	0.4	21
77	A common bean truncated CRINKLY4 kinase controls gene-for-gene resistance to the fungus<i>Colletotrichum lindemuthianum</i>. Journal of Experimental Botany, 2021, 72, 3569-3581.	2.4	21
78	Genetic Diversity, Population Structure, and Andean Introgression in Brazilian Common Bean Cultivars after Half a Century of Genetic Breeding. Genes, 2020, 11, 1298.	1.0	20
79	Characterization of Nutritional Quality Traits of a Common Bean Germplasm Collection. Foods, 2021, 10, 1572.	1.9	20
80	Amplified ribosomal DNA restriction analysis for the characterization of Azotobacteraceae: a contribution to the study of these free-living nitrogen-fixing bacteria. Journal of Microbiological Methods, 2004, 57, 197-206.	0.7	19
81	High Level of Nonsynonymous Changes in Common Bean Suggests That Selection under Domestication Increased Functional Diversity at Target Traits. Frontiers in Plant Science, 2016, 7, 2005.	1.7	19
82	Intelligent Characterization of Lentil Genetic Resources: Evolutionary History, Genetic Diversity of Germplasm, and the Need for Wellâ€Represented Collections. Current Protocols, 2021, 1, e134.	1.3	18
83	Yellow Pigment Determination for Single Kernels of Durum Wheat (<i>Triticum durum</i> Desf.). Cereal Chemistry, 2011, 88, 504-508.	1.1	17
84	Genome-Wide Association Mapping of Prostrate/Erect Growth Habit in Winter Durum Wheat. International Journal of Molecular Sciences, 2020, 21, 394.	1.8	17
85	Integration of Retrotransposons-Based Markers in a Linkage Map of Barley. Molecular Breeding, 2006, 17, 173-184.	1.0	16
86	GWAS Based on RNA-Seq SNPs and High-Throughput Phenotyping Combined with Climatic Data Highlights the Reservoir of Valuable Genetic Diversity in Regional Tomato Landraces. Genes, 2020, 11, 1387.	1.0	14
87	Current State and Perspectives in Population Genomics of the Common Bean. Plants, 2020, 9, 330.	1.6	14
88	The Triticeae Genetic Resources of Central Italy: Collection, Evaluation and Conservation. Hereditas, 2004, 135, 187-192.	0.5	13
89	Towards the Development, Maintenance, and Standardized Phenotypic Characterization of Singleâ€Seedâ€Descent Genetic Resources for Common Bean. Current Protocols, 2021, 1, e133.	1.3	13
90	History of the common bean crop: its evolution beyond its areas of origin and domestication. Arbor, 2016, 192, a317.	0.1	12

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91	Shift in beneficial interactions during crop evolution. Evolutionary Applications, 2022, 15, 905-918.	1.5	10
92	Towards Development, Maintenance, and Standardized Phenotypic Characterization of Singleâ€Seedâ€Descent Genetic Resources for Lupins. Current Protocols, 2021, 1, e191.	1.3	9
93	The Development of a European and Mediterranean Chickpea Association Panel (EMCAP). Agronomy, 2020, 10, 1417.	1.3	7
94	Genetic structure of the Anthyllis vulneraria L. s. l. species complex in Estonia based on AFLPs. Open Life Sciences, 2008, 3, 442-450.	0.6	6
95	Genetic diversity and geographic differentiation in the alternative legume <i>Tripodion tetraphyllum</i> (L.) Fourr. in North African populations. Plant Biology, 2011, 13, 381-390.	1.8	6
96	A Core Set of Snap Bean Genotypes Established by Phenotyping a Large Panel Collected in Europe. Plants, 2022, 11, 577.	1.6	6
97	Towards the Development, Maintenance and Standardized Phenotypic Characterization of Singleâ€Seedâ€Descent Genetic Resources for Chickpea. Current Protocols, 2022, 2, e371.	1.3	6
98	Domestication and Crop History. Compendium of Plant Genomes, 2017, , 21-55.	0.3	5
99	Comparative Analysis Based on Transcriptomics and Metabolomics Data Reveal Differences between Emmer and Durum Wheat in Response to Nitrogen Starvation. International Journal of Molecular Sciences, 2021, 22, 4790.	1.8	5
100	Spatial genetic structure in wild cardoon, the ancestor of cultivated globe artichoke: Limited gene flow, fragmentation and population history. Plant Science, 2016, 253, 194-205.	1.7	3
101	Sustainable Crop Production. , 2020, , 583-600.		2
102	The genomic signature of wild-to-crop introgression during the domestication of scarlet runner bean (<i>Phaseolus coccineus</i>L.). Evolution Letters, 2022, 6, 295-307.	1.6	1