

Jose M Blanca

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

5,396
citations

87888

38
h-index

144013

57
g-index

65
all docs

65
docs citations

65
times ranked

6249
citing authors

#	ARTICLE	IF	CITATIONS
1	Haplotype analyses reveal novel insights into tomato history and domestication driven by long-distance migrations and latitudinal adaptations. <i>Horticulture Research</i> , 2022, 9, .	6.3	13
2	European traditional tomatoes galore: a result of farmersâ€™ selection of a few diversity-rich loci. <i>Journal of Experimental Botany</i> , 2022, 73, 3431-3445.	4.8	11
3	STUDENTâ€™S APPROACH TO LEARNING PER STUDENT BASIS IN TWO SUBJECTS OF BIOTECHNOLOGY DEGREE. <i>EDULEARN Proceedings</i> , 2022, , .	0.0	0
4	A Major QTL Located in Chromosome 8 of <i>Cucurbita moschata</i> Is Responsible for Resistance to Tomato Leaf Curl New Delhi Virus. <i>Frontiers in Plant Science</i> , 2020, 11, 207.	3.6	30
5	Exploiting the diversity of tomato: the development of a phenotypically and genetically detailed germplasm collection. <i>Horticulture Research</i> , 2020, 7, 66.	6.3	49
6	Whole-genome resequencing of <i>Cucurbita pepo</i> morphotypes to discover genomic variants associated with morphology and horticulturally valuable traits. <i>Horticulture Research</i> , 2019, 6, 94.	6.3	34
7	De novo European eel transcriptome provides insights into the evolutionary history of duplicated genes in teleost lineages. <i>PLoS ONE</i> , 2019, 14, e0218085.	2.5	41
8	The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. <i>Nature Genetics</i> , 2019, 51, 1044-1051.	21.4	441
9	Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. <i>Nucleic Acids Research</i> , 2019, 47, D1128-D1136.	14.5	177
10	<i>De novo</i> assembly of the zucchini genome reveals a whole-genome duplication associated with the origin of the <i>Cucurbita</i> genus. <i>Plant Biotechnology Journal</i> , 2018, 16, 1161-1171.	8.3	160
11	Plant Genebanks: Present Situation and Proposals for Their Improvement. the Case of the Spanish Network. <i>Frontiers in Plant Science</i> , 2018, 9, 1794.	3.6	45
12	Resistance to Plum Pox Virus (PPV) in apricot (<i>Prunus armeniaca</i> L.) is associated with down-regulation of two MATHd genes. <i>BMC Plant Biology</i> , 2018, 18, 25.	3.6	35
13	GB3.0: a platform for plant bio-design that connects functional DNA elements with associated biological data. <i>Nucleic Acids Research</i> , 2017, 45, gkw1326.	14.5	70
14	An SNP-based saturated genetic map and QTL analysis of fruit-related traits in Zucchini using Genotyping-by-sequencing. <i>BMC Genomics</i> , 2017, 18, 94.	2.8	93
15	B9â€¦unc-1/stomatin-like modulates aggregation of polyglutamines. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2016, 87, A12.1-A12.	1.9	0
16	The first de novo transcriptome of pepino (<i>Solanum muricatum</i>): assembly, comprehensive analysis and comparison with the closely related species <i>S. caripense</i> , potato and tomato. <i>BMC Genomics</i> , 2016, 17, 321.	2.8	29
17	A modular toolbox for gRNAâ€“Cas9 genome engineering in plants based on the GoldenBraid standard. <i>Plant Methods</i> , 2016, 12, 10.	4.3	119
18	Analysis of the coding-complete genomic sequence of groundnut ringspot virus suggests a common ancestor with tomato chlorotic spot virus. <i>Archives of Virology</i> , 2016, 161, 2311-2316.	2.1	2

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19	Transcriptome analysis and molecular marker discovery in <i>Solanum incanum</i> and <i>S. aethiopicum</i> , two close relatives of the common eggplant (<i>Solanum melongena</i>) with interest for breeding. <i>BMC Genomics</i> , 2016, 17, 300.	2.8	63
20	Genomic variation in tomato, from wild ancestors to contemporary breeding accessions. <i>BMC Genomics</i> , 2015, 16, 257.	2.8	190
21	Software-Assisted Stacking of Gene Modules Using GoldenBraid 2.0 DNA-Assembly Framework. <i>Methods in Molecular Biology</i> , 2015, 1284, 399-420.	0.9	15
22	ABCC transporters mediate insect resistance to multiple Bt toxins revealed by bulk segregant analysis. <i>BMC Biology</i> , 2014, 12, 46.	3.8	144
23	SNP genotyping in melons: genetic variation, population structure, and linkage disequilibrium. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1285-1303.	3.6	85
24	A cytochrome P450 regulates a domestication trait in cultivated tomato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17125-17130.	7.1	257
25	GoldenBraid 2.0: A Comprehensive DNA Assembly Framework for Plant Synthetic Biology. <i>Plant Physiology</i> , 2013, 162, 1618-1631.	4.8	358
26	Application of Genomic Tools in Plant Breeding. <i>Current Genomics</i> , 2012, 13, 179-195.	1.6	236
27	Taxonomy and genetic diversity of domesticated <i>Capsicum</i> species in the Andean region. <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 1077-1088.	1.6	76
28	A Cost-effective Double-Stranded cDNA Synthesis for Plant Microarrays. <i>Plant Molecular Biology Reporter</i> , 2012, 30, 1276-1282.	1.8	1
29	The transcriptome of <i>Spodoptera exigua</i> larvae exposed to different types of microbes. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 557-570.	2.7	70
30	Transcriptome sequencing for SNP discovery across <i>Cucumis melo</i> . <i>BMC Genomics</i> , 2012, 13, 280.	2.8	86
31	High-throughput SNP genotyping in <i>Cucurbita pepo</i> for map construction and quantitative trait loci mapping. <i>BMC Genomics</i> , 2012, 13, 80.	2.8	110
32	The genome of melon (<i>Cucumis melo</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11872-11877.	7.1	654
33	Variation Revealed by SNP Genotyping and Morphology Provides Insight into the Origin of the Tomato. <i>PLoS ONE</i> , 2012, 7, e48198.	2.5	161
34	Melon Transcriptome Characterization: Simple Sequence Repeats and Single Nucleotide Polymorphisms Discovery for High Throughput Genotyping across the Species. <i>Plant Genome</i> , 2011, 4, 118-131.	2.8	53
35	Pattern of genetic variability of <i>Solanum habrochaites</i> in its natural area of distribution. <i>Genetic Resources and Crop Evolution</i> , 2011, 58, 347-360.	1.6	21
36	A consensus linkage map for molecular markers and Quantitative Trait Loci associated with economically important traits in melon (<i>Cucumis melo</i> L.). <i>BMC Plant Biology</i> , 2011, 11, 111.	3.6	156

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37	Transcriptome characterization and high throughput SSRs and SNPs discovery in Cucurbita pepo (Cucurbitaceae). BMC Genomics, 2011, 12, 104.	2.8	177
38	ngs_backbone: a pipeline for read cleaning, mapping and SNP calling using Next Generation Sequence. BMC Genomics, 2011, 12, 285.	2.8	53
39	Analysis of the melon (Cucumis melo) small RNAome by high-throughput pyrosequencing. BMC Genomics, 2011, 12, 393.	2.8	58
40	Analysis of Pathogen Resistance and Fruit Quality Traits in Melon (Cucumis melo L.). , 2011, , 29-46.		0
41	An oligo-based microarray offers novel transcriptomic approaches for the analysis of pathogen resistance and fruit quality traits in melon (Cucumis melo L.). BMC Genomics, 2009, 10, 467.	2.8	61
42	Transcriptomic analysis of tomato carpel development reveals alterations in ethylene and gibberellin synthesis during pat3/pat4 parthenocarpic fruit set. BMC Plant Biology, 2009, 9, 67.	3.6	40
43	A set of EST-SNPs for map saturation and cultivar identification in melon. BMC Plant Biology, 2009, 9, 90.	3.6	90
44	Genetic and bioclimatic variation in Solanum pimpinellifolium. Genetic Resources and Crop Evolution, 2009, 56, 39-51.	1.6	43
45	Classification and phylogenetic relationships in Solanum section Lycopersicon based on AFLP and two nuclear gene sequences. Genetic Resources and Crop Evolution, 2009, 56, 663-678.	1.6	44
46	Bin mapping of genomic and EST-derived SSRs in melon (Cucumis melo L.). Theoretical and Applied Genetics, 2008, 118, 139-150.	3.6	115
47	EST2uni: an open, parallel tool for automated EST analysis and database creation, with a data mining web interface and microarray expression data integration. BMC Bioinformatics, 2008, 9, 5.	2.6	54
48	Tomato torrado virus is Transmitted by <i>Bemisia tabaci</i> and Infects Pepper and Eggplant in Addition to Tomato. Plant Disease, 2008, 92, 1139-1139.	1.4	54
49	Analysis of gene expression during the fruit set of tomato: A comparative approach. Plant Science, 2007, 173, 609-620.	3.6	10
50	AFLP and DNA sequence variation in an Andean domesticate, pepino (<i>Solanum muricatum</i>), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1219-1229.	1.7	30
51	MELOGEN: an EST database for melon functional genomics. BMC Genomics, 2007, 8, 306.	2.8	87
52	Identification of a CAPS marker tightly linked to the Tomato yellow leaf curl disease resistance gene Ty-1 in tomato. European Journal of Plant Pathology, 2007, 117, 347-356.	1.7	49
53	Genetic Structure of Lycopersicon pimpinellifolium (Solanaceae) Populations Collected after the ENSO Event of 1997-1998. Genetic Resources and Crop Evolution, 2007, 54, 359-377.	1.6	12
54	THE SPANISH MELON GENOMICS INITIATIVE. Acta Horticulturae, 2007, , 47-54.	0.2	3

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55	The Implications of AFLP Data for the Systematics of the Wild Species of <i>Solanum</i> Section <i>Basarthurum</i> . <i>Systematic Botany</i> , 2006, 31, 208-216.	0.5	14
56	Relationships, origin, and diversity of Galápagos tomatoes: implications for the conservation of natural populations. <i>American Journal of Botany</i> , 2004, 91, 86-99.	1.7	58
57	Mutations in Myosin VIIA (MYO7A) and Usherin (USH2A) in Spanish patients with usher syndrome types I and II, respectively. <i>Human Mutation</i> , 2002, 20, 76-77.	2.5	47
58	dfh is a <i>Drosophila</i> homolog of the Friedreich's ataxia disease gene. <i>Gene</i> , 2000, 256, 35-42.	2.2	34
59	Incipient GAA repeats in the primate Friedreich ataxia homologous genes. <i>Molecular Biology and Evolution</i> , 1999, 16, 880-883.	8.9	10
60	Phenotype Correlation and Intergenerational Dynamics of the Friedreich Ataxia GAA Trinucleotide Repeat. <i>American Journal of Human Genetics</i> , 1997, 61, 101-110.	6.2	161