

# 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	The genome of melon ( <i>Cucumis melo</i> L.). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11872-11877.	7.1	654
2	The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. Nature Genetics, 2019, 51, 1044-1051.	21.4	441
3	GoldenBraid 2.0: A Comprehensive DNA Assembly Framework for Plant Synthetic Biology. Plant Physiology, 2013, 162, 1618-1631.	4.8	358
4	A cytochrome P450 regulates a domestication trait in cultivated tomato. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17125-17130.	7.1	257
5	Application of Genomic Tools in Plant Breeding. Current Genomics, 2012, 13, 179-195.	1.6	236
6	Genomic variation in tomato, from wild ancestors to contemporary breeding accessions. BMC Genomics, 2015, 16, 257.	2.8	190
7	Transcriptome characterization and high throughput SSRs and SNPs discovery in Cucurbita pepo (Cucurbitaceae). BMC Genomics, 2011, 12, 104.	2.8	177
8	Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. Nucleic Acids Research, 2019, 47, D1128-D1136.	14.5	177
9	Phenotype Correlation and Intergenerational Dynamics of the Friedreich Ataxia GAA Trinucleotide Repeat. American Journal of Human Genetics, 1997, 61, 101-110.	6.2	161
10	Variation Revealed by SNP Genotyping and Morphology Provides Insight into the Origin of the Tomato. PLoS ONE, 2012, 7, e48198.	2.5	161
11	<i>De novo</i> assembly of the zucchini genome reveals a whole-genome duplication associated with the origin of the <i>Cucurbita</i> genus. Plant Biotechnology Journal, 2018, 16, 1161-1171.	8.3	160
12	A consensus linkage map for molecular markers and Quantitative Trait Loci associated with economically important traits in melon ( <i>Cucumis melo</i> L.). BMC Plant Biology, 2011, 11, 111.	3.6	156
13	ABCC transporters mediate insect resistance to multiple Bt toxins revealed by bulk segregant analysis. BMC Biology, 2014, 12, 46.	3.8	144
14	A modular toolbox for gRNA-Cas9 genome engineering in plants based on the GoldenBraid standard. Plant Methods, 2016, 12, 10.	4.3	119
15	Bin mapping of genomic and EST-derived SSRs in melon ( <i>Cucumis melo</i> L.). Theoretical and Applied Genetics, 2008, 118, 139-150.	3.6	115
16	High-throughput SNP genotyping in Cucurbita pepo for map construction and quantitative trait loci mapping. BMC Genomics, 2012, 13, 80.	2.8	110
17	An SNP-based saturated genetic map and QTL analysis of fruit-related traits in Zucchini using Genotyping-by-sequencing. BMC Genomics, 2017, 18, 94.	2.8	93
18	A set of EST-SNPs for map saturation and cultivar identification in melon. BMC Plant Biology, 2009, 9, 90.	3.6	90

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19	MELOGEN: an EST database for melon functional genomics. BMC Genomics, 2007, 8, 306.	2.8	87
20	Transcriptome sequencing for SNP discovery across Cucumis melo. BMC Genomics, 2012, 13, 280.	2.8	86
21	SNP genotyping in melons: genetic variation, population structure, and linkage disequilibrium. Theoretical and Applied Genetics, 2013, 126, 1285-1303.	3.6	85
22	Taxonomy and genetic diversity of domesticated Capsicum species in the Andean region. Genetic Resources and Crop Evolution, 2012, 59, 1077-1088.	1.6	76
23	The transcriptome of Spodoptera exigua larvae exposed to different types of microbes. Insect Biochemistry and Molecular Biology, 2012, 42, 557-570.	2.7	70
24	GB3.0: a platform for plant bio-design that connects functional DNA elements with associated biological data. Nucleic Acids Research, 2017, 45, gkw1326.	14.5	70
25	Transcriptome analysis and molecular marker discovery in Solanum incanum and S. aethiopicum, two close relatives of the common eggplant (Solanum melongena) with interest for breeding. BMC Genomics, 2016, 17, 300.	2.8	63
26	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
27	Relationships, origin, and diversity of Galápagos tomatoes: implications for the conservation of natural populations. American Journal of Botany, 2004, 91, 86-99.	1.7	58
28	Analysis of the melon (Cucumis melo) small RNAome by high-throughput pyrosequencing. BMC Genomics, 2011, 12, 393.	2.8	58
29	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
30	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
31	Melon Transcriptome Characterization: Simple Sequence Repeats and Single Nucleotide Polymorphisms Discovery for High Throughput Genotyping across the Species. Plant Genome, 2011, 4, 118-131.	2.8	53
32	ngs_backbone: a pipeline for read cleaning, mapping and SNP calling using Next Generation Sequence. BMC Genomics, 2011, 12, 285.	2.8	53
33	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
34	Exploiting the diversity of tomato: the development of a phenotypically and genetically detailed germplasm collection. Horticulture Research, 2020, 7, 66.	6.3	49
35	Mutations in Myosin VIIA (MYO7A) and Usherin (USH2A) in Spanish patients with usher syndrome types I and II, respectively. Human Mutation, 2002, 20, 76-77.	2.5	47
36	Plant Genebanks: Present Situation and Proposals for Their Improvement. the Case of the Spanish Network. Frontiers in Plant Science, 2018, 9, 1794.	3.6	45

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37	Classification and phylogenetic relationships in <i>Solanum</i> section <i>Lycopersicon</i> based on AFLP and two nuclear gene sequences. <i>Genetic Resources and Crop Evolution</i> , 2009, 56, 663-678.	1.6	44
38	Genetic and bioclimatic variation in <i>Solanum pimpinellifolium</i> . <i>Genetic Resources and Crop Evolution</i> , 2009, 56, 39-51.	1.6	43
39	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
40	Transcriptomic analysis of tomato carpel development reveals alterations in ethylene and gibberellin synthesis during pat3/pat4 parthenocarpic fruit set. <i>BMC Plant Biology</i> , 2009, 9, 67.	3.6	40
41	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
42	dfh is a <i>Drosophila</i> homolog of the Friedreich's ataxia disease gene. <i>Gene</i> , 2000, 256, 35-42.	2.2	34
43	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
44	AFLP and DNA sequence variation in an Andean domesticate, pepino ( <i>Solanum muricatum</i> L.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1219-1229.	1.7	30
45	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
46	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
47	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
48	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
49	The Implications of AFLP Data for the Systematics of the Wild Species of <i>Solanum</i> Section <i>Basarthrum</i> . <i>Systematic Botany</i> , 2006, 31, 208-216.	0.5	14
50	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
51	Genetic Structure of <i>Lycopersicon pimpinellifolium</i> (Solanaceae) Populations Collected after the ENSO Event of 1997â€“1998. <i>Genetic Resources and Crop Evolution</i> , 2007, 54, 359-377.	1.6	12
52	European traditional tomatoes galore: a result of farmers' selection of a few diversity-rich loci. <i>Journal of Experimental Botany</i> , 2022, 73, 3431-3445.	4.8	11
53	Incipient GAA repeats in the primate Friedreich ataxia homologous genes. <i>Molecular Biology and Evolution</i> , 1999, 16, 880-883.	8.9	10
54	Analysis of gene expression during the fruit set of tomato: A comparative approach. <i>Plant Science</i> , 2007, 173, 609-620.	3.6	10

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55	THE SPANISH MELON GENOMICS INITIATIVE. Acta Horticulturae, 2007, , 47-54.	0.2	3
56	Analysis of the coding-complete genomic sequence of groundnut ringspot virus suggests a common ancestor with tomato chlorotic spot virus. Archives of Virology, 2016, 161, 2311-2316.	2.1	2
57	A Cost-effective Double-Stranded cDNA Synthesis for Plant Microarrays. Plant Molecular Biology Reporter, 2012, 30, 1276-1282.	1.8	1
58	B9â€¦unc-1/stomatin-like modulates aggregation of polyglutamines. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A12.1-A12.	1.9	0
59	Analysis of Pathogen Resistance and Fruit Quality Traits in Melon (Cucumis melo L.). , 2011, , 29-46.		0
60	STUDENTâ€™S APPROACH TO LEARNING PER STUDENT BASIS IN TWO SUBJECTS OF BIOTECHNOLOGY DEGREE. EDULEARN Proceedings, 2022, , .	0.0	0