Rafael Lozano

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/219064/publications.pdf

Version: 2024-02-01

82	2,842	126708 33	197535 49
papers	citations	h-index	g-index

84	84	84	2982
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	FALSIFLORA, the tomato orthologue of FLORICAULA and LEAFY, controls flowering time and floral meristem identity. Plant Journal, 1999, 20, 685-693.	2.8	251
2	Tomato Flower Abnormalities Induced by Low Temperatures Are Associated with Changes of Expression of MADS-Box Genes1. Plant Physiology, 1998, 117, 91-100.	2.3	108
3	<i>ENO</i>regulates tomato fruit size through the floral meristem development network. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 8187-8195.	3.3	108
4	Functional Analysis of the Arlequin Mutant Corroborates the Essential Role of the ARLEQUIN/TAGL1 Gene during Reproductive Development of Tomato. PLoS ONE, 2010, 5, e14427.	1.1	108
5	SINGLE FLOWER TRUSS regulates the transition and maintenance of flowering in tomato. Planta, 2004, 218, 427-434.	1.6	104
6	The Evolution of Reproductive Systems and Sex-Determining Mechanisms Within Rumex (Polygonaceae) Inferred from Nuclear and Chloroplastidial Sequence Data. Molecular Biology and Evolution, 2005, 22, 1929-1939.	3.5	99
7	Genetic relationships among melon breeding lines revealed by RAPD markers and agronomic traits. Theoretical and Applied Genetics, 1998, 96, 878-885.	1.8	92
8	Wide-genome QTL mapping of fruit quality traits in a tomato RIL population derived from the wild-relative species Solanum pimpinellifolium L.. Theoretical and Applied Genetics, 2015, 128, 2019-2035.	1.8	63
9	Transcriptional Activity of the MADS Box <i>ARLEQUIN</i>/<i>TOMATO AGAMOUS-LIKE1</i> Gene Is Required for Cuticle Development of Tomato Fruit. Plant Physiology, 2015, 168, 1036-1048.	2.3	62
10	The tomato mutant <i>ars1</i> (<i>altered response to salt stress 1</i>) identifies an R1â€•type <scp>MYB</scp> transcription factor involved in stomatal closure under salt acclimation. Plant Biotechnology Journal, 2016, 14, 1345-1356.	4.1	58
11	Reduced Rates of Sequence Evolution of Y-Linked Satellite DNA in Rumex (Polygonaceae). Journal of Molecular Evolution, 2005, 60, 391-399.	0.8	55
12	Transcriptional and hormonal regulation of petal and stamen development by STAMENLESS, the tomato (Solanum lycopersicum L.) orthologue to the B-class APETALA3 gene. Journal of Experimental Botany, 2014, 65, 2243-2256.	2.4	55
13	Genetic mapping of two QTL from the wild tomato Solanum pimpinellifolium L. controlling resistance against two-spotted spider mite (Tetranychus urticae Koch). Theoretical and Applied Genetics, 2013, 126, 83-92.	1.8	54
14	TOMATO AGAMOUS1 and ARLEQUIN/TOMATO AGAMOUS-LIKE1 MADS-box genes have redundant and divergent functions required for tomato reproductive development. Plant Molecular Biology, 2016, 91, 513-531.	2.0	54
15	Cloning and characterization of a fish centromeric satellite DNA. Cytogenetic and Genome Research, 1994, 65, 233-237.	0.6	49
16	Genetic analysis of reproductive development in tomato. International Journal of Developmental Biology, 2009, 53, 1635-1648.	0.3	48
17	Multi-environment QTL mapping reveals genetic architecture of fruit cracking in a tomato RIL Solanum lycopersicumÂÃ—ÂS. pimpinellifolium population. Theoretical and Applied Genetics, 2017, 130, 213-222.	1.8	48
18	Evolution of Centromeric Satellite DNA and Its Use in Phylogenetic Studies of the Sparidae Family (Pisces, Perciformes). Molecular Phylogenetics and Evolution, 1999, 12, 200-204.	1.2	47

#	ARTICLE	IF	CITATIONS
19	Characterization of the potato MADS-box gene STMADS16 and expression analysis in tobacco transgenic plants. Plant Molecular Biology, 2000, 42, 499-513.	2.0	47
20	The <i>Eco</i>RI centromeric satellite DNA of the Sparidae family (Pisces, Perciformes) contains a sequence motive common to other vertebrate centromeric satellite DNAs. Cytogenetic and Genome Research, 1995, 71, 345-351.	0.6	46
21	Genetic linkage map of melon (Cucumis melo L.) and localization of a major QTL for powdery mildew resistance. Molecular Breeding, 2011, 27, 181-192.	1.0	46
22	Characterization of vegetative inflorescence (mc-vin) mutant provides new insight into the role of MACROCALYX in regulating inflorescence development of tomato. Scientific Reports, 2016, 6, 18796.	1.6	45
23	The SlCBL10 Calcineurin B-Like Protein Ensures Plant Growth under Salt Stress by Regulating Na⁺ and Ca²⁺ Homeostasis. Plant Physiology, 2018, 176, 1676-1693.	2.3	45
24	Uncovering the genetic architecture of Colletotrichum lindemuthianum resistance through QTL mapping and epistatic interaction analysis in common bean. Frontiers in Plant Science, 2015, 6, 141.	1.7	44
25	The parthenocarpic <i>hydra</i> mutant reveals a new function for a <i>SPOROCYTELESS</i>â€•like gene in the control of fruit set in tomato. New Phytologist, 2017, 214, 1198-1212.	3.5	44
26	Parallel origins of photoperiod adaptation following dual domestications of common bean. Journal of Experimental Botany, 2019, 70, 1209-1219.	2.4	44
27	Stamenless , a tomato mutant with homeotic conversions in petals and stamens. Planta, 1999, 209, 172-179.	1.6	40
28	Chronic dietary exposure to chlorpyrifos causes behavioral impairments, low activity of brain membrane-bound acetylcholinesterase, and increased brain acetylcholinesterase-R mRNA. Toxicology, 2013, 308, 41-49.	2.0	39
29	Major Contribution of Flowering Time and Vegetative Growth to Plant Production in Common Bean As Deduced from a Comparative Genetic Mapping. Frontiers in Plant Science, 2016, 7, 1940.	1.7	38
30	Chlorpyrifos-, Diisopropylphosphorofluoridate-, and Parathion-Induced Behavioral and Oxidative Stress Effects: Are They Mediated by Analogous Mechanisms of Action?. Toxicological Sciences, 2013, 131, 206-216.	1.4	37
31	Chromosomal structure of populations of Scilla autumnalis in the Iberian Peninsula. Heredity, 1991, 67, 287-297.	1.2	36
32	Quantitative genetic analysis of flowering time in tomato. Genome, 2007, 50, 303-315.	0.9	36
33	Codominant PCR-based markers and candidate genes for powdery mildew resistance in melon (Cucumis) Tj ETQq1 1 0.784314 rgBT /Ov	1.8	36
34	Comparative study on short- and long-term behavioral consequences of organophosphate exposure: Relationship to AChE mRNA expression. NeuroToxicology, 2014, 40, 57-64.	1.4	35
35	Cloning and characterization of dispersed repetitive DNA derived from microdissected sex chromosomes of Rumex acetosa. Genome, 2006, 49, 114-121.	0.9	34
36	An insertional mutagenesis programme with an enhancer trap for the identification and tagging of genes involved in abiotic stress tolerance in the tomato wild-related species Solanum pennellii. Plant Cell Reports, 2011, 30, 1865-1879.	2.8	34

#	ARTICLE	IF	CITATIONS
37	The tomato <i>res</i> mutant which accumulates <scp>JA</scp> in roots in nonâ€stressed conditions restores cell structure alterations under salinity. Physiologia Plantarum, 2015, 155, 296-314.	2.6	33
38	A collection of enhancer trap insertional mutants for functional genomics in tomato. Plant Biotechnology Journal, 2017, 15, 1439-1452.	4.1	33
39	Ecology, genetic diversity and phylogeography of the Iberian endemic plant Jurinea pinnata (Lag.) DC. (Compositae) on two special edaphic substrates: dolomite and gypsum. Plant and Soil, 2014, 374, 233-250.	1.8	32
40	Albino T-DNA tomato mutant reveals a key function of 1-deoxy-D-xylulose-5-phosphate synthase (DXS1) in plant development and survival. Scientific Reports, 2017, 7, 45333.	1.6	29
41	Genetic variation underlying pod size and color traits of common bean depends on quantitative trait loci with epistatic effects. Molecular Breeding, 2014, 33, 939-952.	1.0	27
42	Development and mapping of a codominant SCAR marker linked to the andromonoecious gene of melon. Theoretical and Applied Genetics, 2005, 110, 714-720.	1.8	26
43	A Method for Increasing the Number of Mitoses Available for Cytogenetic Analysis in Rainbow Trout. Biotechnic & Histochemistry, 1988, 63, 335-338.	0.4	23
44	An analysis of coho salmon chromatin by means of C-banding, AG- and fluorochrome staining, and in situ digestion with restriction endonucleases. Heredity, 1991, 66, 403-409.	1.2	23
45	Phylogenetic Relationships of the Sparidae Family (Pisces, Perciformes) Inferred from Satellite-DNA. Hereditas, 2004, 122, 1-6.	0.5	23
46	Marker-based linkage map of Andean common bean (Phaseolus vulgaris L.) and mapping of QTLs underlying popping ability traits. BMC Plant Biology, 2012, 12, 136.	1.6	23
47	Genetic and Physiological Characterization of the Arlequin Insertional Mutant Reveals a Key Regulator of Reproductive Development in Tomato. Plant and Cell Physiology, 2010, 51, 435-447.	1.5	22
48	Expression of Arabidopsis APETALA1 in tomato reduces its vegetative cycle without affecting plant production. Molecular Breeding, 2004, 13, 155-163.	1.0	21
49	Developmental role of the tomato Mediator complex subunit <scp>MED</scp>18 in pollen ontogeny. Plant Journal, 2018, 96, 300-315.	2.8	21
50	QTL mapping of fruit mineral contents provides new chances for molecular breeding of tomato nutritional traits. Theoretical and Applied Genetics, 2017, 130, 903-913.	1.8	20
51	rDNA site number polymorphism and NOR inactivation in natural populations ofAllium schoenoprasum. Genetica, 1994, 94, 67-71.	0.5	18
52	Cytogenetic analysis of gilthead seabream <i>Sparus aurata</i> (Pisces, Perciformes), a deletion affecting the NOR in a hatchery stock. Cytogenetic and Genome Research, 1995, 68, 3-7.	0.6	18
53	The Ca2+ Sensor Calcineurin Bâ€"Like Protein 10 in Plants: Emerging New Crucial Roles for Plant Abiotic Stress Tolerance. Frontiers in Plant Science, 2020, 11, 599944.	1.7	18
54	Induction of triploidy in offspring of gilthead seabream (Sparus aurata) by means of heat shock. Journal of Applied Ichthyology, 1996, 12, 53-55.	0.3	16

#	ARTICLE	IF	CITATIONS
55	Genetic analysis of single-locus and epistatic QTLs for seed traits in an adapted Ã— nuÃ±a RIL population of common bean (Phaseolus vulgaris L.). Theoretical and Applied Genetics, 2014, 127, 897-912.	1.8	15
56	The <i>res</i> (<i>restored cell structure by salinity</i>) tomato mutant reveals the role of the <scp>DEAD</scp>â€box <scp>RNA</scp> helicase <scp>SlDEAD39</scp> in plant development and salt response. Plant, Cell and Environment, 2020, 43, 1722-1739.	2.8	15
57	Identification of key genes involved in the phenotypic alterations of res (restored cell structure by) Tj ETQq1 1 0.784314 rgBT /Overlock Plant Biology, 2018, 18, 213.	1.6	14
58	Characterization of QTL and Environmental Interactions Controlling Flowering Time in Andean Common Bean (Phaseolus vulgaris L.). Frontiers in Plant Science, 2020, 11, 599462.	1.7	13
59	Characterization of the chromatin of some liliaceous species after digestion with restriction endonucleases and sequential Giemsa, fluorochrome and silver staining. Heredity, 1990, 64, 185-195.	1.2	12
60	Asphodelus tenuifolius andA. fistulosus (Liliaceae) are morphologically, genetically, and biologically different species. Plant Systematics and Evolution, 1990, 169, 1-12.	0.3	12
61	Genetic Mapping and QTL Analysis in Common Bean. Compendium of Plant Genomes, 2017, , 69-107.	0.3	12
62	Impact of novel SNPs identified in Cynara cardunculus genes on functionality of proteins regulating phenylpropanoid pathway and their association with biological activities. BMC Genomics, 2017, 18, 183.	1.2	11
63	Tomato <i>CRABS CLAW</i> paralogues interact with chromatin remodelling factors to mediate carpel development and floral determinacy. New Phytologist, 2022, 234, 1059-1074.	3.5	11
64	Mutation at the tomato EXCESSIVE NUMBER OF FLORAL ORGANS (ENO) locus impairs floral meristem development, thus promoting an increased number of floral organs and fruit size. Plant Science, 2015, 232, 41-48.	1.7	10
65	Phenotypic and genetic characterization of tomato mutants provides new insights into leaf development and its relationship to agronomic traits. BMC Plant Biology, 2019, 19, 141.	1.6	10
66	The Salt Sensitivity Induced by Disruption of Cell Wall-Associated Kinase 1 (SlWAK1) Tomato Gene Is Linked to Altered Osmotic and Metabolic Homeostasis. International Journal of Molecular Sciences, 2020, 21, 6308.	1.8	10
67	Exploring the quantitative resistance to Pseudomonas syringae pv. phaseolicola in common bean (Phaseolus vulgaris L.). Molecular Breeding, 2016, 36, 1.	1.0	9
68	In situ digestion of satellite DNA of Scilla siberica. Chromosoma, 1991, 100, 439-442.	1.0	7
69	A cytogenetical and molecular analysis of the ribosomal cistrons of Allium sphaerocephalon L. (Liliaceae). Heredity, 1992, 69, 43-49.	1.2	7
70	Effective Mapping by Sequencing to Isolate Causal Mutations in the Tomato Genome. Methods in Molecular Biology, 2021, 2264, 89-103.	0.4	7
71	A Factor Linking Floral Organ Identity and Growth Revealed by Characterization of the Tomato Mutant unfinished flower development (ufd). Frontiers in Plant Science, 2016, 7, 1648.	1.7	6
72	Alq mutation increases fruit set rate and allows the maintenance of fruit yield under moderate saline conditions. Journal of Experimental Botany, 2019, 70, 5731-5744.	2.4	6

#	ARTICLE	IF	CITATIONS
73	The phenotype alterations showed by the <i>res</i> tomato mutant disappear when the plants are grown under semi-arid conditions: Is the <i>res</i> mutant tolerant to multiple stresses?. Plant Signaling and Behavior, 2017, 12, e1146847.	1.2	5
74	Haplotype analysis of the germacrene A synthase gene and association with cynaropicrin content and biological activities in Cynara cardunculus. Molecular Genetics and Genomics, 2018, 293, 417-433.	1.0	5
75	Dissecting the genetic basis of popping ability in nuÃ±a bean, an ancient cultivar of common bean. Euphytica, 2014, 196, 349-363.	0.6	4
76	Transcriptional Dynamics and Candidate Genes Involved in Pod Maturation of Common Bean (Phaseolus vulgaris L.). Plants, 2020, 9, 545.	1.6	4
77	Functional characterization of the tomato <i>HAIRPLUS</i> gene reveals the implication of the epigenome in the control of glandular trichome formation. Horticulture Research, 2022, 9, .	2.9	4
78	A segregating population from a tomato second cycle hybrid allows the identification of novel QTL for fruit quality traits. Euphytica, 2021, 217, 1.	0.6	3
79	Genetic interactions of the unfinished flower development (ufd) mutant support a significant role of the tomato UFD gene in regulating floral organogenesis. Plant Reproduction, 2016, 29, 227-238.	1.3	2
80	Approaching the genetic dissection of indirect adventitious organogenesis process in tomato explants. Plant Science, 2021, 302, 110721.	1.7	2
81	Genotyping selection for resistance against tomato yellow leaf curl virus (TYLCV) conferred by Ty-1 and Ty-3 genes in tomato. Molecular Breeding, 2012, 30, 1131-1142.	1.0	1
82	The Tomato SlVIPP1 Gene Is Required for Plant Survival Through the Proper Development of Chloroplast Thylakoid Membrane. Frontiers in Plant Science, 2020, 11, 1305.	1.7	1