Jesus Vicente-Carbajosa

List of Publications by Year
in descending order

48	6,039	136740	205818
papers	citations	32 h-index	48 g-index

48	48	48	6380
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The targeted overexpression of SlCDF4 in the fruit enhances tomato size and yield involving gibberellin signalling. Scientific Reports, 2020, 10, 10645.	1.6	14
2	The Arabidopsis Transcription Factor CDF3 Is Involved in Nitrogen Responses and Improves Nitrogen Use Efficiency in Tomato. Frontiers in Plant Science, 2020, 11, 601558.	1.7	18
3	CDF transcription factors: plant regulators to deal with extreme environmental conditions. Journal of Experimental Botany, 2020, 71, 3803-3815.	2.4	29
4	Harnessing symbiotic plantâ€“fungus interactions to unleash hidden forces from extreme plant ecosystems. Journal of Experimental Botany, 2020, 71, 3865-3877.	2.4	17
5	A Possible Role of the Aleurone Expressed Gene HvMAN1 in the Hydrolysis of the Cell Wall Mannans of the Starchy Endosperm in Germinating Hordeum vulgare L. Seeds. Frontiers in Plant Science, 2019, 10, 1706.	1.7	9
6	WRKY7, -11 and -17 transcription factors are modulators of the bZIP28 branch of the unfolded protein response during PAMP-triggered immunity in Arabidopsis thaliana. Plant Science, 2018, 277, 242-250.	1.7	20
7	Identification of Two Auxin-Regulated Potassium Transporters Involved in Seed Maturation. International Journal of Molecular Sciences, 2018, 19, 2132.	1.8	21
8	When Transcriptomics and Metabolomics Work Hand in Hand: A Case Study Characterizing Plant CDF Transcription Factors. High-Throughput, 2018, 7, 7.	4.4	4
9	The AFL subfamily of B3 transcription factors: evolution and function in angiosperm seeds. Journal of Experimental Botany, 2017, 68, erw458.	2.4	57
10	Multifaceted role of cycling DOF factor 3 (CDF3) in the regulation of flowering time and abiotic stress responses in Arabidopsis. Plant, Cell and Environment, 2017, 40, 748-764.	2.8	110
11	An active Mitochondrial Complex II Present in Mature Seeds Contains an Embryo-Specific Ironâ€“Sulfur Subunit Regulated by ABA and bZIP53 and Is Involved in Germination and Seedling Establishment. Frontiers in Plant Science, 2017, 8, 277.	1.7	37
12	Ectopic Expression of CDF3 Genes in Tomato Enhances Biomass Production and Yield under Salinity Stress Conditions. Frontiers in Plant Science, 2017, 8, 660.	1.7	45
13	Identification of Novel Components of the Unfolded Protein Response in Arabidopsis. Frontiers in Plant Science, 2016, 7, 650.	1.7	18
14	A Developmental Switch of Gene Expression in the Barley Seed Mediated by HvVP1 (Viviparous-1) and HvGAMYB Interactions. Plant Physiology, 2016, 170, 2146-2158.	2.3	38
15	Transcriptional Control of Glutaredoxin GRXC9 Expression by a Salicylic Acid-Dependent and NPR1-Independent Pathway in Arabidopsis. Plant Molecular Biology Reporter, 2015, 33, 624-637.	1.0	76
16	Crosstalk between Two bZIP Signaling Pathways Orchestrates Salt-Induced Metabolic Reprogramming in Arabidopsis Roots. Plant Cell, 2015, 27, 2244-2260.	3.1	115
17	SnRK1-triggered switch of bZIP63 dimerization mediates the low-energy response in plants. ELife, 2015, 4, .	2.8	184
18	The <scp>TRANSPLANTA</scp> collection of <scp>A</scp>rabidopsis lines: a resource for functional analysis of transcription factors based on their conditional overexpression. Plant Journal, 2014, 77, 944-953.	2.8	104

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19	Characterization of tomato Cycling Dof Factors reveals conserved and new functions in the control of flowering time and abiotic stress responses. Journal of Experimental Botany, 2014, 65, 995-1012.	2.4	161
20	Parenclitic networks: uncovering new functions in biological data. Scientific Reports, 2014, 4, 5112.	1.6	19
21	Salinity Assay in Arabidopsis. Bio-protocol, 2014, 4, .	0.2	9
22	YUCCA8andYUCCA9overexpression reveals a link between auxin signaling and lignification through the induction of ethylene biosynthesis. Plant Signaling and Behavior, 2013, 8, e26363.	1.2	33
23	The role of phosphorylatable serine residues in the DNA-binding domain of Arabidopsis bZIP transcription factors. European Journal of Cell Biology, 2010, 89, 175-183.	1.6	42
24	A Nuclear Gene Encoding the Iron-Sulfur Subunit of Mitochondrial Complex II Is Regulated by B3 Domain Transcription Factors during Seed Development in Arabidopsis Â Â. Plant Physiology, 2009, 150, 84-95.	2.3	51
25	A Pivotal Role of the Basic Leucine Zipper Transcription Factor bZIP53 in the Regulation ofArabidopsisSeed Maturation Gene Expression Based on Heterodimerization and Protein Complex Formation. Plant Cell, 2009, 21, 1747-1761.	3.1	196
26	Expression patterns within the Arabidopsis C/S1 bZIP transcription factor network: availability of heterodimerization partners controls gene expression during stress response and development. Plant Molecular Biology, 2009, 69, 107-119.	2.0	139
27	FUSCA3 from barley unveils a common transcriptional regulation of seedâ€specific genes between cereals and Arabidopsis. Plant Journal, 2008, 53, 882-894.	2.8	60
28	The maize Dof protein PBF activates transcription of Î³-zein during maize seed development. Plant Molecular Biology, 2008, 67, 441-454.	2.0	63
29	DNA-free RNA isolation protocols for Arabidopsis thaliana, including seeds and siliques. BMC Research Notes, 2008, 1, 93.	0.6	374
30	The family of DOF transcription factors: from green unicellular algae to vascular plants. Molecular Genetics and Genomics, 2007, 277, 379-390.	1.0	140
31	Two-hybrid protein-protein interaction analysis in Arabidopsis protoplasts: establishment of a heterodimerization map of group C and group S bZIP transcription factors. Plant Journal, 2006, 46, 890-900.	2.8	200
32	Combinatorial control of Arabidopsis proline dehydrogenase transcription by specific heterodimerisation of bZIP transcription factors. EMBO Journal, 2006, 25, 3133-3143.	3.5	184
33	Seed maturation: developing an intrusive phase to accomplish a quiescent state. International Journal of Developmental Biology, 2005, 49, 645-651.	0.3	173
34	Genome-wide comparative phylogenetic analysis of the rice and Arabidopsis Dof gene families. BMC Evolutionary Biology, 2003, 3, 17.	3.2	295
35	Synergistic Activation of Seed Storage Protein Gene Expression in Arabidopsis by ABI3 and Two bZIPs Related to OPAQUE2. Journal of Biological Chemistry, 2003, 278, 21003-21011.	1.6	154
36	bZIP transcription factors in Arabidopsis. Trends in Plant Science, 2002, 7, 106-111.	4.3	1,585

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37	The GAMYB protein from barley interacts with the DOF transcription factor BPBF and activates endosperm-specific genes during seed development. Plant Journal, 2002, 29, 453-464.	2.8	208
38	A constitutive cystatin-encoding gene from barley (Icy) responds differentially to abiotic stimuli. Plant Molecular Biology, 2001, 45, 599-608.	2.0	91
39	Barley BLZ2, a Seed-specific bZIP Protein That Interacts with BLZ1 in Vivo and Activates Transcription from the GCN4-like motif of B-hordein Promoters in Barley Endosperm. Journal of Biological Chemistry, 1999, 274, 9175-9182.	1.6	113
40	Barley BLZ1: a bZIP transcriptional activator that interacts with endospermâ€specific gene promoters. Plant Journal, 1998, 13, 629-640.	2.8	87
41	An endosperm-specific DOF protein from barley, highly conserved in wheat, binds to and activates transcription from the prolamin-box of a native B-hordein promoter in barley endosperm. Plant Journal, 1998, 16, 53-62.	2.8	207
42	A maize zinc-finger protein binds the prolamin box in zein gene promoters and interacts with the basic leucine zipper transcriptional activator Opaque2. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 7685-7690.	3.3	383
43	Differential expression of two barley SNF1-related protein kinase genes. Plant Molecular Biology, 1995, 27, 1235-1240.	2.0	44
44	Sucrose synthase genes in barley. FEBS Letters, 1993, 320, 177-181.	1.3	29
45	Homologous sucrose synthase genes in barley (Hordeum vulgare) are located in chromosomes 7H		