

# JosÃ© M Franco-Zorrilla

## List of Publications by Year in descending order

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61  
papers

8,847  
citations

71102

41  
h-index

123424

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64  
all docs

64  
docs citations

64  
times ranked

10780  
citing authors

#	ARTICLE	IF	CITATIONS
1	Target mimicry provides a new mechanism for regulation of microRNA activity. <i>Nature Genetics</i> , 2007, 39, 1033-1037.	21.4	1,845
2	The <i>Arabidopsis</i> bHLH Transcription Factors MYC3 and MYC4 Are Targets of JAZ Repressors and Act Additively with MYC2 in the Activation of Jasmonate Responses. <i>Plant Cell</i> , 2011, 23, 701-715.	6.6	906
3	DNA-binding specificities of plant transcription factors and their potential to define target genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2367-2372.	7.1	585
4	Phytochrome interacting factors 4 and 5 control seedling growth in changing light conditions by directly controlling auxin signaling. <i>Plant Journal</i> , 2012, 71, 699-711.	5.7	498
5	SPX1 is a phosphate-dependent inhibitor of PHOSPHATE STARVATION RESPONSE 1 in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14947-14952.	7.1	372
6	Structural Basis for DNA Binding Specificity by the Auxin-Dependent ARF Transcription Factors. <i>Cell</i> , 2014, 156, 577-589.	28.9	348
7	A Mutant of the <i>Arabidopsis</i> Phosphate Transporter PHT1;1 Displays Enhanced Arsenic Accumulation. <i>Plant Cell</i> , 2007, 19, 1123-1133.	6.6	295
8	Interaction between Phosphate-Starvation, Sugar, and Cytokinin Signaling in <i>Arabidopsis</i> and the Roles of Cytokinin Receptors CRE1/AHK4 and AHK3. <i>Plant Physiology</i> , 2005, 138, 847-857.	4.8	261
9	The transcriptional control of plant responses to phosphate limitation. <i>Journal of Experimental Botany</i> , 2004, 55, 285-293.	4.8	232
10	Abscisic acid signaling is controlled by a <i>BRANCHED1/HD-ZIP I</i> cascade in <i>Arabidopsis</i> axillary buds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E245-E254.	7.1	211
11	Ligand-receptor co-evolution shaped the jasmonate pathway in land plants. <i>Nature Chemical Biology</i> , 2018, 14, 480-488.	8.0	194
12	Mutations at CRE1 impair cytokinin-induced repression of phosphate starvation responses in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2002, 32, 353-360.	5.7	165
13	Cytokinin induces genome-wide binding of the type-B response regulator ARR10 to regulate growth and development in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5995-E6004.	7.1	154
14	The bHLH Transcription Factors TSAR1 and TSAR2 Regulate Triterpene Saponin Biosynthesis in <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2016, 170, 194-210.	4.8	152
15	PIF4-induced BR synthesis is critical to diurnal and thermomorphogenic growth. <i>EMBO Journal</i> , 2018, 37, .	7.8	127
16	Improved protein-binding microarrays for the identification of DNA-binding specificities of transcription factors. <i>Plant Journal</i> , 2011, 66, 700-711.	5.7	117
17	A Single JAZ Repressor Controls the Jasmonate Pathway in <i>Marchantia polymorpha</i> . <i>Molecular Plant</i> , 2019, 12, 185-198.	8.3	107
18	A MYB/ZML Complex Regulates Wound-Induced Lignin Genes in Maize. <i>Plant Cell</i> , 2015, 27, 3245-3259.	6.6	104

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19	bHLH003, bHLH013 and bHLH017 Are New Targets of JAZ Repressors Negatively Regulating JA Responses. <i>PLoS ONE</i> , 2014, 9, e86182.	2.5	104
20	The cytokinin response factors modulate root and shoot growth and promote leaf senescence in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2016, 85, 134-147.	5.7	101
21	Molecular mechanisms of Evening Complex activity in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6901-6909.	7.1	101
22	An R2R3-MYB Transcription Factor Regulates Eugenol Production in Ripe Strawberry Fruit Receptacles. <i>Plant Physiology</i> , 2015, 168, 598-614.	4.8	98
23	Catastrophic Unbalanced Genome Rearrangements Cause Somatic Loss of Berry Color in Grapevine. <i>Plant Physiology</i> , 2017, 175, 786-801.	4.8	98
24	FILAMENTOUS FLOWER Is a Direct Target of JAZ3 and Modulates Responses to Jasmonate. <i>Plant Cell</i> , 2015, 27, 3160-3174.	6.6	93
25	Potato StCONSTANS-like1 Suppresses Storage Organ Formation by Directly Activating the FT-like StSP5G Repressor. <i>Current Biology</i> , 2016, 26, 872-881.	3.9	93
26	A Recently Evolved Alternative Splice Site in the BRANCHED1a Gene Controls Potato Plant Architecture. <i>Current Biology</i> , 2015, 25, 1799-1809.	3.9	91
27	The <i>Solanum lycopersicum</i> WRKY3 Transcription Factor SlWRKY3 Is Involved in Salt Stress Tolerance in Tomato. <i>Frontiers in Plant Science</i> , 2017, 8, 1343.	3.6	89
28	Coordination of Chloroplast Development through the Action of the GNC and GLK Transcription Factor Families. <i>Plant Physiology</i> , 2018, 178, 130-147.	4.8	85
29	Jasmonate-Related MYC Transcription Factors Are Functionally Conserved in <i>Marchantia polymorpha</i> . <i>Plant Cell</i> , 2019, 31, 2491-2509.	6.6	73
30	early bolting in short days: An <i>Arabidopsis</i> Mutation That Causes Early Flowering and Partially Suppresses the Floral Phenotype of leafy. <i>Plant Cell</i> , 2001, 13, 1011-1024.	6.6	71
31	An Ancient CO11-Independent Function for Reactive Electrophilic Oxylipins in Thermotolerance. <i>Current Biology</i> , 2020, 30, 962-971.e3.	3.9	68
32	CUL3 <sup>BPM</sup> E3 ubiquitin ligases regulate MYC2, MYC3, and MYC4 stability and JA responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6205-6215.	7.1	67
33	PIF transcription factors link a neighbor threat cue to accelerated reproduction in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2019, 10, 4005.	12.8	65
34	The transcription factor bZIP14 regulates the TCA cycle in the diatom <i>Phaeodactylum tricornutum</i> . <i>EMBO Journal</i> , 2017, 36, 1559-1576.	7.8	64
35	Potato CYCLING DOF FACTOR1 and its lncRNA counterpart <i>StFLORE</i> link tuber development and drought response. <i>Plant Journal</i> , 2021, 105, 855-869.	5.7	64
36	<i>Arabidopsis</i> SWC4 Binds DNA and Recruits the SWR1 Complex to Modulate Histone H2A.Z Deposition at Key Regulatory Genes. <i>Molecular Plant</i> , 2018, 11, 815-832.	8.3	60

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37	ceRNAs: miRNA Target Mimic Mimics. <i>Cell</i> , 2011, 147, 1431-1432.	28.9	54
38	The <i>Solanum lycopersicum</i> Zinc Finger2 Cysteine-2/Histidine-2 Repressor-Like Transcription Factor Regulates Development and Tolerance to Salinity in Tomato and Arabidopsis. <i>Plant Physiology</i> , 2014, 164, 1967-1990.	4.8	54
39	Transcription factor DUO1 generated by neo-functionalization is associated with evolution of sperm differentiation in plants. <i>Nature Communications</i> , 2018, 9, 5283.	12.8	54
40	Deciphering the molecular mechanisms underpinning the transcriptional control of gene expression by L-AFL proteins in Arabidopsis seed. <i>Plant Physiology</i> , 2016, 171, pp.00034.2016.	4.8	53
41	<i>AtREM1</i> , a Member of a New Family of B3 Domain-Containing Genes, Is Preferentially Expressed in Reproductive Meristems. <i>Plant Physiology</i> , 2002, 128, 418-427.	4.8	52
42	The JA pathway MYC transcription factors regulate photomorphogenic responses by targeting HY5 gene expression. <i>Plant Journal</i> , 2020, 102, 138-152.	5.7	47
43	The fruit-specific transcription factor FaDOF2 regulates the production of eugenol in ripe fruit receptacles. <i>Journal of Experimental Botany</i> , 2017, 68, 4529-4543.	4.8	46
44	The Myb-domain protein ULTRAPETALA1 INTERACTING FACTOR 1 controls floral meristem activities in Arabidopsis. <i>Development (Cambridge)</i> , 2016, 143, 1108-19.	2.5	45
45	Interallelic complementation at the Arabidopsis CRE1 locus uncovers independent pathways for the proliferation of vascular initials and canonical cytokinin signalling. <i>Plant Journal</i> , 2004, 38, 70-79.	5.7	38
46	Characterization of the cytokinin-responsive transcriptome in rice. <i>BMC Plant Biology</i> , 2016, 16, 260.	3.6	38
47	Identification of plant transcription factor target sequences. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 21-30.	1.9	36
48	Target Validation of Plant microRNAs. <i>Methods in Molecular Biology</i> , 2011, 732, 187-208.	0.9	25
49	Autoregulation of RCO by Low-Affinity Binding Modulates Cytokinin Action and Shapes Leaf Diversity. <i>Current Biology</i> , 2019, 29, 4183-4192.e6.	3.9	21
50	Genome-wide identification of small RNA targets based on target enrichment and microarray hybridizations. <i>Plant Journal</i> , 2009, 59, 840-850.	5.7	18
51	DNA features beyond the transcription factor binding site specify target recognition by plant MYC2-related bHLH proteins. <i>Plant Communications</i> , 2021, 2, 100232.	7.7	18
52	Identification of genes specifically expressed in cauliflower reproductive meristems. Molecular characterization of BoREM1. <i>Plant Molecular Biology</i> , 1999, 39, 427-436.	3.9	16
53	A non-DNA binding activity for the ATHB4 transcription factor in the control of vegetation proximity. <i>New Phytologist</i> , 2017, 216, 798-813.	7.3	14
54	PthA4 <sup>AT</sup> , a 7.5 repeats transcription activator-like (TAL) effector from <i>Xanthomonas citri</i> ssp. <i>citri</i> , triggers citrus canker resistance. <i>Molecular Plant Pathology</i> , 2019, 20, 1394-1407.	4.2	13

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55	An evolutionarily ancient fatty acid desaturase is required for the synthesis of hexadecatrienoic acid, which is the main source of the bioactive jasmonate in <i>Marchantia polymorpha</i> . <i>New Phytologist</i> , 2022, 233, 1401-1413.	7.3	12
56	The MYB transcription factor Emission of Methyl Anthranilate 1 stimulates emission of methyl anthranilate from <i>Medicago truncatula</i> hairy roots. <i>Plant Journal</i> , 2019, 99, 637-654.	5.7	10
57	High-Throughput Analysis of Protein-DNA Binding Affinity. <i>Methods in Molecular Biology</i> , 2014, 1062, 697-709.	0.9	7
58	Screening of Protein-Protein and Protein-DNA Interactions Using Microarrays. <i>Advances in Protein Chemistry and Structural Biology</i> , 2014, 95, 231-281.	2.3	6
59	TDTHub, a web server tool for the analysis of transcription factor binding sites in plants. <i>Plant Journal</i> , 2022, 111, 1203-1215.	5.7	5
60	Basal differences in the transcriptional profiles of tomato leaves associated with the presence/absence of the resistance gene Mi-1 and changes in these differences after infestation by the whitefly <i>Bemisia tabaci</i> . <i>Bulletin of Entomological Research</i> , 2020, 110, 463-479.	1.0	1
61	DAP-Seq Identification of Transcription Factor-Binding Sites in Potato. <i>Methods in Molecular Biology</i> , 2021, 2354, 123-142.	0.9	1