

# Francois Parcy

## List of Publications by Year in descending order

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69  
papers

14,541  
citations

53794

45  
h-index

88630

70  
g-index

121  
all docs

121  
docs citations

121  
times ranked

22258  
citing authors

#	ARTICLE	IF	CITATIONS
1	bZIP transcription factors in Arabidopsis. Trends in Plant Science, 2002, 7, 106-111.	8.8	1,585
2	JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. Nucleic Acids Research, 2018, 46, D260-D266.	14.5	1,232
3	JASPAR 2020: update of the open-access database of transcription factor binding profiles. Nucleic Acids Research, 2020, 48, D87-D92.	14.5	1,039
4	JASPAR 2016: a major expansion and update of the open-access database of transcription factor binding profiles. Nucleic Acids Research, 2016, 44, D110-D115.	14.5	968
5	JASPAR 2014: an extensively expanded and updated open-access database of transcription factor binding profiles. Nucleic Acids Research, 2014, 42, D142-D147.	14.5	915
6	JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles. Nucleic Acids Research, 2022, 50, D165-D173.	14.5	902
7	A Molecular Link between Stem Cell Regulation and Floral Patterning in Arabidopsis. Cell, 2001, 105, 793-803.	28.9	650
8	Organization of cellulose synthase complexes involved in primary cell wall synthesis in <i>Arabidopsis thaliana</i> . Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15572-15577.	7.1	542
9	A genetic framework for floral patterning. Nature, 1998, 395, 561-566.	27.8	525
10	Characterization of MADS-domain transcription factor complexes in <i>Arabidopsis</i> flower development. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1560-1565.	7.1	439
11	Deciphering gene regulatory networks that control seed development and maturation in Arabidopsis. Plant Journal, 2008, 54, 608-620.	5.7	391
12	A Network of Local and Redundant Gene Regulation Governs Arabidopsis Seed Maturation. Plant Cell, 2006, 18, 1642-1651.	6.6	350
13	Regulation of storage protein gene expression in Arabidopsis. Development (Cambridge), 2003, 130, 6065-6073.	2.5	244
14	LEAFY Target Genes Reveal Floral Regulatory Logic, cis Motifs, and a Link to Biotic Stimulus Response. Developmental Cell, 2011, 20, 430-443.	7.0	239
15	The mRNA of the Arabidopsis Gene FT Moves from Leaf to Shoot Apex and Induces Flowering. Science, 2005, 309, 1694-1696.	12.6	238
16	Cytokinin signalling inhibitory fields provide robustness to phyllotaxis. Nature, 2014, 505, 417-421.	27.8	236
17	The Homologous ABI5 and EEL Transcription Factors Function Antagonistically to Fine-Tune Gene Expression during Late Embryogenesis. Plant Cell, 2002, 14, 1391-1403.	6.6	232
18	Flowering: a time for integration. International Journal of Developmental Biology, 2005, 49, 585-593.	0.6	223

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19	AtGA3ox2, a Key Gene Responsible for Bioactive Gibberellin Biosynthesis, Is Regulated during Embryogenesis by LEAFY COTYLEDON2 and FUSCA3 in Arabidopsis. <i>Plant Physiology</i> , 2004, 136, 3660-3669.	4.8	216
20	LEAFY blossoms. <i>Trends in Plant Science</i> , 2010, 15, 346-352.	8.8	174
21	<i>Arabidopsis</i> TONNEAU1 Proteins Are Essential for Preprophase Band Formation and Interact with Centrin. <i>Plant Cell</i> , 2008, 20, 2146-2159.	6.6	166
22	How Floral Meristems are Built. <i>Plant Molecular Biology</i> , 2006, 60, 855-870.	3.9	160
23	Prediction of Regulatory Interactions from Genome Sequences Using a Biophysical Model for the <i>Arabidopsis</i> LEAFY Transcription Factor Å. <i>Plant Cell</i> , 2011, 23, 1293-1306.	6.6	148
24	Structural basis for oligomerization of auxin transcriptional regulators. <i>Nature Communications</i> , 2014, 5, 3617.	12.8	145
25	Analysis of an activated ABI5 allele using a new selection method for transgenic Arabidopsis seeds. <i>FEBS Letters</i> , 2004, 561, 127-131.	2.8	144
26	Characterization of three homologous basic leucine zipper transcription factors (bZIP) of the ABI5 family during Arabidopsis thaliana embryo maturation. <i>Journal of Experimental Botany</i> , 2005, 56, 597-603.	4.8	127
27	A Promiscuous Intermediate Underlies the Evolution of LEAFY DNA Binding Specificity. <i>Science</i> , 2014, 343, 645-648.	12.6	117
28	Interactions between the ABI1 and the ectopically expressed ABI3 genes in controlling abscisic acid responses in Arabidopsis vegetative tissues. <i>Plant Journal</i> , 1997, 11, 693-702.	5.7	105
29	A Novel Mechanism for the Formation of Actin-Filament Bundles by a Nonprocessive Formin. <i>Current Biology</i> , 2006, 16, 1924-1930.	3.9	97
30	Structural basis for LEAFY floral switch function and similarity with helix-turn-helix proteins. <i>EMBO Journal</i> , 2008, 27, 2628-2637.	7.8	97
31	Structural Basis for the Oligomerization of the MADS Domain Transcription Factor SEPALLATA3 in <i>Arabidopsis</i> Å. <i>Plant Cell</i> , 2014, 26, 3603-3615.	6.6	97
32	Structure of the <i>Arabidopsis</i> TOPLESS corepressor provides insight into the evolution of transcriptional repression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8107-8112.	7.1	90
33	Tetramerization of MADS family transcription factors SEPALLATA3 and AGAMOUS is required for floral meristem determinacy in Arabidopsis. <i>Nucleic Acids Research</i> , 2018, 46, 4966-4977.	14.5	81
34	A SAM oligomerization domain shapes the genomic binding landscape of the LEAFY transcription factor. <i>Nature Communications</i> , 2016, 7, 11222.	12.8	76
35	A variant of <sc>LEAFY</sc> reveals its capacity to stimulate meristem development by inducing <sc>RAX1</sc>. <i>Plant Journal</i> , 2013, 74, 678-689.	5.7	71
36	Building Transcription Factor Binding Site Models to Understand Gene Regulation in Plants. <i>Molecular Plant</i> , 2019, 12, 743-763.	8.3	71

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37	A flower is born: an update on Arabidopsis floral meristem formation. <i>Current Opinion in Plant Biology</i> , 2017, 35, 15-22.	7.1	66
38	FUSCA3 from barley unveils a common transcriptional regulation of seed-specific genes between cereals and Arabidopsis. <i>Plant Journal</i> , 2008, 53, 882-894.	5.7	60
39	Evolution of the Plant Reproduction Master Regulators LFY and the MADS Transcription Factors: The Role of Protein Structure in the Evolutionary Development of the Flower. <i>Frontiers in Plant Science</i> , 2015, 6, 1193.	3.6	58
40	Evidence for functional interaction between brassinosteroids and cadmium response in Arabidopsis thaliana. <i>Journal of Experimental Botany</i> , 2012, 63, 1185-1200.	4.8	57
41	Integrating long-day flowering signals: a LEAFY binding site is essential for proper photoperiodic activation of <i>APETALA1</i> . <i>Plant Journal</i> , 2011, 67, 1094-1102.	5.7	56
42	A network of transcriptional repressors modulates auxin responses. <i>Nature</i> , 2021, 589, 116-119.	27.8	56
43	The LEAFY Floral Regulators in Angiosperms: Conserved Proteins with Diverse Roles. <i>Journal of Plant Biology</i> , 2009, 52, 177-185.	2.1	53
44	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
45	Interaction of LEAFY, AGAMOUS and TERMINAL FLOWER1 in maintaining floral meristem identity in Arabidopsis. <i>Development (Cambridge)</i> , 2002, 129, 2519-27.	2.5	49
46	The LEAFY floral regulator displays pioneer transcription factor properties. <i>Molecular Plant</i> , 2021, 14, 829-837.	8.3	48
47	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
48	Genome-wide binding of SEPALLATA3 and AGAMOUS complexes determined by sequential DNA-affinity purification sequencing. <i>Nucleic Acids Research</i> , 2020, 48, 9637-9648.	14.5	39
49	Capturing Auxin Response Factors Syntax Using DNA Binding Models. <i>Molecular Plant</i> , 2019, 12, 822-832.	8.3	38
50	Cauliflower fractal forms arise from perturbations of floral gene networks. <i>Science</i> , 2021, 373, 192-197.	12.6	37
51	Evolution of the Auxin Response Factors from charophyte ancestors. <i>PLoS Genetics</i> , 2019, 15, e1008400.	3.5	35
52	A link between LEAFY and <i>W</i> gene homologues in <i>Welwitschia mirabilis</i> sheds light on ancestral mechanisms prefiguring floral development. <i>New Phytologist</i> , 2017, 216, 469-481.	7.3	33
53	<i>LEAFY</i> activity is post-transcriptionally regulated by <i>BLADE ON PETIOLE</i> 2 and <i>CULLIN</i> 3 in Arabidopsis. <i>New Phytologist</i> , 2018, 220, 579-592.	7.3	32
54	The intervening domain is required for DNA-binding and functional identity of plant MADS transcription factors. <i>Nature Communications</i> , 2021, 12, 4760.	12.8	29

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55	Contrasted evolutionary trajectories of plant transcription factors. <i>Current Opinion in Plant Biology</i> , 2020, 54, 101-107.	7.1	26
56	Differential regulation of two ABA-inducible genes from <i>Craterostigma plantagineum</i> in transgenic <i>Arabidopsis</i> plants. <i>Plant Molecular Biology</i> , 1996, 30, 343-349.	3.9	21
57	Conservation vs divergence in <i>LEAFY</i> and <i>APETALA1</i> functions between <i>Arabidopsis thaliana</i> and <i>Cardamine hirsuta</i> . <i>New Phytologist</i> , 2017, 216, 549-561.	7.3	21
58	Plant SAM-Domain Proteins Start to Reveal Their Roles. <i>Trends in Plant Science</i> , 2017, 22, 718-725.	8.8	21
59	OsFD4 promotes the rice floral transition via florigen activation complex formation in the shoot apical meristem. <i>New Phytologist</i> , 2021, 229, 429-443.	7.3	21
60	A Glimpse beyond Structures in Auxin-Dependent Transcription. <i>Trends in Plant Science</i> , 2016, 21, 574-583.	8.8	20
61	Crystal structure of the transcriptional repressor DdrO: insight into the metalloprotease/repressor-controlled radiation response in <i>Deinococcus</i> . <i>Nucleic Acids Research</i> , 2019, 47, 11403-11417.	14.5	18
62	Differential activation of <i>ABI3</i> and <i>LEA</i> genes upon plant parasitic nematode infection. <i>Molecular Plant Pathology</i> , 2005, 6, 321-325.	4.2	16
63	MORPHEUS, a Webtool for Transcription Factor Binding Analysis Using Position Weight Matrices with Dependency. <i>PLoS ONE</i> , 2015, 10, e0135586.	2.5	16
64	The analysis of entire gene promoters by surface plasmon resonance. <i>Plant Journal</i> , 2009, 59, 851-858.	5.7	15
65	Use of the <i>lacZ</i> reporter gene as an internal control for GUS activity in microprojectile bombarded plant tissue. <i>Plant Science</i> , 1996, 120, 153-160.	3.6	8
66	Response to Comment on "A promiscuous intermediate underlies the evolution of <i>LEAFY</i> DNA binding specificity". <i>Science</i> , 2015, 347, 621-621.	12.6	4
67	Transcriptional reprogramming during floral fate acquisition. <i>Science</i> , 2022, 25, 104683.	4.1	2
68	Self-Assembly of a Ginkgo Oligomerization Domain Creates a Sub-10-nm Honeycomb Architecture on Carbon and Silicon Surfaces with Customizable Pores: Implications for Nanoelectronics, Biosensing, and Biocatalysis. <i>ACS Applied Nano Materials</i> , 2021, 4, 9518-9526.	5.0	0
69	Floral development: an integrated view. , 2016, , 43-116.		0