

Francois Parcy

List of Publications by Year in descending order

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Version: 2024-02-01

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	JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2022, 50, D165-D173.	14.5	902
2	Transcriptional reprogramming during floral fate acquisition. <i>IScience</i> , 2022, 25, 104683.	4.1	2
3	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
4	A network of transcriptional repressors modulates auxin responses. <i>Nature</i> , 2021, 589, 116-119.	27.8	56
5	The LEAFY floral regulator displays pioneer transcription factor properties. <i>Molecular Plant</i> , 2021, 14, 829-837.	8.3	48
6	Cauliflower fractal forms arise from perturbations of floral gene networks. <i>Science</i> , 2021, 373, 192-197.	12.6	37
7	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
8	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
9	JASPAR 2020: update of the open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2020, 48, D87-D92.	14.5	1,039
10	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
11	Contrasted evolutionary trajectories of plant transcription factors. <i>Current Opinion in Plant Biology</i> , 2020, 54, 101-107.	7.1	26
12	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
13	Evolution of the Auxin Response Factors from charophyte ancestors. <i>PLoS Genetics</i> , 2019, 15, e1008400.	3.5	35
14	Building Transcription Factor Binding Site Models to Understand Gene Regulation in Plants. <i>Molecular Plant</i> , 2019, 12, 743-763.	8.3	71
15	Capturing Auxin Response Factors Syntax Using DNA Binding Models. <i>Molecular Plant</i> , 2019, 12, 822-832.	8.3	38
16	JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. <i>Nucleic Acids Research</i> , 2018, 46, D260-D266.	14.5	1,232
17	Tetramerization of MADS family transcription factors SEPALLATA3 and AGAMOUS is required for floral meristem determinacy in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2018, 46, 4966-4977.	14.5	81
18	<sc>LEAFY</sc> activity is post-transcriptionally regulated by <sc>BLADE ON PETIOLE</sc>2 and <sc>CULLIN</sc>3 in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2018, 220, 579-592.	7.3	32

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19	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
20	A link between <i>LEAFY</i> 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
21	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
22	Plant SAM-Domain Proteins Start to Reveal Their Roles. <i>Trends in Plant Science</i> , 2017, 22, 718-725.	8.8	21
23	A flower is born: an update on <i>Arabidopsis</i> floral meristem formation. <i>Current Opinion in Plant Biology</i> , 2017, 35, 15-22.	7.1	66
24	A Glimpse beyond Structures in Auxin-Dependent Transcription. <i>Trends in Plant Science</i> , 2016, 21, 574-583.	8.8	20
25	Deciphering the molecular mechanisms underpinning the transcriptional control of gene expression by L-AFL proteins in <i>Arabidopsis</i> seed.. <i>Plant Physiology</i> , 2016, 171, pp.00034.2016.	4.8	53
26	A SAM oligomerization domain shapes the genomic binding landscape of the <i>LEAFY</i> transcription factor. <i>Nature Communications</i> , 2016, 7, 11222.	12.8	76
27	JASPAR 2016: a major expansion and update of the open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2016, 44, D110-D115.	14.5	968
28	The Myb-domain protein ULTRAPETALA1 INTERACTING FACTOR 1 controls floral meristem activities in <i>Arabidopsis</i> . <i>Development (Cambridge)</i> , 2016, 143, 1108-19.	2.5	45
29	Floral development: an integrated view. , 2016, , 43-116.		0
30	MORPHEUS, a Webtool for Transcription Factor Binding Analysis Using Position Weight Matrices with Dependency. <i>PLoS ONE</i> , 2015, 10, e0135586.	2.5	16
31	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
32	Evolution of the Plant Reproduction Master Regulators <i>LFY</i> and the <i>MADS</i> 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
33	JASPAR 2014: an extensively expanded and updated open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2014, 42, D142-D147.	14.5	915
34	Cytokinin signalling inhibitory fields provide robustness to phyllotaxis. <i>Nature</i> , 2014, 505, 417-421.	27.8	236
35	A Promiscuous Intermediate Underlies the Evolution of <i>LEAFY</i> DNA Binding Specificity. <i>Science</i> , 2014, 343, 645-648.	12.6	117
36	Structural basis for oligomerization of auxin transcriptional regulators. <i>Nature Communications</i> , 2014, 5, 3617.	12.8	145

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37	Structural Basis for the Oligomerization of the MADS Domain Transcription Factor SEPALLATA3 in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 3603-3615.	6.6	97
38	A variant of <i>LEAFY</i> reveals its capacity to stimulate meristem development by inducing <i>RAX1</i> . <i>Plant Journal</i> , 2013, 74, 678-689.	5.7	71
39	Evidence for functional interaction between brassinosteroids and cadmium response in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2012, 63, 1185-1200.	4.8	57
40	Characterization of MADS-domain transcription factor complexes in <i>Arabidopsis</i> flower development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1560-1565.	7.1	439
41	<i>LEAFY</i> Target Genes Reveal Floral Regulatory Logic, cis Motifs, and a Link to Biotic Stimulus Response. <i>Developmental Cell</i> , 2011, 20, 430-443.	7.0	239
42	Integrating long-day flowering signals: a <i>LEAFY</i> binding site is essential for proper photoperiodic activation of <i>APETALA1</i> . <i>Plant Journal</i> , 2011, 67, 1094-1102.	5.7	56
43	Prediction of Regulatory Interactions from Genome Sequences Using a Biophysical Model for the <i>Arabidopsis</i> <i>LEAFY</i> Transcription Factor. <i>Plant Cell</i> , 2011, 23, 1293-1306.	6.6	148
44	<i>LEAFY</i> blossoms. <i>Trends in Plant Science</i> , 2010, 15, 346-352.	8.8	174
45	The <i>LEAFY</i> Floral Regulators in Angiosperms: Conserved Proteins with Diverse Roles. <i>Journal of Plant Biology</i> , 2009, 52, 177-185.	2.1	53
46	The analysis of entire gene promoters by surface plasmon resonance. <i>Plant Journal</i> , 2009, 59, 851-858.	5.7	15
47	<i>FUSCA3</i> from barley unveils a common transcriptional regulation of seed-specific genes between cereals and <i>Arabidopsis</i> . <i>Plant Journal</i> , 2008, 53, 882-894.	5.7	60
48	Structural basis for <i>LEAFY</i> floral switch function and similarity with helix-turn-helix proteins. <i>EMBO Journal</i> , 2008, 27, 2628-2637.	7.8	97
49	Deciphering gene regulatory networks that control seed development and maturation in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2008, 54, 608-620.	5.7	391
50	<i>Arabidopsis</i> <i>TONNEAU1</i> Proteins Are Essential for Preprophase Band Formation and Interact with Centrin. <i>Plant Cell</i> , 2008, 20, 2146-2159.	6.6	166
51	Organization of cellulose synthase complexes involved in primary cell wall synthesis in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15572-15577.	7.1	542
52	How Floral Meristems are Built. <i>Plant Molecular Biology</i> , 2006, 60, 855-870.	3.9	160
53	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
54	A Network of Local and Redundant Gene Regulation Governs <i>Arabidopsis</i> Seed Maturation. <i>Plant Cell</i> , 2006, 18, 1642-1651.	6.6	350

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55	Differential activation ofABI3andLEAgenes upon plant parasitic nematode infection. <i>Molecular Plant Pathology</i> , 2005, 6, 321-325.	4.2	16
56	Flowering: a time for integration. <i>International Journal of Developmental Biology</i> , 2005, 49, 585-593.	0.6	223
57	Characterization of three homologous basic leucine zipper transcription factors (bZIP) of the ABI5 family during <i>Arabidopsis thaliana</i> embryo maturation. <i>Journal of Experimental Botany</i> , 2005, 56, 597-603.	4.8	127
58	The mRNA of the <i>Arabidopsis</i> Gene FT Moves from Leaf to Shoot Apex and Induces Flowering. <i>Science</i> , 2005, 309, 1694-1696.	12.6	238
59	AtGA3ox2, a Key Gene Responsible for Bioactive Gibberellin Biosynthesis, Is Regulated during Embryogenesis by LEAFY COTYLEDON2 and FUSCA3 in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2004, 136, 3660-3669.	4.8	216
60	Analysis of an activated ABI5 allele using a new selection method for transgenic <i>Arabidopsis</i> seeds. <i>FEBS Letters</i> , 2004, 561, 127-131.	2.8	144
61	Regulation of storage protein gene expression in <i>Arabidopsis</i> . <i>Development (Cambridge)</i> , 2003, 130, 6065-6073.	2.5	244
62	The Homologous ABI5 and EEL Transcription Factors Function Antagonistically to Fine-Tune Gene Expression during Late Embryogenesis. <i>Plant Cell</i> , 2002, 14, 1391-1403.	6.6	232
63	bZIP transcription factors in <i>Arabidopsis</i> . <i>Trends in Plant Science</i> , 2002, 7, 106-111.	8.8	1,585
64	Interaction of LEAFY, AGAMOUS and TERMINAL FLOWER1 in maintaining floral meristem identity in <i>Arabidopsis</i> . <i>Development (Cambridge)</i> , 2002, 129, 2519-27.	2.5	49
65	A Molecular Link between Stem Cell Regulation and Floral Patterning in <i>Arabidopsis</i> . <i>Cell</i> , 2001, 105, 793-803.	28.9	650
66	A genetic framework for floral patterning. <i>Nature</i> , 1998, 395, 561-566.	27.8	525
67	Interactions between the ABI1 and the ectopically expressed ABI3 genes in controlling abscisic acid responses in <i>Arabidopsis</i> vegetative tissues. <i>Plant Journal</i> , 1997, 11, 693-702.	5.7	105
68	Use of the lacZ 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
69	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