

# Franziska Turck

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4780933/publications.pdf>

Version: 2024-02-01

59  
papers

6,170  
citations

126907

33  
h-index

155660

55  
g-index

63  
all docs

63  
docs citations

63  
times ranked

7078  
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulation and Identity of Florigen: FLOWERING LOCUS T Moves Center Stage. Annual Review of Plant Biology, 2008, 59, 573-594.	18.7	889
2	The transcription factor FLC confers a flowering response to vernalization by repressing meristem competence and systemic signaling in Arabidopsis. Genes and Development, 2006, 20, 898-912.	5.9	744
3	Arabidopsis TFL2/LHP1 Specifically Associates with Genes Marked by Trimethylation of Histone H3 Lysine 27. PLoS Genetics, 2007, 3, e86.	3.5	537
4	CONSTANS and the CCAAT Box Binding Complex Share a Functionally Important Domain and Interact to Regulate Flowering of Arabidopsis. Plant Cell, 2006, 18, 2971-2984.	6.6	512
5	PEP1 regulates perennial flowering in Arabis alpina. Nature, 2009, 459, 423-427.	27.8	325
6	<i>cis</i> -Regulatory Elements and Chromatin State Coordinately Control Temporal and Spatial Expression of FLOWERING LOCUS T in Arabidopsis. Plant Cell, 2010, 22, 1425-1440.	6.6	274
7	ATAF1 transcription factor directly regulates abscisic acid biosynthetic gene <i>NCED3</i> in Arabidopsis thaliana. FEBS Open Bio, 2013, 3, 321-327.	2.3	182
8	Stimulus-Dependent, Promoter-Specific Binding of Transcription Factor WRKY1 to Its Native Promoter and the Defense-Related Gene PcPR1-1 in Parsley[W]. Plant Cell, 2004, 16, 2573-2585.	6.6	180
9	VAL- and AtBMI1-Mediated H2Aub Initiate the Switch from Embryonic to Postgerminative Growth in Arabidopsis. Current Biology, 2013, 23, 1324-1329.	3.9	172
10	Unequally redundant RCD1 and SRO1 mediate stress and developmental responses and interact with transcription factors. Plant Journal, 2009, 60, 268-279.	5.7	156
11	Mutation identification by direct comparison of whole-genome sequencing data from mutant and wild-type individuals using k-mers. Nature Biotechnology, 2013, 31, 325-330.	17.5	149
12	Genome-wide mapping of transcriptional enhancer candidates using DNA and chromatin features in maize. Genome Biology, 2017, 18, 137.	8.8	134
13	Telobox motifs recruit CLF/SWN-PRC2 for H3K27me3 deposition via TRB factors in Arabidopsis. Nature Genetics, 2018, 50, 638-644.	21.4	123
14	Fast Isogenic Mapping-by-Sequencing of Ethyl Methanesulfonate-Induced Mutant Bulks. Plant Physiology, 2012, 160, 591-600.	4.8	119
15	<i>miR824</i> Regulated AGAMOUS-LIKE16 Contributes to Flowering Time Repression in Arabidopsis. Plant Cell, 2014, 26, 2024-2037.	6.6	112
16	Phytohormones Participate in an S6 Kinase Signal Transduction Pathway in Arabidopsis. Plant Physiology, 2004, 134, 1527-1535.	4.8	106
17	Induced and natural variation of promoter length modulates the photoperiodic response of FLOWERING LOCUS T. Nature Communications, 2014, 5, 4558.	12.8	93
18	The age of multiplexity: recruitment and interactions of Polycomb complexes in plants. Current Opinion in Plant Biology, 2016, 29, 169-178.	7.1	79

#	ARTICLE	IF	CITATIONS
19	Speeding Cis-Trans Regulation Discovery by Phylogenomic Analyses Coupled with Screenings of an Arrayed Library of Arabidopsis Transcription Factors. PLoS ONE, 2011, 6, e21524.	2.5	78
20	From Decision to Commitment: The Molecular Memory of Flowering. Molecular Plant, 2009, 2, 628-642.	8.3	75
21	H2A monoubiquitination in Arabidopsis thaliana is generally independent of LHP1 and PRC2 activity. Genome Biology, 2017, 18, 69.	8.8	71
22	Tissue-Specific Expression of <i>FLOWERING LOCUS T</i> in <i>Arabidopsis</i> Is Maintained Independently of Polycomb Group Protein Repression. Plant Cell, 2011, 23, 3204-3214.	6.6	70
23	The impact of chromatin regulation on the floral transition. Seminars in Cell and Developmental Biology, 2008, 19, 560-573.	5.0	69
24	Kicking against the PRCs – A Domesticated Transposase Antagonises Silencing Mediated by Polycomb Group Proteins and Is an Accessory Component of Polycomb Repressive Complex 2. PLoS Genetics, 2015, 11, e1005660.	3.5	68
25	Complementary Activities of TELOMERE REPEAT BINDING Proteins and Polycomb Group Complexes in Transcriptional Regulation of Target Genes. Plant Cell, 2016, 28, 87-101.	6.6	67
26	A Heat-Sensitive Arabidopsis thaliana Kinase Substitutes for Human p70 s6k Function In Vivo. Molecular and Cellular Biology, 1998, 18, 2038-2044.	2.3	66
27	AP2 transcription factor CBX1 with a specific function in symbiotic exchange of nutrients in mycorrhizal <i>Lotus japonicus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E9239-E9246.	7.1	63
28	Brahma Is Required for Proper Expression of the Floral Repressor FLC in Arabidopsis. PLoS ONE, 2011, 6, e17997.	2.5	50
29	Molecular memories in the regulation of seasonal flowering: from competence to cessation. Genome Biology, 2015, 16, 192.	8.8	50
30	Multiple loci and genetic interactions involving flowering time genes regulate stem branching among natural variants of Arabidopsis. New Phytologist, 2013, 199, 843-857.	7.3	44
31	Targeted DNA methylation represses two enhancers of FLOWERING LOCUS T in Arabidopsis thaliana. Nature Plants, 2019, 5, 300-307.	9.3	44
32	NATURAL VARIATION IN EPIGENETIC GENE REGULATION AND ITS EFFECTS ON PLANT DEVELOPMENTAL TRAITS. Evolution; International Journal of Organic Evolution, 2014, 68, 620-631.	2.3	38
33	The Arabidopsis Polycomb Repressive Complex 1 (PRC1) Components AtBMI1A, B, and C Impact Gene Networks throughout All Stages of Plant Development. Plant Physiology, 2017, 173, 627-641.	4.8	38
34	The Arabidopsis DNA Polymerase $\delta$ Has a Role in the Deposition of Transcriptionally Active Epigenetic Marks, Development and Flowering. PLoS Genetics, 2015, 11, e1004975.	3.5	36
35	Ctf4-related protein recruits LHP1-PRC2 to maintain H3K27me3 levels in dividing cells in <i>Arabidopsis thaliana</i> . Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4833-4838.	7.1	36
36	Genome-wide Analysis of Cis-regulatory Divergence between Species in the Arabidopsis Genus. Molecular Biology and Evolution, 2012, 29, 3385-3395.	8.9	34

#	ARTICLE	IF	CITATIONS
37	Natural variation of H3K27me3 distribution between two Arabidopsis accessions and its association with flanking transposable elements. <i>Genome Biology</i> , 2012, 13, R117.	9.6	34
38	Elevated Levels of MYB30 in the Phloem Accelerate Flowering in Arabidopsis through the Regulation of FLOWERING LOCUS T. <i>PLoS ONE</i> , 2014, 9, e89799.	2.5	30
39	Post-fertilization expression of FLOWERING LOCUS T suppresses reproductive reversion. <i>Frontiers in Plant Science</i> , 2014, 5, 164.	3.6	30
40	Widespread Interspecific Divergence in Cis-Regulation of Transposable Elements in the Arabidopsis Genus. <i>Molecular Biology and Evolution</i> , 2012, 29, 1081-1091.	8.9	29
41	Genome-Wide Mapping of Protein-DNA Interaction by Chromatin Immunoprecipitation and DNA Microarray Hybridization (ChIP-chip). Part A: ChIP-chip Molecular Methods. <i>Methods in Molecular Biology</i> , 2010, 631, 139-160.	0.9	29
42	<i>DEVELOPMENT-RELATED PcG TARGET IN THE APEX 4</i> controls leaf margin architecture in <i>Arabidopsis thaliana</i>. <i>Development (Cambridge)</i> , 2012, 139, 2566-2575.	2.5	28
43	Photoperiod-responsive changes in chromatin accessibility in phloem companion and epidermis cells of Arabidopsis leaves. <i>Plant Cell</i> , 2021, 33, 475-491.	6.6	23
44	The domesticated transposase ALP2 mediates formation of a novel Polycomb protein complex by direct interaction with MSI1, a core subunit of Polycomb Repressive Complex 2 (PRC2). <i>PLoS Genetics</i> , 2020, 16, e1008681.	3.5	22
45	When Vernalization Makes Sense. <i>Science</i> , 2011, 331, 36-37.	12.6	17
46	Quality control and evaluation of plant epigenomics data. <i>Plant Cell</i> , 2022, 34, 503-513.	6.6	13
47	Genome-Wide Mapping of Protein-DNA Interaction by Chromatin Immunoprecipitation and DNA Microarray Hybridization (ChIP-chip). Part B: ChIP-chip Data Analysis. <i>Methods in Molecular Biology</i> , 2010, 631, 161-184.	0.9	9
48	Plant H3K27me3 has finally found its readers. <i>Nature Genetics</i> , 2018, 50, 1206-1208.	21.4	5
49	Information integration and decision making in flowering time control. <i>PLoS ONE</i> , 2020, 15, e0239417.	2.5	3
50	Epigenetic Control of Flowering Time. <i>Signaling and Communication in Plants</i> , 2013, , 77-105.	0.7	3
51	Control of perennial flowering and perenniality in Arabis alpina, a relative of Arabidopsis thaliana. <i>Comparative Biochemistry and Physiology Part A, Molecular &amp; Integrative Physiology</i> , 2009, 153, S195-S196.	1.8	2
52	Meta-analysis of Genome-Wide Chromatin Data. <i>Methods in Molecular Biology</i> , 2017, 1456, 33-50.	0.9	2
53	Metaanalysis of ChIP-chip Data. <i>Methods in Molecular Biology</i> , 2010, 631, 185-207.	0.9	2
54	Arabidopsis TFL2/LHP1 Specifically Associates with Genes Marked by Trimethylation of Histone H3 Lysine 27. <i>PLoS Genetics</i> , 2005, preprint, e86.	3.5	2

#	ARTICLE	IF	CITATIONS
55	Molekulare Mechanismen der Datenintegration und Entscheidung zur Einleitung der Reproduktiven Phase in Pflanzen. Lecture Notes in Bioengineering, 2018, , 331-339.	0.4	0
56	Title is missing!. , 2020, 16, e1008681.		0
57	Title is missing!. , 2020, 16, e1008681.		0
58	Title is missing!. , 2020, 16, e1008681.		0
59	Title is missing!. , 2020, 16, e1008681.		0