

# Kai Tang

## List of Publications by Year in descending order

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Version: 2024-02-01

46  
papers

3,779  
citations

109321

35  
h-index

243625

44  
g-index

50  
all docs

50  
docs citations

50  
times ranked

4040  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reciprocal Regulation of the TOR Kinase and ABA Receptor Balances Plant Growth and Stress Response. <i>Molecular Cell</i> , 2018, 69, 100-112.e6.	9.7	385
2	Critical roles of DNA demethylation in the activation of ripening-induced genes and inhibition of ripening-repressed genes in tomato fruit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4511-E4519.	7.1	342
3	A Histone Acetyltransferase Regulates Active DNA Demethylation in <i>Arabidopsis</i> . <i>Science</i> , 2012, 336, 1445-1448.	12.6	224
4	Regulatory link between DNA methylation and active demethylation in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3553-3557.	7.1	204
5	Global increase in DNA methylation during orange fruit development and ripening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1430-1436.	7.1	190
6	DTF1 is a core component of RNA-directed DNA methylation and may assist in the recruitment of Pol IV. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8290-8295.	7.1	158
7	The DNA demethylase ROS1 targets genomic regions with distinct chromatin modifications. <i>Nature Plants</i> , 2016, 2, 16169.	9.3	147
8	Transcriptome-wide high-throughput deep m6A-seq reveals unique differential m6A methylation patterns between three organs in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2015, 16, 272.	8.8	145
9	The Methyl-CpG-Binding Protein MBD7 Facilitates Active DNA Demethylation to Limit DNA Hyper-Methylation and Transcriptional Gene Silencing. <i>Molecular Cell</i> , 2015, 57, 971-983.	9.7	112
10	<i>Arabidopsis</i> EDM2 promotes IBM1 distal polyadenylation and regulates genome DNA methylation patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 527-532.	7.1	102
11	Dicer-independent RNA-directed DNA methylation in <i>Arabidopsis</i> . <i>Cell Research</i> , 2016, 26, 66-82.	12.0	95
12	RNA-binding protein regulates plant DNA methylation by controlling mRNA processing at the intronic heterochromatin-containing gene IBM1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15467-15472.	7.1	91
13	Specific but interdependent functions for <i>Arabidopsis</i> AGO4 and AGO6 in RNA-directed DNA methylation. <i>EMBO Journal</i> , 2015, 34, 581-592.	7.8	90
14	The SnRK2 kinases modulate miRNA accumulation in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2017, 13, e1006753.	3.5	87
15	The transcription factor ICE1 functions in cold stress response by binding to the promoters of CBF and COR genes. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 258-263.	8.5	82
16	A DNA 3' Phosphatase Functions in Active DNA Demethylation in <i>Arabidopsis</i> . <i>Molecular Cell</i> , 2012, 45, 357-370.	9.7	81
17	A pair of transposon-derived proteins function in a histone acetyltransferase complex for active DNA demethylation. <i>Cell Research</i> , 2017, 27, 226-240.	12.0	80
18	A protein complex regulates RNA processing of intronic heterochromatin-containing genes in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7377-E7384.	7.1	74

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19	Histone acetylation recruits the SWR1 complex to regulate active DNA demethylation in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16641-16650.	7.1	73
20	An <i>Arabidopsis</i> Nucleoporin NUP85 modulates plant responses to ABA and salt stress. <i>PLoS Genetics</i> , 2017, 13, e1007124.	3.5	72
21	<i>Arabidopsis</i> AGDP1 links H3K9me2 to DNA methylation in heterochromatin. <i>Nature Communications</i> , 2018, 9, 4547.	12.8	66
22	Rhizobacterium-derived diacetyl modulates plant immunity in a phosphate-dependent manner. <i>EMBO Journal</i> , 2020, 39, e102602.	7.8	66
23	A Pre-mRNA-Splicing Factor Is Required for RNA-Directed DNA Methylation in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2013, 9, e1003779.	3.5	58
24	A Role for PICKLE in the Regulation of Cold and Salt Stress Tolerance in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 900.	3.6	58
25	Genome-wide identification and comparative analysis of grafting-responsive mRNA in watermelon grafted onto bottle gourd and squash rootstocks by high-throughput sequencing. <i>Molecular Genetics and Genomics</i> , 2016, 291, 621-633.	2.1	55
26	An AP Endonuclease Functions in Active DNA Demethylation and Gene Imprinting in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2015, 11, e1004905.	3.5	53
27	CDK8 is associated with RAP2.6 and SnRK2.6 and positively modulates abscisic acid signaling and drought response in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2020, 228, 1573-1590.	7.3	50
28	The LRXs-RALFs-FER module controls plant growth and salt stress responses by modulating multiple plant hormones. <i>National Science Review</i> , 2021, 8, nwa149.	9.5	50
29	Critical function of DNA methyltransferase 1 in tomato development and regulation of the DNA methylome and transcriptome. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 1224-1242.	8.5	49
30	DNA demethylases are required for myo-inositol-mediated mutualism between plants and beneficial rhizobacteria. <i>Nature Plants</i> , 2020, 6, 983-995.	9.3	48
31	DNA demethylase ROS1 negatively regulates the imprinting of <i>DOGL4</i> and seed dormancy in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9962-E9970.	7.1	46
32	An Rrp6-like Protein Positively Regulates Noncoding RNA Levels and DNA Methylation in <i>Arabidopsis</i> . <i>Molecular Cell</i> , 2014, 54, 418-430.	9.7	45
33	Regulation of Active DNA Demethylation by an $\hat{\pm}$ -Crystallin Domain Protein in <i>Arabidopsis</i> . <i>Molecular Cell</i> , 2014, 55, 361-371.	9.7	44
34	High-throughput m6A-seq reveals RNA m6A methylation patterns in the chloroplast and mitochondria transcriptomes of <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2017, 12, e0185612.	2.5	43
35	MET18 Connects the Cytosolic Iron-Sulfur Cluster Assembly Pathway to Active DNA Demethylation in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2015, 11, e1005559.	3.5	43
36	The PRP6-like splicing factor STA1 is involved in RNA-directed DNA methylation by facilitating the production of Pol V-dependent scaffold RNAs. <i>Nucleic Acids Research</i> , 2013, 41, 8489-8502.	14.5	40

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37	Protocol: a beginner's guide to the analysis of RNA-directed DNA methylation in plants. <i>Plant Methods</i> , 2014, 10, 18.	4.3	32
38	Four putative SWI2/SNF2 chromatin remodelers have dual roles in regulating DNA methylation in <i>Arabidopsis</i> . <i>Cell Discovery</i> , 2018, 4, 55.	6.7	22
39	SAC3B, a central component of the mRNA export complex TREX-2, is required for prevention of epigenetic gene silencing in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2017, 45, 181-197.	14.5	21
40	A histone H3K4me1-specific binding protein is required for siRNA accumulation and DNA methylation at a subset of loci targeted by RNA-directed DNA methylation. <i>Nature Communications</i> , 2021, 12, 3367.	12.8	21
41	A domesticated <i>Harbinger</i> transposase forms a complex with HDA6 and promotes histone H3 deacetylation at genes but not TEs in <i>Arabidopsis</i> . <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1462-1474.	8.5	14
42	EXPORTIN 1A prevents transgene silencing in <i>Arabidopsis</i> by modulating nucleocytoplasmic partitioning of HDA6. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 1243-1254.	8.5	11
43	Non-CG DNA methylation-deficiency mutations enhance mutagenesis rates during salt adaptation in cultured <i>Arabidopsis</i> cells. <i>Stress Biology</i> , 2021, 1, 1.	3.1	7
44	Small RNA and DNA methylation in plants. , 2020, , 353-376.		2
45	Computational Analysis of Genome-Wide ARGONAUTE-Dependent DNA Methylation in Plants. <i>Methods in Molecular Biology</i> , 2017, 1640, 219-225.	0.9	1
46	Editorial: The Interplay Between Epigenetic Regulation and Other Cellular Processes. <i>Frontiers in Genetics</i> , 2021, 12, 691202.	2.3	0