

# Claude Becker

## List of Publications by Year in descending order

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Version: 2024-02-01

46  
papers

6,957  
citations

147801

31  
h-index

223800

46  
g-index

66  
all docs

66  
docs citations

66  
times ranked

8602  
citing authors

#	ARTICLE	IF	CITATIONS
1	1,135 Genomes Reveal the Global Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2016, 166, 481-491.	28.9	1,107
2	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <i>Nature Genetics</i> , 2017, 49, 1099-1106.	21.4	693
3	Spontaneous epigenetic variation in the <i>Arabidopsis thaliana</i> methylome. <i>Nature</i> , 2011, 480, 245-249.	27.8	681
4	Epigenomic Diversity in a Global Collection of <i>Arabidopsis thaliana</i> Accessions. <i>Cell</i> , 2016, 166, 492-505.	28.9	594
5	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	21.4	413
6	Hyperosmotic stress memory in <i>Arabidopsis</i> is mediated by distinct epigenetically labile sites in the genome and is restricted in the male germline by DNA glycosylase activity. <i>ELife</i> , 2016, 5, .	6.0	282
7	Ecological plant epigenetics: Evidence from model and non-model species, and the way forward. <i>Ecology Letters</i> , 2017, 20, 1576-1590.	6.4	279
8	Genome-wide analysis of local chromatin packing in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2015, 25, 246-256.	5.5	254
9	Mutation bias reflects natural selection in <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2022, 602, 101-105.	27.8	206
10	Genome-wide analysis of chromatin packing in <i>Arabidopsis thaliana</i> at single-gene resolution. <i>Genome Research</i> , 2016, 26, 1057-1068.	5.5	187
11	Evolution of DNA Methylation Patterns in the Brassicaceae is Driven by Differences in Genome Organization. <i>PLoS Genetics</i> , 2014, 10, e1004785.	3.5	184
12	Transposons: a blessing curse. <i>Current Opinion in Plant Biology</i> , 2018, 42, 23-29.	7.1	163
13	Genome expansion of <i>Arabis alpina</i> linked with retrotransposition and reduced symmetric DNA methylation. <i>Nature Plants</i> , 2015, 1, 14023.	9.3	156
14	Century-scale Methylome Stability in a Recently Diverged <i>Arabidopsis thaliana</i> Lineage. <i>PLoS Genetics</i> , 2015, 11, e1004920.	3.5	148
15	Nt-RhoGDI2 regulates Rac/Rop signaling and polar cell growth in tobacco pollen tubes. <i>Plant Journal</i> , 2006, 46, 1018-1031.	5.7	138
16	The role of plant epigenetics in biotic interactions. <i>New Phytologist</i> , 2019, 221, 731-737.	7.3	116
17	The rate and potential relevance of new mutations in a colonizing plant lineage. <i>PLoS Genetics</i> , 2018, 14, e1007155.	3.5	116
18	Epigenetic variation: origin and transgenerational inheritance. <i>Current Opinion in Plant Biology</i> , 2012, 15, 562-567.	7.1	110

#	ARTICLE	IF	CITATIONS
19	Fine-Grained Analysis of Spontaneous Mutation Spectrum and Frequency in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2019, 211, 703-714.	2.9	97
20	Epigenome confrontation triggers immediate reprogramming of DNA methylation and transposon silencing in <i>Arabidopsis thaliana</i> F1 epihybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2083-92.	7.1	90
21	Plants Release Precursors of Histone Deacetylase Inhibitors to Suppress Growth of Competitors. <i>Plant Cell</i> , 2015, 27, 3175-3189.	6.6	86
22	Altered chromatin compaction and histone methylation drive non-additive gene expression in an interspecific <i>Arabidopsis</i> hybrid. <i>Genome Biology</i> , 2017, 18, 157.	8.8	86
23	Allelopathic Plants: Models for Studying Plant-Plant Interkingdom Interactions. <i>Trends in Plant Science</i> , 2020, 25, 176-185.	8.8	85
24	The causes and consequences of DNA methylome variation in plants. <i>Current Opinion in Plant Biology</i> , 2017, 36, 56-63.	7.1	71
25	Partial maintenance of organ-specific epigenetic marks during plant asexual reproduction leads to heritable phenotypic variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9145-E9152.	7.1	65
26	Characterization of Phytochrome Interacting Factors from the Moss <i>Physcomitrella patens</i> Illustrates Conservation of Phytochrome Signaling Modules in Land Plants. <i>Plant Cell</i> , 2017, 29, 310-330.	6.6	61
27	DNA sequence properties that predict susceptibility to epiallelic switching. <i>EMBO Journal</i> , 2017, 36, 617-628.	7.8	56
28	Tissue-Specific Silencing of <i>Arabidopsis</i> SU(VAR)3-9 HOMOLOG8 by miR171a. <i>Plant Physiology</i> , 2013, 161, 805-812.	4.8	53
29	Signatures of antagonistic pleiotropy in a bacterial flagellin epitope. <i>Cell Host and Microbe</i> , 2021, 29, 620-634.e9.	11.0	44
30	Characterization of auxin transporter PIN6 plasma membrane targeting reveals a function for PIN6 in plant bolting. <i>New Phytologist</i> , 2018, 217, 1610-1624.	7.3	39
31	Nitric oxide coordinates growth, development, and stress response via histone modification and gene expression. <i>Plant Physiology</i> , 2021, 187, 336-360.	4.8	37
32	<i>Arabidopsis</i> proteins with a transposon-related domain act in gene silencing. <i>Nature Communications</i> , 2017, 8, 15122.	12.8	32
33	Repression of CHROMOMETHYLASE 3 prevents epigenetic collateral damage in <i>Arabidopsis</i> . <i>ELife</i> , 2021, 10, .	6.0	28
34	Epigenetics in plant organismic interactions. <i>Current Opinion in Plant Biology</i> , 2021, 61, 102060.	7.1	25
35	EFFECTOR OF TRANSCRIPTION factors are novel plant-specific regulators associated with genomic DNA methylation in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2019, 221, 261-278.	7.3	20
36	ARADEEPOPSIS, an Automated Workflow for Top-View Plant Phenomics using Semantic Segmentation of Leaf States. <i>Plant Cell</i> , 2020, 32, 3674-3688.	6.6	20

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37	Allelopathy in rice: a story of momilactones, kin recognition, and weed management. <i>Journal of Experimental Botany</i> , 2021, 72, 4022-4037.	4.8	20
38	Chromosome-level <i>Thlaspi arvense</i> genome provides new tools for translational research and for a newly domesticated cash cover crop of the cooler climates. <i>Plant Biotechnology Journal</i> , 2022, 20, 944-963.	8.3	18
39	Allelochemicals of the phenoxazinone class act at physiologically relevant concentrations. <i>Plant Signaling and Behavior</i> , 2016, 11, e1176818.	2.4	11
40	How to Design a Whole-Genome Bisulfite Sequencing Experiment. <i>Epigenomes</i> , 2018, 2, 21.	1.8	11
41	GSNOR Contributes to Demethylation and Expression of Transposable Elements and Stress-Responsive Genes. <i>Antioxidants</i> , 2021, 10, 1128.	5.1	10
42	The EpiDiverse Plant Epigenome-Wide Association Studies (EWAS) Pipeline. <i>Epigenomes</i> , 2021, 5, 12.	1.8	6
43	Like father, like son. <i>ELife</i> , 2017, 6, .	6.0	4
44	Assessing Distribution and Variation of Genome-Wide DNA Methylation Using Short-Read Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1610, 61-72.	0.9	1
45	A Critical Guide for Studies on Epigenetic Inheritance in Plants. <i>Methods in Molecular Biology</i> , 2020, 2093, 261-270.	0.9	1
46	MicroRNA as an Integral Part of Cell Communication: Regularized Target Prediction and Network Prediction. <i>Lecture Notes in Bioengineering</i> , 2018, , 85-100.	0.4	0