Claudia KÃ¶hler

List of Publications by Year
in descending order

114 papers	9,420 citations	31902 53 h-index	45213 90 g-index
138 all docs	138 docs citations	138 times ranked	6654 citing authors

#	Article	IF	Citations
1	The Polycomb-group protein MEDEA regulates seed development by controlling expression of the MADS-box gene PHERES1. Genes and Development, 2003, 17, 1540-1553.	2.7	390
2	Arabidopsis MSI1 is a component of the MEA/FIE Polycomb group complex and required for seed development. EMBO Journal, 2003, 22, 4804-4814.	3.5	379
3	HLM1, an Essential Signaling Component in the Hypersensitive Response, Is a Member of the Cyclic Nucleotideâ€“Gated Channel Ion Channel Family[W]. Plant Cell, 2003, 15, 365-379.	3.1	329
4	The Arabidopsis thaliana MEDEA Polycomb group protein controls expression of PHERES1 by parental imprinting. Nature Genetics, 2005, 37, 28-30.	9.4	251
5	Different Polycomb group complexes regulate common target genes in Arabidopsis. EMBO Reports, 2006, 7, 947-952.	2.0	242
6	High-Resolution Analysis of Parent-of-Origin Allelic Expression in the Arabidopsis Endosperm. PLoS Genetics, 2011, 7, e1002126.	1.5	237
7	The impact of the triploid block on the origin and evolution of polyploid plants. Trends in Genetics, 2010, 26, 142-148.	2.9	225
8	Polycomb-group proteins repressthe floral activator AGL19 in the FLC-independent vernalization pathway. Genes and Development, 2006, 20, 1667-1678.	2.7	222
9	Epigenetic Mechanisms Underlying Genomic Imprinting in Plants. Annual Review of Plant Biology, 2012, 63, 331-352.	8.6	196
10	Endosperm cellularization defines an important developmental transition for embryo development. Development (Cambridge), 2012, 139, 2031-2039.	1.2	191
11	Silencing in sperm cells is directed by RNA movement from the surrounding nurse cell. Nature Plants, 2016, 2, 16030.	4.7	191
12	Characterisation of a novel gene family of putative cyclic nucleotide- and calmodulin-regulated ion channels in Arabidopsis thaliana. Plant Journal, 1999, 18, 97-104.	2.8	176
13	H3K27me3 Profiling of the Endosperm Implies Exclusion of Polycomb Group Protein Targeting by DNA Methylation. PLoS Genetics, 2010, 6, e1001152.	1.5	174
14	Nuclear export of proteins in plants: AtXPO1 is the export receptor for leucine-rich nuclear export signals in Arabidopsis thaliana. Plant Journal, 1999, 20, 695-705.	2.8	165
15	Unreduced gamete formation in plants: mechanisms and prospects. Journal of Experimental Botany, 2011, 62, 1659-1668.	2.4	159
16	Auxin production in the endosperm drives seed coat development in Arabidopsis. ELife, 2016, 5, .	2.8	158
17	Programming of gene expression by Polycomb group proteins. Trends in Cell Biology, 2008, 18, 236-243.	3.6	156
18	The CHD3 Chromatin Remodeler PICKLE and Polycomb Group Proteins Antagonistically Regulate Meristem Activity in the <i>Arabidopsis</i> Root Â. Plant Cell, 2011, 23, 1047-1060.	3.1	150

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19	Embryo and endosperm, partners in seed development. Current Opinion in Plant Biology, 2014, 17, 64-69.	3.5	143
20	Auxin production couples endosperm development to fertilization. Nature Plants, 2015, 1, 15184.	4.7	143
21	Interaction of the Arabidopsis Polycomb group proteins FIE and MEA mediates their common phenotypes. Current Biology, 2000, 10, 1535-1538.	1.8	142
22	Imprinting of the Polycomb Group Gene MEDEA Serves as a Ploidy Sensor in Arabidopsis. PLoS Genetics, 2009, 5, e1000663.	1.5	141
23	CHD3 Proteins and Polycomb Group Proteins Antagonistically Determine Cell Identity in Arabidopsis. PLoS Genetics, 2009, 5, e1000605.	1.5	141
24	Mechanism of <i>PHERES1</i> imprinting in <i>Arabidopsis</i>. Journal of Cell Science, 2008, 121, 906-912.	1.2	138
25	Keeping the gate closed: functions of the polycomb repressive complex <scp>PRC</scp>2 in development. Plant Journal, 2015, 83, 121-132.	2.8	133
26	Characterisation of calmodulin binding to cyclic nucleotide-gated ion channels fromArabidopsis thaliana. FEBS Letters, 2000, 471, 133-136.	1.3	127
27	Genomic imprinting and seed development: endosperm formation with and without sex. Current Opinion in Plant Biology, 2001, 4, 21-27.	3.5	127
28	An Imprinted Gene Underlies Postzygotic Reproductive Isolation in Arabidopsis thaliana. Developmental Cell, 2013, 26, 525-535.	3.1	127
29	Transposon-derived small RNAs triggered by miR845 mediate genome dosage response in Arabidopsis. Nature Genetics, 2018, 50, 186-192.	9.4	126
30	Paternal easiRNAs regulate parental genome dosage in Arabidopsis. Nature Genetics, 2018, 50, 193-198.	9.4	125
31	Parental epigenetic asymmetry of <scp>PRC</scp> 2â€mediated histone modifications in the <i>Arabidopsis</i> endosperm. EMBO Journal, 2016, 35, 1298-1311.	3.5	124
32	Auxin: a molecular trigger of seed development. Genes and Development, 2018, 32, 479-490.	2.7	124
33	The Chromodomain of LIKE HETEROCHROMATIN PROTEIN 1 Is Essential for H3K27me3 Binding and Function during Arabidopsis Development. PLoS ONE, 2009, 4, e5335.	1.1	120
34	Transcriptional Programs of Early Reproductive Stages in Arabidopsis. Plant Physiology, 2004, 135, 1765-1775.	2.3	119
35	Endospermâ€based postzygotic hybridization barriers: developmental mechanisms and evolutionary drivers. Molecular Ecology, 2016, 25, 2620-2629.	2.0	114
36	Genomic imprinting in plantsâ€”revisiting existing models. Genes and Development, 2020, 34, 24-36.	2.7	114

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37	age Mutants of Arabidopsis Exhibit Altered Auxin-Regulated Gene Expression. Plant Cell, 1998, 10, 1649-1662.	3.1	113
38	Epigenetic mechanisms governing seed development in plants. EMBO Reports, 2006, 7, 1223-1227.	2.0	103
39	Endosperm-based hybridization barriers explain the pattern of gene flow between <i>Arabidopsis lyrata</i> and <i>Arabidopsis arenosa</i> in Central Europe. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1027-E1035.	3.3	103
40	Polycomb group proteins are required to couple seed coat initiation to fertilization. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20826-20831.	3.3	101
41	Paternally expressed imprinted genes establish postzygotic hybridization barriers in Arabidopsis thaliana. ELife, 2015, 4, .	2.8	101
42	Non-reciprocal Interspecies Hybridization Barriers in the Capsella Genus Are Established in the Endosperm. PLoS Genetics, 2015, 11, e1005295.	1.5	88
43	Rapid Evolution of Genomic Imprinting in Two Species of the Brassicaceae. Plant Cell, 2016, 28, 1815-1827.	3.1	84
44	Regulation of cell identity by plant Polycomb and trithorax group proteins. Current Opinion in Genetics and Development, 2010, 20, 541-547.	1.5	83
45	Paternally expressed imprinted genes associate with hybridization barriers in Capsella. Nature Plants, 2018, 4, 352-357.	4.7	81
46	H3K36ac Is an Evolutionary Conserved Plant Histone Modification That Marks Active Genes. Plant Physiology, 2016, 170, 1566-1577.	2.3	77
47	Mechanisms and evolution of genomic imprinting in plants. Heredity, 2010, 105, 57-63.	1.2	73
48	The MADS-box transcription factor PHERES1 controls imprinting in the endosperm by binding to domesticated transposons. ELife, 2019, 8, .	2.8	73
49	Auxin regulates endosperm cellularization in <i>Arabidopsis</i>. Genes and Development, 2019, 33, 466-476.	2.7	68
50	Evolution, function, and regulation of genomic imprinting in plant seed development. Journal of Experimental Botany, 2012, 63, 4713-4722.	2.4	66
51	H2A deubiquitinases UBP12/13 are part of the Arabidopsis polycomb group protein system. Nature Plants, 2016, 2, 16126.	4.7	66
52	Epigenetic inheritance of expression states in plant development: the role of Polycomb group proteins. Current Opinion in Cell Biology, 2002, 14, 773-779.	2.6	61
53	Control of PHERES1 Imprinting in Arabidopsis by Direct Tandem Repeats. Molecular Plant, 2009, 2, 654-660.	3.9	61
54	Ectopic application of the repressive histone modification H3K9me2 establishes post-zygotic reproductive isolation in<i>Arabidopsis thaliana</i>. Genes and Development, 2017, 31, 1272-1287.	2.7	61

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55	Arabidopsis SWC4 Binds DNA and Recruits the SWR1 Complex to Modulate Histone H2A.Z Deposition at Key Regulatory Genes. Molecular Plant, 2018, 11, 815-832.	3.9	60
56	Characterization of two members (ACS1 and ACS3) of the 1-aminocyclopropane-1-carboxylate synthase gene family of Arabidopsis thaliana. Gene, 1995, 167, 17-24.	1.0	59
57	Genetic Interaction of an Origin Recognition Complex Subunit and the Polycomb Group Gene MEDEA during Seed Development[W]. Plant Cell, 2004, 16, 1035-1046.	3.1	58
58	Signalling events regulating seed coat development. Biochemical Society Transactions, 2014, 42, 358-363.	1.6	57
59	Epigenetic processes in flowering plant reproduction. Journal of Experimental Botany, 2017, 68, erw486.	2.4	57
60	Increased Maternal Genome Dosage Bypasses the Requirement of the FIS Polycomb Repressive Complex 2 in Arabidopsis Seed Development. PLoS Genetics, 2013, 9, e1003163.	1.5	56
61	Applying the INTACT method to purify endosperm nuclei and to generate parental-specific epigenome profiles. Nature Protocols, 2017, 12, 238-254.	5.5	56
62	BRR2a Affects Flowering Time via FLC Splicing. PLoS Genetics, 2016, 12, e1005924.	1.5	51
63	Role of small RNAs in epigenetic reprogramming during plant sexual reproduction. Current Opinion in Plant Biology, 2017, 36, 22-28.	3.5	51
64	Hypomethylated Pollen Bypasses the Interploidy Hybridization Barrier in<i>Arabidopsis</i>Â Â. Plant Cell, 2014, 26, 3556-3568.	3.1	49
65	Epigenetic mechanisms of postzygotic reproductive isolation in plants. Current Opinion in Plant Biology, 2015, 23, 39-44.	3.5	49
66	Identification of imprinted genes subject to parent-of-origin specific expression in Arabidopsis thaliana seeds. BMC Plant Biology, 2011, 11, 113.	1.6	46
67	Polymerase IV Plays a Crucial Role in Pollen Development in <i>Capsella</i>. Plant Cell, 2020, 32, 950-966.	3.1	46
68	Tearing down barriers: understanding the molecular mechanisms of interploidy hybridizations. Journal of Experimental Botany, 2012, 63, 6059-6067.	2.4	44
69	Polycomb group proteins function in the female gametophyte to determine seed development in plants. Development (Cambridge), 2007, 134, 3639-3648.	1.2	43
70	Sequestration of a Transposon-Derived siRNA by a Target Mimic Imprinted Gene Induces Postzygotic Reproductive Isolation in Arabidopsis. Developmental Cell, 2018, 46, 696-705.e4.	3.1	40
71	Epigenetic signatures associated with imprinted paternally expressed genes in the Arabidopsis endosperm. Genome Biology, 2019, 20, 41.	3.8	40
72	Role of H1 and DNA methylation in selective regulation of transposable elements during heat stress. New Phytologist, 2021, 229, 2238-2250.	3.5	40

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73	Plant Chromatin Immunoprecipitation. Methods in Molecular Biology, 2010, 655, 401-411.	0.4	37
74	Organelles maintain spindle position in plant meiosis. Nature Communications, 2015, 6, 6492.	5.8	37
75	Intrachromosomal excision of a hybrid Ds element induces large genomic deletions in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2969-2974.	3.3	35
76	Removal of H2Aub1 by ubiquitin-specific proteases 12 and 13 is required for stable Polycomb-mediated gene repression in Arabidopsis. Genome Biology, 2020, 21, 144.	3.8	34
77	Mobility connects: transposable elements wire new transcriptional networks by transferring transcription factor binding motifs. Biochemical Society Transactions, 2020, 48, 1005-1017.	1.6	33
78	Bridging the generation gap: communication between maternal sporophyte, female gametophyte and fertilization products. Current Opinion in Plant Biology, 2016, 29, 16-20.	3.5	28
79	Postzygotic reproductive isolation established in the endosperm: mechanisms, drivers and relevance. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200118.	1.8	28
80	Genetic basis and timing of a major mating system shift in <i>Capsella</i>. New Phytologist, 2019, 224, 505-517.	3.5	23
81	Seed Development and Genomic Imprinting in Plants. , 2005, 38, 237-262.		22
82	Endosperm-specific transcriptome analysis by applying the INTACT system. Plant Reproduction, 2019, 32, 55-61.	1.3	22
83	INT-Hi-C reveals distinct chromatin architecture in endosperm and leaf tissues of<i>Arabidopsis</i>. Nucleic Acids Research, 2021, 49, 4371-4385.	6.5	22
84	Intercellular communication in Arabidopsis thaliana pollen discovered via AHG3 transcript movement from the vegetative cell to sperm. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13378-13383.	3.3	21
85	Epigenetic mechanisms in the endosperm and their consequences for the evolution of flowering plants. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2011, 1809, 438-443.	0.9	20
86	H3K23me1 is an evolutionarily conserved histone modification associated with <scp>CG DNA</scp> methylation in Arabidopsis. Plant Journal, 2017, 90, 293-303.	2.8	19
87	SYBR Green-activated sorting of Arabidopsis pollen nuclei based on different DNA/RNA content. Plant Reproduction, 2015, 28, 61-72.	1.3	18
88	Plant epigenomicsâ€"deciphering the mechanisms of epigenetic inheritance and plasticity in plants. Genome Biology, 2017, 18, 132.	3.8	18
89	Epigenetics: The Flowers That Come In From The Cold. Current Biology, 2002, 12, R129-R131.	1.8	17
90	Hybrid seed incompatibility in Capsella is connected to chromatin condensation defects in the endosperm. PLoS Genetics, 2021, 17, e1009370.	1.5	17

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91	The miRNome function transitions from regulating developmental genes to transposable elements during pollen maturation. Plant Cell, 2022, 34, 784-801.	3.1	17
92	Evolution and function of epigenetic processes in the endosperm. Frontiers in Plant Science, 2015, 6, 130.	1.7	16
93	Bypassing reproductive barriers in hybrid seeds using chemically induced epimutagenesis. Plant Cell, 2022, 34, 989-1001.	3.1	16
94	Transgenerational phenotype aggravation in <scp>CAF</scp>â€1 mutants reveals parentâ€ofâ€origin specific epigenetic inheritance. New Phytologist, 2018, 220, 908-921.	3.5	15
95	Polycomb Repressive Complex 2 and KRYPTONITE regulate pathogen-induced programmed cell death in Arabidopsis. Plant Physiology, 2021, 185, 2003-2021.	2.3	15
96	Transgenerational effect of mutants in the RNA-directed DNA methylation pathway on the triploid block in Arabidopsis. Genome Biology, 2021, 22, 141.	3.8	13
97	Tissue-specific transposon-associated small RNAs in the gymnosperm tree, Norway spruce. BMC Genomics, 2019, 20, 997.	1.2	12
98	Polycomb Repressive Complex 2-mediated histone modification H3K27me3 is associated with embryogenic potential in Norway spruce. Journal of Experimental Botany, 2020, 71, 6366-6378.	2.4	12
99	On the origin of the widespread self-compatible allotetraploid Capsella bursa-pastoris (Brassicaceae). Heredity, 2021, 127, 124-134.	1.2	12
100	Endosperm Evolution by Duplicated and Neofunctionalized Type I MADS-Box Transcription Factors. Molecular Biology and Evolution, 2022, 39, .	3.5	12
101	age Mutants of Arabidopsis Exhibit Altered Auxin-Regulated Gene Expression. Plant Cell, 1998, 10, 1649.	3.1	11
102	Dark-Induced Senescence Causes Localized Changes in DNA Methylation. Plant Physiology, 2020, 182, 949-961.	2.3	11
103	Combinations of maternal-specific repressive epigenetic marks in the endosperm control seed dormancy. ELife, 2021, 10, .	2.8	10
104	Endosperm-Specific Chromatin Profiling by Fluorescence-Activated Nuclei Sorting and Chip-on-Chip. Methods in Molecular Biology, 2014, 1112, 105-115.	0.4	9
105	Bisulphite Sequencing of Plant Genomic DNA. Methods in Molecular Biology, 2010, 655, 433-443.	0.4	8
106	DNA-sequence-specific erasers of epigenetic memory. Nature Genetics, 2016, 48, 591-592.	9.4	8
107	H2A ubiquitination is essential for Polycomb Repressive Complex 1-mediated gene regulation in Marchantia polymorpha. Genome Biology, 2021, 22, 253.	3.8	8
108	Antagonizing Polycomb group-mediated gene repression by chromatin remodelers. Epigenetics, 2010, 5, 20-23.	1.3	6

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109	The meiotic regulator JASON utilizes alternative translation initiation sites to produce differentially localized forms. Journal of Experimental Botany, 2017, 68, 4205-4217.	2.4	6
110	Epigenetic Regulation of Seed Development. , 2007, , 309-311.		0
111	Function of Polycomb group proteins in the transition to flowering in plants. , 0, 2008, .		0
112	Role of the Mi-2 homolog PICKLE in repression of Polycomb group target genes in Arabidopsis. , 0, 2008, .		0
113	Case studies for transcriptional profiling. , 2007, 97, 87-97.		0
114	Kingdom Come. PLoS Genetics, 2020, 16, e1009178.	1.5	0