

Renate H Schmidt

List of Publications by Year in descending order

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59
papers

5,161
citations

117625

34
h-index

168389

53
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61
all docs

61
docs citations

61
times ranked

5122
citing authors

#	ARTICLE	IF	CITATIONS
1	Unlocking big data doubled the accuracy in predicting the grain yield in hybrid wheat. <i>Science Advances</i> , 2021, 7, .	10.3	22
2	Selecting Closely-Linked SNPs Based on Local Epistatic Effects for Haplotype Construction Improves Power of Association Mapping. <i>C3: Genes, Genomes, Genetics</i> , 2019, 9, 4115-4126.	1.8	17
3	Haplotype-Based Genome-Wide Prediction Models Exploit Local Epistatic Interactions Among Markers. <i>C3: Genes, Genomes, Genetics</i> , 2018, 8, 1687-1699.	1.8	50
4	Chromosome identification for the carnivorous plant <i>Genlisea margaretae</i> . <i>Chromosoma</i> , 2017, 126, 389-397.	2.2	7
5	A quantitative genetic framework highlights the role of epistatic effects for grain-yield heterosis in bread wheat. <i>Nature Genetics</i> , 2017, 49, 1741-1746.	21.4	144
6	Extracting genotype information of <i>Arabidopsis thaliana</i> recombinant inbred lines from transcript profiles established with high-density oligonucleotide arrays. <i>Plant Cell Reports</i> , 2017, 36, 1871-1881.	5.6	1
7	Tailoring high-density oligonucleotide arrays for transcript profiling of different <i>Arabidopsis thaliana</i> accessions using a sequence-based approach. <i>Plant Cell Reports</i> , 2017, 36, 1323-1332.	5.6	1
8	Genetic dissection of metabolite variation in <i>Arabidopsis</i> seeds: evidence for mQTL hotspots and a master regulatory locus of seed metabolism. <i>Journal of Experimental Botany</i> , 2017, 68, 1655-1667.	4.8	36
9	Intergenomic single nucleotide polymorphisms as a tool for bacterial artificial chromosome contig building of homoeologous <i>Brassica napus</i> regions. <i>BMC Genomics</i> , 2014, 15, 560.	2.8	0
10	Screening of a <i>Brassica napus</i> bacterial artificial chromosome library using highly parallel single nucleotide polymorphism assays. <i>BMC Genomics</i> , 2013, 14, 603.	2.8	7
11	Heterosis manifestation during early <i>Arabidopsis</i> seedling development is characterized by intermediate gene expression and enhanced metabolic activity in the hybrids. <i>Plant Journal</i> , 2012, 71, 669-683.	5.7	117
12	Perspectives on Genetics and Genomics of the Brassicaceae. , 2011, , 617-632.		5
13	Comparative Genome Analysis at the Sequence Level in the Brassicaceae. , 2011, , 171-194.		1
14	Local DNA features affect RNA-directed transcriptional gene silencing and DNA methylation. <i>Plant Journal</i> , 2008, 53, 1-10.	5.7	36
15	Epigenetic Mechanisms for Breakdown of Self-Incompatibility in Interspecific Hybrids. <i>Genetics</i> , 2007, 175, 1965-1973.	2.9	69
16	Mechanisms of chromosome number reduction in <i>Arabidopsis thaliana</i> and related Brassicaceae species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5224-5229.	7.1	360
17	Plant Genome Analysis: The State of the Art. <i>International Review of Cytology</i> , 2005, 247, 223-284.	6.2	14
18	Silencing in <i>Arabidopsis</i> T-DNA Transformants: The Predominant Role of a Gene-Specific RNA Sensing Mechanism versus Position Effects. <i>Plant Cell</i> , 2004, 16, 2561-2572.	6.6	251

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19	The Arabidopsis Genome Sequence as a Tool for Genome Analysis in Brassicaceae. A Comparison of the Arabidopsis and Capsella rubella Genomes. <i>Plant Physiology</i> , 2004, 135, 735-744.	4.8	87
20	Essential role of the V-ATPase in male gametophyte development. <i>Plant Journal</i> , 2004, 41, 117-124.	5.7	106
21	A comprehensive characterization of single-copy T-DNA insertions in the Arabidopsis thaliana genome. <i>Plant Molecular Biology</i> , 2003, 52, 161-176.	3.9	160
22	Neither inverted repeat T-DNA configurations nor arrangements of tandemly repeated transgenes are sufficient to trigger transgene silencing. <i>Plant Journal</i> , 2003, 34, 507-517.	5.7	118
23	MOR1/GEM1 has an essential role in the plant-specific cytokinetic phragmoplast. <i>Nature Cell Biology</i> , 2002, 4, 711-714.	10.3	220
24	Plant genome evolution: lessons from comparative genomics at the DNA level. <i>Plant Molecular Biology</i> , 2002, 48, 21-37.	3.9	71
25	Plant genome evolution: lessons from comparative genomics at the DNA level. , 2002, , 21-37.		6
26	Plant genome evolution: lessons from comparative genomics at the DNA level. <i>Plant Molecular Biology</i> , 2002, 48, 21-37.	3.9	33
27	Comparative Sequence Analysis Reveals Extensive Microcolinearity in the Lateral Suppressor Regions of the Tomato, Arabidopsis, and Capsella Genomes. <i>Plant Cell</i> , 2001, 13, 979.	6.6	2
28	Comparative structural genomics in the Brassicaceae family. <i>Plant Physiology and Biochemistry</i> , 2001, 39, 253-262.	5.8	93
29	Comparative Sequence Analysis Reveals Extensive Microcolinearity in the Lateral Suppressor Regions of the Tomato, Arabidopsis, and Capsella Genomes. <i>Plant Cell</i> , 2001, 13, 979-988.	6.6	116
30	Comparative genome analysis reveals extensive conservation of genome organisation for Arabidopsis thaliana and Capsella rubella. <i>Plant Journal</i> , 2000, 23, 55-62.	5.7	86
31	Synten: recent advances and future prospects. <i>Current Opinion in Plant Biology</i> , 2000, 3, 97-102.	7.1	82
32	TOM1, an Arabidopsis gene required for efficient multiplication of a tobamovirus, encodes a putative transmembrane protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 10107-10112.	7.1	176
33	The arabinose kinase, ARA1, gene of Arabidopsis is a novel member of the galactose kinase gene family. <i>Plant Molecular Biology</i> , 1999, 39, 1003-1012.	3.9	40
34	Physical mapping of the Arabidopsis thaliana genome. <i>Plant Physiology and Biochemistry</i> , 1998, 36, 1-8.	5.8	6
35	The Arabidopsis downy mildew resistance gene RPP5 shares similarity to the toll and interleukin-1 receptors with N and L6.. <i>Plant Cell</i> , 1997, 9, 879-894.	6.6	434
36	FCA, a Gene Controlling Flowering Time in Arabidopsis, Encodes a Protein Containing RNA-Binding Domains. <i>Cell</i> , 1997, 89, 737-745.	28.9	480

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37	A Novel Zinc Finger Protein Is Encoded by the Arabidopsis LSD1 Gene and Functions as a Negative Regulator of Plant Cell Death. <i>Cell</i> , 1997, 88, 685-694.	28.9	452
38	Identification of mutants in metabolically regulated gene expression. <i>Plant Journal</i> , 1997, 11, 53-62.	5.7	114
39	Description of 31 YAC contigs spanning the majority of Arabidopsis thaliana chromosome 5. <i>Plant Journal</i> , 1997, 11, 563-572.	5.7	70
40	A novel repetitive sequence associated with the centromeric regions of Arabidopsis thaliana chromosomes. <i>Molecular Genetics and Genomics</i> , 1996, 253, 247-252.	2.4	36
41	Detailed description of four YAC contigs representing 17 Mb of chromosome 4 of Arabidopsis thaliana ecotype Columbia. <i>Plant Journal</i> , 1996, 9, 755-765.	5.7	53
42	Analysis of the occurrence and nature of repeated DNA in an 850 kb region of Arabidopsis thaliana chromosome 4. <i>Plant Molecular Biology</i> , 1996, 32, 553-557.	3.9	10
43	Identification and distribution of seven classes of middle-repetitive DNA in the Arabidopsis thaliana genome. <i>Nucleic Acids Research</i> , 1996, 24, 3017-3022.	14.5	51
44	Physical Mapping of the Arabidopsis thaliana Genome. <i>Stadler Genetics Symposia Series</i> , 1996, , 73-86.	0.0	1
45	Arabidopsis Phosphoribosylanthranilate Isomerase: Molecular Genetic Analysis of Triplicate Tryptophan Pathway Genes. <i>Plant Cell</i> , 1995, 7, 447.	6.6	13
46	Plant Genomes: A Current Molecular Description. <i>Annual Review of Plant Biology</i> , 1995, 46, 395-418.	14.3	50
47	Physical Map and Organization of Arabidopsis thaliana Chromosome 4. <i>Science</i> , 1995, 270, 480-483.	12.6	230
48	Easy determination of ploidy level in Arabidopsis thaliana plants by means of pollen size measurement. <i>Plant Cell Reports</i> , 1994, 13, 652-6.	5.6	46
49	Analysis of clones carrying repeated DNA sequences in two YAC libraries of Arabidopsis thaliana DNA. <i>Plant Journal</i> , 1994, 5, 735-744.	5.7	34
50	Genes and genomes: Towards construction of an overlapping YAC library of the Arabidopsis thaliana genome. <i>BioEssays</i> , 1993, 15, 63-69.	2.5	10
51	PFGE-resolved RFLP analysis and long range restriction mapping of the DNA of Arabidopsis thaliana using whole YAC clones as probes. <i>Nucleic Acids Research</i> , 1992, 20, 6201-6207.	14.5	19
52	Non-destructive assay systems for detection of β -glucuronidase activity in higher plants. <i>Plant Molecular Biology Reporter</i> , 1992, 10, 37-46.	1.8	29
53	Construction of an Overlapping YAC Library of the Arabidopsis thaliana Genome. <i>Functional Plant Biology</i> , 1992, 19, 341.	2.1	9
54	Identification and map position of YAC clones comprising one-third of the Arabidopsis genome.. <i>Plant Journal</i> , 1991, 1, 367-374.	5.7	64

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55	Arabidopsis Regeneration and Transformation (Leaf & Cotyledon Explant System). , 1991, , 97-113.		3
56	Efficient transformation of Arabidopsis thaliana using direct gene transfer to protoplasts. Molecular Genetics and Genomics, 1989, 217, 6-12.	2.4	138
57	The maize autonomous element Activator (Ac) shows a minimal germinal excision frequency of 0.2%â€”0.5% in transgenic Arabidopsis thaliana plants. Molecular Genetics and Genomics, 1989, 220, 17-24.	2.4	64
58	High efficiency Agrobacterium tumefaciens-mediated transformation of Arabidopsis thaliana leaf and cotyledon explants. Plant Cell Reports, 1988, 7, 583-586.	5.6	109
59	Isolation and characterization of a gene from Solanum tuberosum encoding patatin, the major storage protein of potato tubers. Molecular Genetics and Genomics, 1986, 203, 214-220.	2.4	101