

# Kai Wang

## List of Publications by Year in descending order

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72  
papers

16,047  
citations

159525

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85498

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76  
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76  
docs citations

76  
times ranked

36664  
citing authors

#	ARTICLE	IF	CITATIONS
1	A comprehensive molecular cytogenetic analysis of the genome architecture in modern sugarcane cultivars. <i>Chromosome Research</i> , 2022, 30, 29-41.	1.0	7
2	Genome-wide identification and characterization of the CLASP_N gene family in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>PeerJ</i> , 2022, 10, e12733.	0.9	2
3	Genome-wide analysis reveals the spatiotemporal expression patterns of SOS3 genes in the maize B73 genome in response to salt stress. <i>BMC Genomics</i> , 2022, 23, 60.	1.2	2
4	Characterization of Repetitive DNA in <i>Saccharum officinarum</i> and <i>Saccharum spontaneum</i> by Genome Sequencing and Cytological Assays. <i>Frontiers in Plant Science</i> , 2022, 13, 814620.	1.7	1
5	Genome-wide identification and analysis of the GUB_WAK_bind gene family in <i>Gossypium hirsutum</i> . <i>Molecular Biology Reports</i> , 2022, , 1.	1.0	0
6	The genome and gene editing system of sea barleygrass provide a novel platform for cereal domestication and stress tolerance studies. <i>Plant Communications</i> , 2022, 3, 100333.	3.6	8
7	Brachypodium: 20 years as a grass biology model system; the way forward?. <i>Trends in Plant Science</i> , 2022, 27, 1002-1016.	4.3	21
8	Genome sequence of <i>Gossypium anomalum</i> facilitates interspecific introgression breeding. <i>Plant Communications</i> , 2022, 3, 100350.	3.6	14
9	Optimization of protoplast isolation, transformation and its application in sugarcane ( <i>Saccharum</i> ) Tj ETQq1 1 0.784314 rgBT/Overlo	2.3	32
10	Considerations regarding centromere assembly in plant whole-genome sequencing. <i>Methods</i> , 2021, 187, 54-56.	1.9	5
11	The formation and evolution of centromeric satellite repeats in <i>Saccharum</i> species. <i>Plant Journal</i> , 2021, 106, 616-629.	2.8	24
12	Genome-wide Identification of DNase I Hypersensitive Sites in Plants. <i>Current Protocols</i> , 2021, 1, e148.	1.3	4
13	Transcriptome analysis reveals genes potentially related to high fiber strength in a <i>Gossypium hirsutum</i> line IL9 with <i>Gossypium mustelinum</i> introgression. <i>Genome</i> , 2021, 64, 985-995.	0.9	3
14	Chromosome Painting Provides Insights Into the Genome Structure and Evolution of Sugarcane. <i>Frontiers in Plant Science</i> , 2021, 12, 731664.	1.7	13
15	Megabase-scale presence-absence variation with <i>Tripsacum</i> origin was under selection during maize domestication and adaptation. <i>Genome Biology</i> , 2021, 22, 237.	3.8	21
16	<i>Verticillium dahliae</i> effector VDAL protects MYB6 from degradation by interacting with PUB25 and PUB26 E3 ligases to enhance <i>Verticillium</i> wilt resistance. <i>Plant Cell</i> , 2021, 33, 3675-3699.	3.1	39
17	Characterization of a <i>Saccharum spontaneum</i> with a basic chromosome number of $x=10$ provides new insights on genome evolution in genus <i>Saccharum</i> . <i>Theoretical and Applied Genetics</i> , 2020, 133, 187-199.	1.8	42
18	Species-specific abundant retrotransposons elucidate the genomic composition of modern sugarcane cultivars. <i>Chromosoma</i> , 2020, 129, 45-55.	1.0	12

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19	The water lily genome and the early evolution of flowering plants. <i>Nature</i> , 2020, 577, 79-84.	13.7	238
20	Progressive refinement of the karyotyping of <i>Brachypodium</i> genomes. <i>New Phytologist</i> , 2020, 227, 1668-1675.	3.5	8
21	Genome-Wide Characterization of DNase I-Hypersensitive Sites and Cold Response Regulatory Landscapes in Grasses. <i>Plant Cell</i> , 2020, 32, 2457-2473.	3.1	29
22	<i>Arabidopsis thaliana</i> trehalose-6-phosphate phosphatase gene TPPI enhances drought tolerance by regulating stomatal apertures. <i>Journal of Experimental Botany</i> , 2020, 71, 4285-4297.	2.4	55
23	Horizontal gene transfer of <i>Fhb7</i> from fungus underlies <i>Fusarium</i> head blight resistance in wheat. <i>Science</i> , 2020, 368, .	6.0	398
24	Genome-Wide Identification of Regulatory DNA Elements in Crop Plants. <i>Methods in Molecular Biology</i> , 2020, 2072, 85-99.	0.4	1
25	The wild sweetpotato ( <i>Ipomoea trifida</i> ) genome provides insights into storage root development. <i>BMC Plant Biology</i> , 2019, 19, 119.	1.6	33
26	Optimization of Mature Embryo-Based Tissue Culture and <i>Agrobacterium</i> -Mediated Transformation in Model Grass <i>Brachypodium distachyon</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 5448.	1.8	7
27	Overexpression of the trehalose-6-phosphate phosphatase family gene <i>AtTPPF</i> improves the drought tolerance of <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2019, 19, 381.	1.6	70
28	Genome-Wide Identification, Evolution, and Expression Analysis of TPS and TPP Gene Families in <i>Brachypodium distachyon</i> . <i>Plants</i> , 2019, 8, 362.	1.6	13
29	Centromere histone H3- and phospholipase-mediated haploid induction in plants. <i>Plant Methods</i> , 2019, 15, 42.	1.9	29
30	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. <i>Nature Genetics</i> , 2019, 51, 739-748.	9.4	568
31	Genome-wide selection footprints and deleterious variations in young Asian allotetraploid rapeseed. <i>Plant Biotechnology Journal</i> , 2019, 17, 1998-2010.	4.1	54
32	Centromeric DNA characterization in the model grass <i>Brachypodium distachyon</i> provides insights on the evolution of the genus. <i>Plant Journal</i> , 2018, 93, 1088-1101.	2.8	28
33	3C and 3C-based techniques: the powerful tools for spatial genome organization deciphering. <i>Molecular Cytogenetics</i> , 2018, 11, 21.	0.4	61
34	New insights into the evolution and functional divergence of the SWEET family in <i>Saccharum</i> based on comparative genomics. <i>BMC Plant Biology</i> , 2018, 18, 270.	1.6	42
35	Comprehensively Characterizing the Cytological Features of <i>Saccharum spontaneum</i> by the Development of a Complete Set of Chromosome-Specific Oligo Probes. <i>Frontiers in Plant Science</i> , 2018, 9, 1624.	1.7	42
36	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	9.4	463

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37	Comparative Analysis of Homologous Sequences of <i>Saccharum officinarum</i> and <i>Saccharum spontaneum</i> Reveals Independent Polyploidization Events. <i>Frontiers in Plant Science</i> , 2018, 9, 1414.	1.7	3
38	Development and Applications of Chromosome-Specific Cytogenetic BAC-FISH Probes in <i>S. spontaneum</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 218.	1.7	23
39	Global Involvement of Lysine Crotonylation in Protein Modification and Transcription Regulation in Rice. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1922-1936.	2.5	62
40	Isolation and characterization of centromeric repetitive DNA sequences in <i>Saccharum spontaneum</i> . <i>Scientific Reports</i> , 2017, 7, 41659.	1.6	31
41	The <i>Aegilops tauschii</i> genome reveals multiple impacts of transposons. <i>Nature Plants</i> , 2017, 3, 946-955.	4.7	164
42	Chromosome Nomenclature and Cytological Characterization of Sacred Lotus. <i>Cytogenetic and Genome Research</i> , 2017, 153, 223-231.	0.6	12
43	Chromatin states responsible for the regulation of differentially expressed genes under $60\text{Co-}\gamma$ radiation in rice. <i>BMC Genomics</i> , 2017, 18, 778.	1.2	12
44	Chromosome Preparation in Rice ( <i>Oryza sativa</i> ). <i>Current Protocols in Plant Biology</i> , 2016, 1, 67-77.	2.8	4
45	Rapid proliferation and nucleolar organizer targeting centromeric retrotransposons in cotton. <i>Plant Journal</i> , 2016, 88, 992-1005.	2.8	33
46	In Situ Hybridization in Rice ( <i>Oryza sativa</i> ). <i>Current Protocols in Plant Biology</i> , 2016, 1, 89-106.	2.8	2
47	Comprehensive cytological characterization of the <i>Gossypium hirsutum</i> genome based on the development of a set of chromosome cytological markers. <i>Crop Journal</i> , 2016, 4, 256-265.	2.3	7
48	Gene Expression and Chromatin Modifications Associated with Maize Centromeres. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 183-192.	0.8	30
49	A and D genomes spatial separation at somatic metaphase in tetraploid cotton: evidence for genomic disposition in a polyploid plant. <i>Plant Journal</i> , 2015, 84, 1167-1177.	2.8	13
50	Stable Patterns of CENH3 Occupancy Through Maize Lineages Containing Genetically Similar Centromeres. <i>Genetics</i> , 2015, 200, 1105-1116.	1.2	20
51	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
52	Distinct Copy Number, Coding Sequence, and Locus Methylation Patterns Underlie Rhg1-Mediated Soybean Resistance to Soybean Cyst Nematode. <i>Plant Physiology</i> , 2014, 165, 630-647.	2.3	136
53	Maize centromeres expand and adopt a uniform size in the genetic background of oat. <i>Genome Research</i> , 2014, 24, 107-116.	2.4	77
54	Construction of a complete set of alien chromosome addition lines from <i>Gossypium australe</i> in <i>Gossypium hirsutum</i> : morphological, cytological, and genotypic characterization. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1105-1121.	1.8	34

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55	Identification of centromeric regions on the linkage map of cotton using centromere-related repeats. <i>Genomics</i> , 2014, 104, 587-593.	1.3	15
56	Boom-Bust Turnovers of Megabase-Sized Centromeric DNA in <i>Solanum</i> Species: Rapid Evolution of DNA Sequences Associated with Centromeres. <i>Plant Cell</i> , 2014, 26, 1436-1447.	3.1	73
57	Systematic Application of DNA Fiber-FISH Technique in Cotton. <i>PLoS ONE</i> , 2013, 8, e75674.	1.1	25
58	Repeatless and Repeat-Based Centromeres in Potato: Implications for Centromere Evolution. <i>Plant Cell</i> , 2012, 24, 3559-3574.	3.1	221
59	Copy Number Variation of Multiple Genes at <i>Rhg1</i> Mediates Nematode Resistance in Soybean. <i>Science</i> , 2012, 338, 1206-1209.	6.0	535
60	Localization of high level of sequence conservation and divergence regions in cotton. <i>Theoretical and Applied Genetics</i> , 2012, 124, 1173-1182.	1.8	11
61	Stable integration of an engineered megabase repeat array into the maize genome. <i>Plant Journal</i> , 2012, 70, 357-365.	2.8	17
62	Structure and size variations between 12A and 12D homoeologous chromosomes based on high-resolution cytogenetic map in allotetraploid cotton. <i>Chromosoma</i> , 2010, 119, 255-266.	1.0	32
63	ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2010, 38, e164-e164.	6.5	10,960
64	Higher axial-resolution and sensitivity pachytene fluorescence in situ hybridization protocol in tetraploid cotton. <i>Chromosome Research</i> , 2009, 17, 1041-1050.	1.0	15
65	Establishment of a Multi-color Genomic <i>in situ</i> Hybridization Technique to Simultaneously Discriminate the Three Interspecific Hybrid Genomes in <i>Gossypium</i> . <i>Journal of Integrative Plant Biology</i> , 2008, 50, 345-351.	4.1	10
66	Completely Distinguishing Individual A-Genome Chromosomes and Their Karyotyping Analysis by Multiple Bacterial Artificial Chromosome Fluorescence <i>in Situ</i> Hybridization. <i>Genetics</i> , 2008, 178, 1117-1122.	1.2	39
67	A Microsatellite-Based, Gene-Rich Linkage Map Reveals Genome Structure, Function and Evolution in <i>Gossypium</i> . <i>Genetics</i> , 2007, 176, 527-541.	1.2	265
68	Detection and mapping of homologous and homoeologous segments in homoeologous groups of allotetraploid cotton by BAC-FISH. <i>BMC Genomics</i> , 2007, 8, 178.	1.2	24
69	Development of one set of chromosome-specific microsatellite-containing BACs and their physical mapping in <i>Gossypium hirsutum</i> L. <i>Theoretical and Applied Genetics</i> , 2007, 115, 675-682.	1.8	48
70	Complete assignment of the chromosomes of <i>Gossypium hirsutum</i> L. by translocation and fluorescence in situ hybridization mapping. <i>Theoretical and Applied Genetics</i> , 2006, 113, 73-80.	1.8	147
71	A comparison of genetic maps constructed from haploid and BC1 mapping populations from the same crossing between <i>Gossypium hirsutum</i> L. and <i>Gossypium barbadense</i> L. <i>Genome</i> , 2005, 48, 378-390.	0.9	75
72	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. , 0, .		1