

# Kai Wang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2909366/publications.pdf>

Version: 2024-02-01

72  
papers

16,047  
citations

159358

30  
h-index

85405

71  
g-index

76  
all docs

76  
docs citations

76  
times ranked

36664  
citing authors

#	ARTICLE	IF	CITATIONS
1	ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2010, 38, e164-e164.	6.5	10,960
2	<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
3	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
4	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
5	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	9.4	463
6	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
7	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
8	The water lily genome and the early evolution of flowering plants. <i>Nature</i> , 2020, 577, 79-84.	13.7	238
9	Repeatless and Repeat-Based Centromeres in Potato: Implications for Centromere Evolution. <i>Plant Cell</i> , 2012, 24, 3559-3574.	3.1	221
10	The <i>Aegilops tauschii</i> genome reveals multiple impacts of transposons. <i>Nature Plants</i> , 2017, 3, 946-955.	4.7	164
11	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
12	Distinct Copy Number, Coding Sequence, and Locus Methylation Patterns Underlie <i>Rhg1</i> -Mediated Soybean Resistance to Soybean Cyst Nematode. <i>Plant Physiology</i> , 2014, 165, 630-647.	2.3	136
13	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
14	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
15	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
16	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
17	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
18	3C and 3C-based techniques: the powerful tools for spatial genome organization deciphering. <i>Molecular Cytogenetics</i> , 2018, 11, 21.	0.4	61

#	ARTICLE	IF	CITATIONS
19	Arabidopsis thaliana 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
20	Genome-wide selection footprints and deleterious variations in young Asian allotetraploid rapeseed. <i>Plant Biotechnology Journal</i> , 2019, 17, 1998-2010.	4.1	54
21	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
22	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
23	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
24	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
25	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
26	<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
27	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
28	Rapid proliferation and nucleolar organizer targeting centromeric retrotransposons in cotton. <i>Plant Journal</i> , 2016, 88, 992-1005.	2.8	33
29	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
30	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
31	Optimization of protoplast isolation, transformation and its application in sugarcane ( <i>Saccharum</i> ) Tj ETQq1 1 0.784314 rgBT/Overlo	2.3	32
32	Isolation and characterization of centromeric repetitive DNA sequences in <i>Saccharum spontaneum</i> . <i>Scientific Reports</i> , 2017, 7, 41659.	1.6	31
33	Gene Expression and Chromatin Modifications Associated with Maize Centromeres. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 183-192.	0.8	30
34	Centromere histone H3- and phospholipase-mediated haploid induction in plants. <i>Plant Methods</i> , 2019, 15, 42.	1.9	29
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	Systematic Application of DNA Fiber-FISH Technique in Cotton. PLoS ONE, 2013, 8, e75674.	1.1	25
38	Detection and mapping of homologous and homoeologous segments in homoeologous groups of allotetraploid cotton by BAC-FISH. BMC Genomics, 2007, 8, 178.	1.2	24
39	The formation and evolution of centromeric satellite repeats in <i>Saccharum</i> species. Plant Journal, 2021, 106, 616-629.	2.8	24
40	Development and Applications of Chromosome-Specific Cytogenetic BAC-FISH Probes in <i>S. spontaneum</i> . Frontiers in Plant Science, 2018, 9, 218.	1.7	23
41	Megabase-scale presence-absence variation with <i>Tripsacum</i> origin was under selection during maize domestication and adaptation. Genome Biology, 2021, 22, 237.	3.8	21
42	Brachypodium: 20 years as a grass biology model system; the way forward?. Trends in Plant Science, 2022, 27, 1002-1016.	4.3	21
43	Stable Patterns of CENH3 Occupancy Through Maize Lineages Containing Genetically Similar Centromeres. Genetics, 2015, 200, 1105-1116.	1.2	20
44	Stable integration of an engineered megabase repeat array into the maize genome. Plant Journal, 2012, 70, 357-365.	2.8	17
45	Higher axial-resolution and sensitivity pachytene fluorescence in situ hybridization protocol in tetraploid cotton. Chromosome Research, 2009, 17, 1041-1050.	1.0	15
46	Identification of centromeric regions on the linkage map of cotton using centromere-related repeats. Genomics, 2014, 104, 587-593.	1.3	15
47	Genome sequence of <i>Gossypium anomalum</i> facilitates interspecific introgression breeding. Plant Communications, 2022, 3, 100350.	3.6	14
48	A and D genomes spatial separation at somatic metaphase in tetraploid cotton: evidence for genomic disposition in a polyploid plant. Plant Journal, 2015, 84, 1167-1177.	2.8	13
49	Genome-Wide Identification, Evolution, and Expression Analysis of TPS and TPP Gene Families in <i>Brachypodium distachyon</i> . Plants, 2019, 8, 362.	1.6	13
50	Chromosome Painting Provides Insights Into the Genome Structure and Evolution of Sugarcane. Frontiers in Plant Science, 2021, 12, 731664.	1.7	13
51	Chromosome Nomenclature and Cytological Characterization of Sacred Lotus. Cytogenetic and Genome Research, 2017, 153, 223-231.	0.6	12
52	Chromatin states responsible for the regulation of differentially expressed genes under $60\text{Co-}\gamma$ radiation in rice. BMC Genomics, 2017, 18, 778.	1.2	12
53	Species-specific abundant retrotransposons elucidate the genomic composition of modern sugarcane cultivars. Chromosoma, 2020, 129, 45-55.	1.0	12
54	Localization of high level of sequence conservation and divergence regions in cotton. Theoretical and Applied Genetics, 2012, 124, 1173-1182.	1.8	11

#	ARTICLE	IF	CITATIONS
55	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
56	Progressive refinement of the karyotyping of <i>Brachypodium</i> genomes. <i>New Phytologist</i> , 2020, 227, 1668-1675.	3.5	8
57	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
58	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
59	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
60	A comprehensive molecular cytogenetic analysis of the genome architecture in modern sugarcane cultivars. <i>Chromosome Research</i> , 2022, 30, 29-41.	1.0	7
61	Considerations regarding centromere assembly in plant whole-genome sequencing. <i>Methods</i> , 2021, 187, 54-56.	1.9	5
62	Chromosome Preparation in Rice ( <i>Oryza sativa</i> ). <i>Current Protocols in Plant Biology</i> , 2016, 1, 67-77.	2.8	4
63	Genome-Wide Identification of DNase I Hypersensitive Sites in Plants. <i>Current Protocols</i> , 2021, 1, e148.	1.3	4
64	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
65	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
66	In Situ Hybridization in Rice ( <i>Oryza sativa</i> ). <i>Current Protocols in Plant Biology</i> , 2016, 1, 89-106.	2.8	2
67	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
68	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
69	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. , 0, .		1
70	Genome-Wide Identification of Regulatory DNA Elements in Crop Plants. <i>Methods in Molecular Biology</i> , 2020, 2072, 85-99.	0.4	1
71	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
72	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