

# Wencai Yang

## List of Publications by Year in descending order

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57  
papers

1,754  
citations

279798

23  
h-index

302126

39  
g-index

60  
all docs

60  
docs citations

60  
times ranked

2142  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping of CaPP2C35 involved in the formation of light-green immature pepper ( <i>Capsicum annuum</i> L.) fruits via GWAS and BSA. <i>Theoretical and Applied Genetics</i> , 2022, 135, 591-604.	3.6	8
2	Advances in the Characterization of the Mechanism Underlying Bacterial Canker Development and Tomato Plant Resistance. <i>Horticulturae</i> , 2022, 8, 209.	2.8	7
3	Mapping and characterization of the Rx3 gene for resistance to <i>Xanthomonas euvesicatoria</i> pv. <i>euvesicatoria</i> race T1 in tomato. <i>Theoretical and Applied Genetics</i> , 2022, , 1.	3.6	1
4	Loci underlying leaf agronomic traits identified by re-sequencing celery accessions based on an assembled genome. <i>IScience</i> , 2022, 25, 104565.	4.1	6
5	Tomato protein Rx4 mediates the hypersensitive response to <i>Xanthomonas euvesicatoria</i> pv. <i>perforans</i> race T3. <i>Plant Journal</i> , 2021, 105, 1630-1644.	5.7	9
6	Tomato SIPUB24 enhances resistance to <i>Xanthomonas euvesicatoria</i> pv. <i>perforans</i> race T3. <i>Horticulture Research</i> , 2021, 8, 30.	6.3	9
7	Auxin Metabolism Is Involved in Fruit Set and Early Fruit Development in the Parthenocarpic Tomato <i>âœR35-Pâ€</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 671713.	3.6	11
8	A high-continuity and annotated tomato reference genome. <i>BMC Genomics</i> , 2021, 22, 898.	2.8	21
9	SLGID1a Is a Putative Candidate Gene for qtph1.1, a Major-Effect Quantitative Trait Locus Controlling Tomato Plant Height. <i>Frontiers in Genetics</i> , 2020, 11, 881.	2.3	5
10	Transcription of lncRNA <i>ACoS-AS1</i> is essential to <i>trans</i> -splicing between <i>SIPsy1</i> and <i>ACoS-AS1</i> that causes yellow fruit in tomato. <i>RNA Biology</i> , 2020, 17, 596-607.	3.1	14
11	Marker-assisted development and characterization of near-isogenic lines carrying the Rx4 gene for hypersensitive resistance to <i>Xanthomonas euvesicatoria</i> pv. <i>perforans</i> race T3 in tomato. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	6
12	Fine mapping and molecular marker development of the Sm gene conferring resistance to gray leaf spot ( <i>Stemphylium</i> spp.) in tomato. <i>Theoretical and Applied Genetics</i> , 2019, 132, 871-882.	3.6	24
13	Breeding for Resistance to Tomato Bacterial Diseases in China: Challenges and Prospects. <i>Horticultural Plant Journal</i> , 2018, 4, 193-207.	5.0	46
14	Analysis and fine mapping of a gene controlling the folded-leaf phenotype of a mutant tomato line. <i>Euphytica</i> , 2018, 214, 1.	1.2	3
15	The Aborted Microspores (AMS)-Like Gene Is Required for Anther and Microspore Development in Pepper ( <i>Capsicum annuum</i> L.). <i>International Journal of Molecular Sciences</i> , 2018, 19, 1341.	4.1	23
16	Improved <i>Brassica rapa</i> reference genome by single-molecule sequencing and chromosome conformation capture technologies. <i>Horticulture Research</i> , 2018, 5, 50.	6.3	224
17	Identification of candidate genes underlying genic male-sterile <i>msc-1</i> locus via genome resequencing in <i>Capsicum annuum</i> L.. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1861-1872.	3.6	26
18	Proteomic analysis reveals strong mitochondrial involvement in cytoplasmic male sterility of pepper ( <i>Capsicum annuum</i> L.). <i>Journal of Proteomics</i> , 2017, 14, 107-117.	2.4	33

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19	Genetic and fruit trait differences between Chinese elite lines/varieties and American varieties of processing tomato. <i>Scientia Horticulturae</i> , 2017, 224, 251-257.	3.6	3
20	Genetic diversity among ‘Qamgur’ varieties in China revealed by SSR markers. <i>Euphytica</i> , 2017, 213, 1.	1.2	5
21	Association and Genetic Identification of Loci for Four Fruit Traits in Tomato Using InDel Markers. <i>Frontiers in Plant Science</i> , 2017, 8, 1269.	3.6	23
22	Enriching Glucoraphanin in <i>Brassica rapa</i> Through Replacement of BrAOP2.2/BrAOP2.3 with Non-functional Genes. <i>Frontiers in Plant Science</i> , 2017, 8, 1329.	3.6	13
23	Molecular mapping of a gene conferring resistance to <i>Phytophthora capsici</i> Leonian race 2 in pepper line PI201234 ( <i>Capsicum annuum</i> L.). <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	23
24	Association Analysis for Bacterial Spot Resistance in a Directionally Selected Complex Breeding Population of Tomato. <i>Phytopathology</i> , 2015, 105, 1437-1445.	2.2	27
25	Impacts of Whole-Genome Triplication on <i>MIRNA</i> Evolution in <i>Brassica rapa</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 3085-3096.	2.5	18
26	Comparative Transcriptome Analysis of Cultivated and Wild Watermelon during Fruit Development. <i>PLoS ONE</i> , 2015, 10, e0130267.	2.5	106
27	Comparative Transcriptome Analysis of Resistant and Susceptible Tomato Lines in Response to Infection by <i>Xanthomonas perforans</i> Race T3. <i>Frontiers in Plant Science</i> , 2015, 6, 1173.	3.6	60
28	Lineage-specific evolution of Methylthioalkylmalate synthases (MAMs) involved in glucosinolates biosynthesis. <i>Frontiers in Plant Science</i> , 2015, 6, 18.	3.6	18
29	Development and validation of a standard area diagram set to aid estimation of bacterial spot severity on tomato leaves. <i>European Journal of Plant Pathology</i> , 2015, 142, 665-675.	1.7	12
30	Transcriptomic analysis reveals the roles of microtubule-related genes and transcription factors in fruit length regulation in cucumber ( <i>Cucumis sativus</i> L.). <i>Scientific Reports</i> , 2015, 5, 8031.	3.3	89
31	Identification of Genes Differentially Expressed between Resistant and Susceptible Tomato Lines during Time-Course Interactions with <i>Xanthomonas perforans</i> Race T3. <i>PLoS ONE</i> , 2014, 9, e93476.	2.5	11
32	A comparison of disease severity measurements using image analysis and visual estimates using a category scale for genetic analysis of resistance to bacterial spot in tomato. <i>European Journal of Plant Pathology</i> , 2014, 139, 125-136.	1.7	20
33	Identification and Analysis of Resistance-like Genes in the Tomato Genome. <i>Journal of Phytopathology</i> , 2014, 162, 137-146.	1.0	7
34	A chimeric transcript containing <i>Psy1</i> and a potential mRNA is associated with yellow flesh color in tomato accession PI 114490. <i>Planta</i> , 2014, 240, 1011-1021.	3.2	27
35	In Silico Identification and Experimental Validation of Insertion-Deletion Polymorphisms in Tomato Genome. <i>DNA Research</i> , 2014, 21, 429-438.	3.4	63
36	Mapping of a Heat-Stable Gene for Resistance to Southern Root-Knot Nematode in <i>Solanum lycopersicum</i> . <i>Plant Molecular Biology Reporter</i> , 2013, 31, 352-362.	1.8	15

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37	Identification of Single-Copy Orthologous Genes between <i>Physalis</i> and <i>Solanum lycopersicum</i> and Analysis of Genetic Diversity in <i>Physalis</i> Using Molecular Markers. <i>PLoS ONE</i> , 2012, 7, e50164.	2.5	27
38	Inheritance of white petiole in celery and development of a tightly linked SCAR marker. <i>Plant Breeding</i> , 2012, 131, 340-344.	1.9	4
39	Fine mapping and analysis of a candidate gene in tomato accession PI128216 conferring hypersensitive resistance to bacterial spot race T3. <i>Theoretical and Applied Genetics</i> , 2012, 124, 533-542.	3.6	43
40	Mapping and linkage disequilibrium analysis with a genome-wide collection of SNPs that detect polymorphism in cultivated tomato. <i>Journal of Experimental Botany</i> , 2011, 62, 1831-1845.	4.8	68
41	Genetic diversity in <i>Apium graveolens</i> and related species revealed by SRAP and SSR markers. <i>Scientia Horticulturae</i> , 2011, 129, 1-8.	3.6	21
42	Natural Variation of Pto and Fen Genes and Marker-Assisted Selection for Resistance to Bacterial Speck in Tomato. <i>Agricultural Sciences in China</i> , 2011, 10, 827-837.	0.6	5
43	Molecular Mapping of Hypersensitive Resistance from Tomato 'Hawaii 7981' to <i>Xanthomonas perforans</i> Race T3. <i>Phytopathology</i> , 2011, 101, 1217-1223.	2.2	30
44	Discovery of intron polymorphisms in cultivated tomato using both tomato and <i>Arabidopsis</i> genomic information. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1199-1207.	3.6	31
45	Identification of QTL associated with resistance to bacterial spot race T4 in tomato. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1275-1287.	3.6	39
46	A Snapshot of the Emerging Tomato Genome Sequence. <i>Plant Genome</i> , 2009, 2, .	2.8	73
47	Genetic variation in tomato populations from four breeding programs revealed by single nucleotide polymorphism and simple sequence repeat markers. <i>Scientia Horticulturae</i> , 2009, 122, 6-16.	3.6	29
48	Sources for Heat-Stable Resistance to Southern Root-Knot Nematode ( <i>Meloidogyne incognita</i> ) in <i>Solanum lycopersicum</i> . <i>Agricultural Sciences in China</i> , 2009, 8, 697-702.	0.6	9
49	Genetics of flesh color and nucleotide sequence analysis of phytoene synthase gene 1 in a yellow-fruited tomato accession PI114490. <i>Scientia Horticulturae</i> , 2008, 118, 20-24.	3.6	20
50	Tomato. , 2007, , 1-125.		14
51	Genetics and Breeding for Resistance to Bacterial Diseases in Tomato. , 2006, , 379-419.		9
52	Genetics of female mate discrimination of heterospecific males in <i>Nasonia</i> (Hymenoptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 Td	1.9	32
53	Resistance in <i>Lycopersicon esculentum</i> Intraspecific Crosses to Race T1 Strains of <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> Causing Bacterial Spot of Tomato. <i>Phytopathology</i> , 2005, 95, 519-527.	2.2	71
54	Marker-assisted Selection for Combining Resistance to Bacterial Spot and Bacterial Speck in Tomato. <i>Journal of the American Society for Horticultural Science</i> , 2005, 130, 716-721.	1.0	56

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55	Discovery of single nucleotide polymorphisms in <i>Lycopersicon esculentum</i> by computer aided analysis of expressed sequence tags. <i>Molecular Breeding</i> , 2004, 14, 21-34.	2.1	101
56	Improved Tomato Fruit Color within an Inbred Backcross Line Derived from <i>Lycopersicon esculentum</i> and <i>L. hirsutum</i> Involves the Interaction of Loci. <i>Journal of the American Society for Horticultural Science</i> , 2004, 129, 250-257.	1.0	43
57	Resistance to Frogeye Leaf Spot in Maturity Groups VI and VII of Soybean Germplasm. <i>Crop Science</i> , 2001, 41, 549-552.	1.8	9