

Tongming Yin

List of Publications by Year in descending order

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103
papers

3,026
citations

186209

28
h-index

197736

49
g-index

110
all docs

110
docs citations

110
times ranked

3114
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic insights into salt adaptation in a desert poplar. <i>Nature Communications</i> , 2013, 4, 2797.	5.8	286
2	Genome structure and emerging evidence of an incipient sex chromosome in <i>Populus</i> . <i>Genome Research</i> , 2008, 18, 422-430.	2.4	177
3	The willow genome and divergent evolution from poplar after the common genome duplication. <i>Cell Research</i> , 2014, 24, 1274-1277.	5.7	148
4	Characterization of microsatellites revealed by genomic sequencing of <i>Populus trichocarpa</i> . <i>Canadian Journal of Forest Research</i> , 2004, 34, 85-93.	0.8	145
5	The F-Box Gene Family Is Expanded in Herbaceous Annual Plants Relative to Woody Perennial Plants. <i>Plant Physiology</i> , 2008, 148, 1189-1200.	2.3	125
6	The nearly complete genome of <i>Ginkgo biloba</i> illuminates gymnosperm evolution. <i>Nature Plants</i> , 2021, 7, 748-756.	4.7	98
7	Phylogenomics of the genus <i>Populus</i> reveals extensive interspecific gene flow and balancing selection. <i>New Phytologist</i> , 2020, 225, 1370-1382.	3.5	93
8	L1-Norm Distance Linear Discriminant Analysis Based on an Effective Iterative Algorithm. <i>IEEE Transactions on Circuits and Systems for Video Technology</i> , 2018, 28, 114-129.	5.6	83
9	Different autosomes evolved into sex chromosomes in the sister genera of <i>Salix</i> and <i>Populus</i> . <i>Scientific Reports</i> , 2015, 5, 9076.	1.6	76
10	Molecular linkage maps of the <i>Populus</i> genome. <i>Genome</i> , 2002, 45, 541-555.	0.9	73
11	Evidences for a role of two Y-specific genes in sex determination in <i>Populus deltoides</i> . <i>Nature Communications</i> , 2020, 11, 5893.	5.8	68
12	Expression of the chickpea <i>CarNAC3</i> gene enhances salinity and drought tolerance in transgenic poplars. <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 120, 141-154.	1.2	64
13	Pathways to sex determination in plants: how many roads lead to Rome?. <i>Current Opinion in Plant Biology</i> , 2020, 54, 61-68.	3.5	54
14	Organellar genome assembly methods and comparative analysis of horticultural plants. <i>Horticulture Research</i> , 2018, 5, 3.	2.9	53
15	A General Model to Explain Repeated Turnovers of Sex Determination in the Salicaceae. <i>Molecular Biology and Evolution</i> , 2021, 38, 968-980.	3.5	53
16	The <i>Acer truncatum</i> genome provides insights into nervonic acid biosynthesis. <i>Plant Journal</i> , 2020, 104, 662-678.	2.8	52
17	Genome-wide identification and characterization of WRKY gene family in <i>Salix suchowensis</i> . <i>PeerJ</i> , 2016, 4, e2437.	0.9	52
18	The obscure events contributing to the evolution of an incipient sex chromosome in <i>Populus</i> : a retrospective working hypothesis. <i>Tree Genetics and Genomes</i> , 2012, 8, 559-571.	0.6	50

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19	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	1.7	50
20	A logistic mixture model for characterizing genetic determinants causing differentiation in growth trajectories. <i>Genetical Research</i> , 2002, 79, 235-245.	0.3	49
21	Transcriptome Analysis of Differentially Expressed Genes Relevant to Variegation in Peach Flowers. <i>PLoS ONE</i> , 2014, 9, e90842.	1.1	48
22	Detection of quantitative trait loci influencing growth trajectories of adventitious roots in <i>Populus</i> using functional mapping. <i>Tree Genetics and Genomes</i> , 2009, 5, 539-552.	0.6	46
23	A Highly Dense Genetic Map for <i>Ginkgo biloba</i> Constructed Using Sequence-Based Markers. <i>Frontiers in Plant Science</i> , 2017, 8, 1041.	1.7	45
24	Transcriptome Analysis of the Differentially Expressed Genes in the Male and Female Shrub Willows (<i>Salix suchowensis</i>). <i>PLoS ONE</i> , 2013, 8, e60181.	1.1	38
25	The chromosome-scale assembly of the willow genome provides insight into Salicaceae genome evolution. <i>Horticulture Research</i> , 2020, 7, 45.	2.9	35
26	Preliminary interspecific genetic maps of the <i>Populus</i> genome constructed from RAPD markers. <i>Genome</i> , 2001, 44, 602-609.	0.9	31
27	Quantitative trait loci for growth trajectories in <i>Populus</i> . <i>Genetical Research</i> , 2003, 81, 51-64.	0.3	31
28	RNA-directed DNA methylation in plants. <i>Plant Cell Reports</i> , 2015, 34, 1857-1862.	2.8	31
29	Functional Analysis of Two Orthologous NAC Genes, CarNAC3, and CarNAC6 from <i>Cicer arietinum</i> , Involved in Abiotic Stresses in Poplar. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1539-1551.	1.0	31
30	Major Chromosomal Rearrangements Distinguish Willow and Poplar After the Ancestral "Salicoid" Genome Duplication. <i>Genome Biology and Evolution</i> , 2016, 8, 1868-1875.	1.1	30
31	Evaluation, characterization, expression profiling, and functional analysis of DXS and DXR genes of <i>Populus trichocarpa</i> . <i>Plant Physiology and Biochemistry</i> , 2019, 142, 94-105.	2.8	30
32	Efficient CRISPR/Cas9-Mediated Gene Editing in an Interspecific Hybrid Poplar With a Highly Heterozygous Genome. <i>Frontiers in Plant Science</i> , 2020, 11, 996.	1.7	27
33	The genomic architecture of the sex-determining region and sex-related metabolic variation in <i>Ginkgo biloba</i> . <i>Plant Journal</i> , 2020, 104, 1399-1409.	2.8	26
34	Sex determination through X-Y heterogamety in <i>Salix nigra</i> . <i>Heredity</i> , 2021, 126, 630-639.	1.2	26
35	Bioinformatics-Based Identification of Candidate Genes from QTLs Associated with Cell Wall Traits in <i>Populus</i> . <i>Bioenergy Research</i> , 2010, 3, 172-182.	2.2	25
36	Confirmation of Single-Locus Sex Determination and Female Heterogamety in Willow Based on Linkage Analysis. <i>PLoS ONE</i> , 2016, 11, e0147671.	1.1	24

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37	DNA fingerprinting of oil camellia cultivars with SSR markers. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	24
38	IGDD: a database of intronless genes in dicots. <i>BMC Bioinformatics</i> , 2016, 17, 289.	1.2	23
39	VGSC: A Web-Based Vector Graph Toolkit of Genome Synteny and Collinearity. <i>BioMed Research International</i> , 2016, 2016, 1-7.	0.9	22
40	Genetic Map Construction and Detection of Genetic Loci Underlying Segregation Distortion in an Intraspecific Cross of <i>Populus deltoides</i> . <i>PLoS ONE</i> , 2015, 10, e0126077.	1.1	21
41	Mapping quantitative trait loci conferring resistance to Marssonina leaf spot disease in <i>Populus deltoides</i> . <i>Trees - Structure and Function</i> , 2019, 33, 697-706.	0.9	19
42	Fine mapping of the sex locus in <i>Salix triandra</i> confirms a consistent sex determination mechanism in genus <i>Salix</i> . <i>Horticulture Research</i> , 2020, 7, 64.	2.9	19
43	Genome-Wide Comparative Analysis of R2R3 MYB Gene Family in <i>Populus</i> and <i>Salix</i> and Identification of Male Flower Bud Development-Related Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 721558.	1.7	19
44	Molecular structure, chemical synthesis, and antibacterial activity of ABP-dHC-cecropin A from drury (<i>Hyphantria cunea</i>). <i>Peptides</i> , 2015, 68, 197-204.	1.2	18
45	Functional analyses of NDPK2 in <i>Populus trichocarpa</i> and overexpression of PtNDPK2 enhances growth and tolerance to abiotic stresses in transgenic poplar. <i>Plant Physiology and Biochemistry</i> , 2017, 117, 61-74.	2.8	17
46	An analytical toolkit for polyploid willow discrimination. <i>Scientific Reports</i> , 2016, 6, 37702.	1.6	16
47	Potential chromosomal introgression barriers revealed by linkage analysis in a hybrid of <i>Pinus massoniana</i> and <i>P. hwangshanensis</i> . <i>BMC Plant Biology</i> , 2010, 10, 37.	1.6	15
48	Uneven selection pressure accelerating divergence of <i>Populus</i> and <i>Salix</i> . <i>Horticulture Research</i> , 2019, 6, 37.	2.9	15
49	Sex-Related Differences in Growth, Herbivory, and Defense of Two <i>Salix</i> Species. <i>Forests</i> , 2020, 11, 450.	0.9	15
50	Genome-wide identification and characterization of the MADS-box gene family in <i>Salix suchowensis</i> . <i>PeerJ</i> , 2019, 7, e8019.	0.9	15
51	Characterization of microsatellites in the coding regions of the <i>Populus</i> genome. <i>Molecular Breeding</i> , 2011, 27, 59-66.	1.0	14
52	Discovery and experimental analysis of microsatellites in an oil woody plant <i>Camellia chekiangoleosa</i> . <i>Plant Systematics and Evolution</i> , 2013, 299, 1387-1393.	0.3	14
53	Physical interaction between SnRK2 and PP2C is conserved in <i>Populus trichocarpa</i> and <i>Populus deltoides</i> . <i>Plant Biotechnology</i> , 2015, 32, 337-341.	0.5	14
54	Heterologous overexpression of the Arabidopsis SnRK2.8 gene enhances drought and salt tolerance in <i>Populus euphratica</i> cv 'Nanlin895'. <i>Plant Biotechnology Reports</i> , 2019, 13, 245-261.	0.9	14

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55	Design, synthesis and biological evaluation of anilide (dicarboxylic acid) shikonin esters as antitumor agents through targeting PI3K/Akt/mTOR signaling pathway. <i>Bioorganic Chemistry</i> , 2021, 111, 104872.	2.0	14
56	Differential retention and expansion of the ancestral genes associated with the paleopolyploidies in modern rosid plants, as revealed by analysis of the extensins super-gene family. <i>BMC Genomics</i> , 2014, 15, 612.	1.2	13
57	Relative density degree induced boundary detection for one-class SVM. <i>Soft Computing</i> , 2016, 20, 4473-4485.	2.1	13
58	Functional analyses of PtRDM1 gene overexpression in poplars and evaluation of its effect on DNA methylation and response to salt stress. <i>Plant Physiology and Biochemistry</i> , 2018, 127, 64-73.	2.8	13
59	High-density genetic map of <i>Populus deltoides</i> constructed by using specific length amplified fragment sequencing. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	13
60	Differential relieving effects of shikonin and its derivatives on inflammation and mucosal barrier damage caused by ulcerative colitis. <i>PeerJ</i> , 2021, 9, e10675.	0.9	13
61	<i>Melampsora larici-populina</i> , the main rust pathogen, causes loss in biomass production of black cottonwood plantations in the south of China. <i>Phytoparasitica</i> , 2013, 41, 337-344.	0.6	12
62	In vitro production and antifungal activity of peptide ABP-dHC-cecropin A. <i>Journal of Biotechnology</i> , 2015, 199, 47-54.	1.9	12
63	Characterization, Expression Profiling, and Functional Analysis of PtDef, a Defensin-Encoding Gene From <i>Populus trichocarpa</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 106.	1.5	12
64	Aux/IAA and ARF Gene Families in <i>Salix suchowensis</i> : Identification, Evolution, and Dynamic Transcriptome Profiling During the Plant Growth Process. <i>Frontiers in Plant Science</i> , 2021, 12, 666310.	1.7	12
65	High-level SUMO-mediated fusion expression of ABP-dHC-cecropin A from multiple joined genes in <i>Escherichia coli</i> . <i>Analytical Biochemistry</i> , 2016, 509, 15-23.	1.1	11
66	The complete mitochondrial genome of <i>Medicago truncatula</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 122-123.	0.2	11
67	Map and analysis of microsatellites in the genome of <i>Populus</i> : The first sequenced perennial plant. <i>Science in China Series C: Life Sciences</i> , 2007, 50, 690-699.	1.3	9
68	Genome-wide identification and characterization of WUSCHEL-related homeobox (WOX) genes in <i>Salix suchowensis</i> . <i>Journal of Forestry Research</i> , 2019, 30, 1811-1822.	1.7	9
69	Sequencing and Analysis of the <i>Pseudomonas fluorescens</i> GcM5-1A Genome: A Pathogen Living in the Surface Coat of <i>Bursaphelenchus xylophilus</i> . <i>PLoS ONE</i> , 2015, 10, e0141515.	1.1	9
70	Plant small RNAs: definition, classification and response against stresses. <i>Biologia (Poland)</i> , 2018, 73, 285-294.	0.8	8
71	Differential microbial assemblages associated with shikonin-producing <i>Borage</i> species in two distinct soil types. <i>Scientific Reports</i> , 2021, 11, 10788.	1.6	8
72	Genetic Introgression and Species Boundary of Two Geographically Overlapping Pine Species Revealed by Molecular Markers. <i>PLoS ONE</i> , 2014, 9, e101106.	1.1	8

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73	Impact of a δ -G2-EPSPS & δ -GAT Dual Transgenic Glyphosate-Resistant Soybean Line on the Soil Microbial Community under Field Conditions Affected by Glyphosate Application. <i>Microbes and Environments</i> , 2020, 35, n/a.	0.7	8
74	Identification and characterization of nucleotide variations in the genome of <i>Ziziphus jujuba</i> (Rhamnaceae) by next generation sequencing. <i>Molecular Biology Reports</i> , 2014, 41, 3219-3223.	1.0	7
75	Identifying candidate genes for wood formation in poplar based on microarray network analysis and graph theory. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	7
76	PreLnc: An Accurate Tool for Predicting lncRNAs Based on Multiple Features. <i>Genes</i> , 2020, 11, 981.	1.0	7
77	Shikonin N-benzyl malonic acid ester derivatives as novel telomerase inhibitors with potent activity against lung cancer cell lines. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2022, 57, 128503.	1.0	7
78	Natural infectious behavior of the urediniospores of <i>Melampsora larici-populina</i> on poplar leaves. <i>Journal of Forestry Research</i> , 2015, 26, 225-231.	1.7	6
79	The Whole Genome Assembly and Comparative Genomic Research of <i>Thellungiella parvula</i> (Extremophile Crucifer) Mitochondrion. <i>International Journal of Genomics</i> , 2016, 2016, 1-13.	0.8	6
80	Incorporating neighbors' distribution knowledge into support vector machines. <i>Soft Computing</i> , 2017, 21, 6407-6420.	2.1	6
81	Identification of Genes Underlying the Resistance to <i>Melampsora larici-populina</i> in an <i>R</i> Gene Supercluster of the <i>Populus deltoides</i> Genome. <i>Plant Disease</i> , 2020, 104, 1133-1143.	0.7	6
82	Cloning and functional analysis of EpGHQH1 in shikonin production of <i>Echium plantagineum</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2021, 144, 533-543.	1.2	6
83	Genome-wide detection of genetic loci triggering uneven descending of gametes from a natural hybrid pine. <i>Tree Genetics and Genomes</i> , 2012, 8, 1371-1377.	0.6	5
84	Marker-Aided Selection of Polyploid Poplars. <i>Bioenergy Research</i> , 2013, 6, 984-990.	2.2	5
85	A novel inclusion complex (β -CD/ABP-dHC-cecropin A) with antibiotic properties for use as an anti-Agrobacterium additive in transgenic poplar rooting medium. <i>Enzyme and Microbial Technology</i> , 2015, 81, 72-79.	1.6	5
86	<i>Pinus massoniana</i> Introgression Hybrids Display Differential Expression of Reproductive Genes. <i>Forests</i> , 2019, 10, 230.	0.9	5
87	Optimization of the cry1Ah1 Sequence Enhances the Hyper-Resistance of Transgenic Poplars to <i>Hyphantria cunea</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 335.	1.7	5
88	Identification of Reference Genes for Quantitative Gene Expression Studies in <i>Pinus massoniana</i> and Its Introgression Hybrid. <i>Forests</i> , 2019, 10, 787.	0.9	4
89	Analysis of topology properties in different tissues of poplar based on gene co-expression networks. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	4
90	Volatile metabolites of willows determining host discrimination by adult <i>Plagiodera versicolora</i> . <i>Journal of Forestry Research</i> , 0, 1.	1.7	4

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91	Differential Assembly and Shifts of the Rhizosphere Bacterial Community by a Dual Transgenic Glyphosate-Tolerant Soybean Line with and without Glyphosate Application. <i>Horticulturae</i> , 2021, 7, 374.	1.2	4
92	Molecular discrimination and ploidy level determination for elite willow cultivars. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	3
93	Discovering Podophyllotoxin Derivatives as Potential Anti-Tubulin Agents: Design, Synthesis and Biological Evaluation. <i>ChemistrySelect</i> , 2020, 5, 10526-10536.	0.7	3
94	Overexpression of a putative 12-oxophytodienoate reductase gene, EpOPR1, enhances acetylshikonin production in <i>Echium plantagineum</i> . <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2022, 58, 311-320.	0.9	3
95	GESearch: An Interactive GUI Tool for Identifying Gene Expression Signature. <i>BioMed Research International</i> , 2015, 2015, 1-8.	0.9	2
96	Gene discovery and marker resource development by transcriptome sequencing from a short-rotation coppice willow, <i>Salix suchowensis</i> . <i>Plant Breeding</i> , 2017, 136, 279-286.	1.0	2
97	Deciphering the rhizobacterial assemblages under the influence of genetically engineered maize carrying <i>mcrY</i> genes. <i>Environmental Science and Pollution Research</i> , 2021, 28, 60154-60166.	2.7	2
98	GEsture: an online hand-drawing tool for gene expression pattern search. <i>PeerJ</i> , 2018, 6, e4927.	0.9	2
99	OUP accepted manuscript. <i>Tree Physiology</i> , 2021, , .	1.4	2
100	A Selection of Reliable Reference Genes for Gene Expression Analysis in the Female and Male Flowers of <i>Salix suchowensis</i> . <i>Plants</i> , 2022, 11, 647.	1.6	2
101	Detecting the Candidate Gender Determinants by Bioinformatic Prediction of miRNAs and Their Targets from Transcriptome Sequences of the Male and Female Flowers in <i>Salix suchowensis</i> . <i>BioMed Research International</i> , 2017, 2017, 1-9.	0.9	1
102	Assessment of shikonin and acetyl-shikonin for mitigating quorum sensing potential of <i>C. violaceum</i> . <i>Plant Growth Regulation</i> , 2021, 94, 233-243.	1.8	1
103	AN OMNI-DIRECTIONAL ELECTRIC PRUNING SAW FOR FOREST TENDING. <i>INMATEH - Agricultural Engineering</i> , 2020, 61, 35-40.	0.1	1