

Tongming Yin

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

101
papers

1,911
citations

22
h-index

41
g-index

110
ext. papers

2,608
ext. citations

4.3
avg, IF

4.68
L-index

#	Paper	IF	Citations
101	Shikonin N-benzyl matricinic acid ester derivatives as novel telomerase inhibitors with potent activity against lung cancer cell lines.. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2021 , 128503	2.9	0
100	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	2.5	0
99	Differential microbial assemblages associated with shikonin-producing Borage species in two distinct soil types. <i>Scientific Reports</i> , 2021 , 11, 10788	4.9	1
98	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	3.2	
97	Aux/IAA and ARF Gene Families in : Identification, Evolution, and Dynamic Transcriptome Profiling During the Plant Growth Process. <i>Frontiers in Plant Science</i> , 2021 , 12, 666310	6.2	2
96	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	5.1	4
95	Deciphering the rhizobacterial assemblages under the influence of genetically engineered maize carrying mcrY genes. <i>Environmental Science and Pollution Research</i> , 2021 , 28, 60154-60166	5.1	1
94	The nearly complete genome of Ginkgo biloba illuminates gymnosperm evolution. <i>Nature Plants</i> , 2021 , 7, 748-756	11.5	11
93	A General Model to Explain Repeated Turnovers of Sex Determination in the Salicaceae. <i>Molecular Biology and Evolution</i> , 2021 , 38, 968-980	8.3	18
92	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	2.7	3
91	Differential relieving effects of shikonin and its derivatives on inflammation and mucosal barrier damage caused by ulcerative colitis. <i>PeerJ</i> , 2021 , 9, e10675	3.1	4
90	Genome-Wide Comparative Analysis of R2R3 MYB Gene Family in and and Identification of Male Flower Bud Development-Related Genes. <i>Frontiers in Plant Science</i> , 2021 , 12, 721558	6.2	3
89	Sex determination through X-Y heterogamety in <i>Salix nigra</i> . <i>Heredity</i> , 2021 , 126, 630-639	3.6	10
88	Fine mapping of the sex locus in confirms a consistent sex determination mechanism in genus. <i>Horticulture Research</i> , 2020 , 7, 64	7.7	11
87	The chromosome-scale assembly of the willow genome provides insight into Salicaceae genome evolution. <i>Horticulture Research</i> , 2020 , 7, 45	7.7	14
86	Characterization, Expression Profiling, and Functional Analysis of , a Defensin-Encoding Gene From. <i>Frontiers in Microbiology</i> , 2020 , 11, 106	5.7	5
85	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	6.2	15

84	Pathways to sex determination in plants: how many roads lead to Rome?. <i>Current Opinion in Plant Biology</i> , 2020 , 54, 61-68	9.9	24
83	Sex-Related Differences in Growth, Herbivory, and Defense of Two <i>Salix</i> Species. <i>Forests</i> , 2020 , 11, 450	2.8	6
82	Impact of a G2-EPSPS & 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,	2.6	4
81	AN OMNI-DIRECTIONAL ELECTRIC PRUNING SAW FOR FOREST TENDING. <i>INMATEH - Agricultural Engineering</i> , 2020 , 61, 35-40	1.2	1
80	Identification of Genes Underlying the Resistance to in an Gene Supercluster of the Genome. <i>Plant Disease</i> , 2020 , 104, 1133-1143	1.5	1
79	Phylogenomics of the genus <i>Populus</i> reveals extensive interspecific gene flow and balancing selection. <i>New Phytologist</i> , 2020 , 225, 1370-1382	9.8	33
78	Analysis of topology properties in different tissues of poplar based on gene co-expression networks. <i>Tree Genetics and Genomes</i> , 2020 , 16, 1	2.1	1
77	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	6.9	8
76	Evidences for a role of two Y-specific genes in sex determination in <i>Populus deltoides</i> . <i>Nature Communications</i> , 2020 , 11, 5893	17.4	17
75	The <i>Acer truncatum</i> genome provides insights into nervonic acid biosynthesis. <i>Plant Journal</i> , 2020 , 104, 662-678	6.9	14
74	Discovering Podophyllotoxin Derivatives as Potential Anti-Tubulin Agents: Design, Synthesis and Biological Evaluation. <i>ChemistrySelect</i> , 2020 , 5, 10526-10536	1.8	2
73	Identification of Reference Genes for Quantitative Gene Expression Studies in <i>Pinus massoniana</i> and Its Introgression Hybrid. <i>Forests</i> , 2019 , 10, 787	2.8	2
72	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	5.4	13
71	Uneven selection pressure accelerating divergence of and. <i>Horticulture Research</i> , 2019 , 6, 37	7.7	11
70	<i>Pinus massoniana</i> Introgression Hybrids Display Differential Expression of Reproductive Genes. <i>Forests</i> , 2019 , 10, 230	2.8	4
69	Optimization of the Sequence Enhances the Hyper-Resistance of Transgenic Poplars to. <i>Frontiers in Plant Science</i> , 2019 , 10, 335	6.2	4
68	Heterologous overexpression of the <i>Arabidopsis</i> SnRK2.8 gene enhances drought and salt tolerance in <i>Populus euramericana</i> cv Nanlin895. <i>Plant Biotechnology Reports</i> , 2019 , 13, 245-261	2.5	5
67	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	2.6	2

66	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	2	4
65	Genome-wide identification and characterization of the MADS-box gene family in. <i>PeerJ</i> , 2019 , 7, e8019	3.1	6
64	Plant small RNAs: definition, classification and response against stresses. <i>Biologia (Poland)</i> , 2018 , 73, 285-294	1.5	5
63	Organellar genome assembly methods and comparative analysis of horticultural plants. <i>Horticulture Research</i> , 2018 , 5, 3	7.7	44
62	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	5.4	8
61	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	6.4	63
60	GEsture: an online hand-drawing tool for gene expression pattern search. <i>PeerJ</i> , 2018 , 6, e4927	3.1	1
59	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018 , 9, 1799	6.2	22
58	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	2.1	6
57	Molecular discrimination and ploidy level determination for elite willow cultivars. <i>Tree Genetics and Genomes</i> , 2018 , 14, 1	2.1	2
56	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	2.4	2
55	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	5.4	11
54	Detecting the Candidate Gender Determinants by Bioinformatic Prediction of miRNAs and Their Targets from Transcriptome Sequences of the Male and Female Flowers in. <i>BioMed Research International</i> , 2017 , 2017, 9614596	3	1
53	Incorporating neighbors' distribution knowledge into support vector machines. <i>Soft Computing</i> , 2017 , 21, 6407-6420	3.5	5
52	A Highly Dense Genetic Map for Constructed Using Sequence-Based Markers. <i>Frontiers in Plant Science</i> , 2017 , 8, 1041	6.2	21
51	The complete mitochondrial genome of. <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 122-123	0.5	7
50	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	2.1	5
49	Major Chromosomal Rearrangements Distinguish Willow and Poplar After the Ancestral "Salicoid" Genome Duplication. <i>Genome Biology and Evolution</i> , 2016 , 8, 1868-75	3.9	22

48	DNA fingerprinting of oil camellia cultivars with SSR markers. <i>Tree Genetics and Genomes</i> , 2016 , 12, 1	2.1	12
47	Relative density degree induced boundary detection for one-class SVM. <i>Soft Computing</i> , 2016 , 20, 4473-4485	3.5	9
46	Genome-wide identification and characterization of WRKY gene family in <i>Salix suchowensis</i> . <i>PeerJ</i> , 2016 , 4, e2437	3.1	25
45	The Whole Genome Assembly and Comparative Genomic Research of <i>Thellungiella parvula</i> (Extremophile Crucifer) Mitochondrion. <i>International Journal of Genomics</i> , 2016 , 2016, 5283628	2.5	3
44	VGSC: A Web-Based Vector Graph Toolkit of Genome Synteny and Collinearity. <i>BioMed Research International</i> , 2016 , 2016, 7823429	3	14
43	IGDD: a database of intronless genes in dicots. <i>BMC Bioinformatics</i> , 2016 , 17, 289	3.6	13
42	Confirmation of Single-Locus Sex Determination and Female Heterogamety in Willow Based on Linkage Analysis. <i>PLoS ONE</i> , 2016 , 11, e0147671	3.7	17
41	An analytical toolkit for polyploid willow discrimination. <i>Scientific Reports</i> , 2016 , 6, 37702	4.9	7
40	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	3.1	9
39	RNA-directed DNA methylation in plants. <i>Plant Cell Reports</i> , 2015 , 34, 1857-62	5.1	24
38	A novel inclusion complex (ECD/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, 72-9	3.8	5
37	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	4.9	60
36	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	1.7	21
35	Expression of the chickpea CarNAC3 gene enhances salinity and drought tolerance in transgenic poplars. <i>Plant Cell, Tissue and Organ Culture</i> , 2015 , 120, 141-154	2.7	39
34	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	3.8	16
33	GESearch: An Interactive GUI Tool for Identifying Gene Expression Signature. <i>BioMed Research International</i> , 2015 , 2015, 853734	3	1
32	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	3.7	15
31	Physical interaction between SnRK2 and PP2C is conserved in <i>Populus trichocarpa</i> . <i>Plant Biotechnology</i> , 2015 , 32, 337-341	1.3	11

30	In vitro production and antifungal activity of peptide ABP-dHC-cecropin A. <i>Journal of Biotechnology</i> , 2015 , 199, 47-54	3.7	9
29	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	2	5
28	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	3.7	7
27	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, 3219-23	2.8	6
26	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	4.5	10
25	Transcriptome analysis of differentially expressed genes relevant to variegation in peach flowers. <i>PLoS ONE</i> , 2014 , 9, e90842	3.7	42
24	The willow genome and divergent evolution from poplar after the common genome duplication. <i>Cell Research</i> , 2014 , 24, 1274-7	24.7	104
23	Genetic introgression and species boundary of two geographically overlapping pine species revealed by molecular markers. <i>PLoS ONE</i> , 2014 , 9, e101106	3.7	4
22	<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	1.5	7
21	Marker-Aided Selection of Polyploid Poplars. <i>Bioenergy Research</i> , 2013 , 6, 984-990	3.1	5
20	Genomic insights into salt adaptation in a desert poplar. <i>Nature Communications</i> , 2013 , 4, 2797	17.4	183
19	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	1.3	11
18	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	3.7	32
17	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	2.1	5
16	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	2.1	41
15	Characterization of microsatellites in the coding regions of the <i>Populus</i> genome. <i>Molecular Breeding</i> , 2011 , 27, 59-66	3.4	11
14	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	3.1	21
13	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	5.3	14

12	Detection of quantitative trait loci influencing growth trajectories of adventitious roots in Populus using functional mapping. <i>Tree Genetics and Genomes</i> , 2009 , 5, 539-552	2.1	39
11	Genome structure and emerging evidence of an incipient sex chromosome in Populus. <i>Genome Research</i> , 2008 , 18, 422-30	9.7	155
10	The F-box gene family is expanded in herbaceous annual plants relative to woody perennial plants. <i>Plant Physiology</i> , 2008 , 148, 1189-200	6.6	106
9	Map and analysis of microsatellites in the genome of Populus: the first sequenced perennial plant. <i>Science in China Series C: Life Sciences</i> , 2007 , 50, 690-9		6
8	Characterization of microsatellites revealed by genomic sequencing of Populus trichocarpa. <i>Canadian Journal of Forest Research</i> , 2004 , 34, 85-93	1.9	129
7	Quantitative trait loci for growth trajectories in Populus. <i>Genetical Research</i> , 2003 , 81, 51-64	1.1	28
6	Molecular linkage maps of the Populus genome. <i>Genome</i> , 2002 , 45, 541-55	2.4	62
5	A logistic mixture model for characterizing genetic determinants causing differentiation in growth trajectories. <i>Genetical Research</i> , 2002 , 79, 235-45	1.1	43
4	Preliminary interspecific genetic maps of the Populus genome constructed from RAPD markers. <i>Genome</i> , 2001 , 44, 602-609	2.4	30
3	Two antagonistic effect genes mediate separation of sexes in a fully dioecious plant		2
2	Volatile metabolites of willows determining host discrimination by adult Plagiodera versicolora. <i>Journal of Forestry Research</i> , 1	2	1
1	Overexpression of a putative 12-oxophytodienoate reductase gene, EpOPR1, enhances acetylshikonin production in Echim plantagineum. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 1	2.3	0