

Zhibiao Ye

List of Publications by Year in descending order

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75
papers

4,442
citations

156536

32
h-index

129628

63
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75
all docs

75
docs citations

75
times ranked

5392
citing authors

#	ARTICLE	IF	CITATIONS
1	VG, encoding a thylakoid formation protein, regulates the formation of variegated leaves in tomato. Horticultural Plant Journal, 2023, 9, 98-108.	2.3	1
2	Hair interacts with SLZFP8-like to regulate the initiation and elongation of trichomes by modulating <i>SLZFP6</i> expression in tomato. Journal of Experimental Botany, 2022, 73, 228-244.	2.4	18
3	Tomato methionine sulfoxide reductase B2 functions in drought tolerance by promoting ROS scavenging and chlorophyll accumulation through interaction with Catalase 2 and RBCS3B. Plant Science, 2022, 318, 111206.	1.7	13
4	Methylation profiling of biosynthetic genes reveals the role of D-galacturonic acid reductase in ascorbic acid accumulation in tomato fruit. Plant Growth Regulation, 2022, 98, 281-288.	1.8	2
5	NF- κ B plays essential roles in flavonoid biosynthesis by modulating histone modifications in tomato. New Phytologist, 2021, 229, 3237-3252.	3.5	36
6	MAPK11 regulates seed germination and ABA signaling in tomato by phosphorylating SnRKs. Journal of Experimental Botany, 2021, 72, 1677-1690.	2.4	20
7	<i>HOMEODOMAIN PROTEIN8</i> mediates jasmonate-triggered trichome elongation in tomato. New Phytologist, 2021, 230, 1063-1077.	3.5	43
8	A novel negative-stranded RNA virus of the order Bunyavirales identified in Brassica campestris L. ssp. chinensis. Archives of Virology, 2021, 166, 1525-1528.	0.9	5
9	Genome-wide association study reveals the genetic architecture of 27 agronomic traits in tomato. Plant Physiology, 2021, 186, 2078-2092.	2.3	18
10	SLRCM1, which encodes tomato Lutescent1, is required for chlorophyll synthesis and chloroplast development in fruits. Horticulture Research, 2021, 8, 128.	2.9	22
11	SLBBX20 interacts with the COP9 signalosome subunit SICSN5-2 to regulate anthocyanin biosynthesis by activating SLDFR expression in tomato. Horticulture Research, 2021, 8, 163.	2.9	27
12	Interactions between ShPP2-1, an F-box family gene, and ACR11A regulate cold tolerance of tomato. Horticulture Research, 2021, 8, 148.	2.9	7
13	A mutation in a C2H2-type zinc finger transcription factor contributed to the transition toward self-pollination in cultivated tomato. Plant Cell, 2021, 33, 3293-3308.	3.1	15
14	Regulation of invertase and sucrose for improving tomato fruit flavor: A review. Vegetable Research, 2021, 1, 1-13.	0.2	0
15	miR156a-targeted SBP-box transcription factor SLSP13 regulates inflorescence morphogenesis by directly activating <i>SFT</i> in tomato. Plant Biotechnology Journal, 2020, 18, 1670-1682.	4.1	51
16	The loss of function of HEL, which encodes a cellulose synthase interactive protein, causes helical and vine-like growth of tomato. Horticulture Research, 2020, 7, 180.	2.9	6
17	A CCAAT-binding factor, SINFYA10, negatively regulates ascorbate accumulation by modulating the d-mannose/l-galactose pathway in tomato. Horticulture Research, 2020, 7, 200.	2.9	19
18	NDW, encoding a receptor-like protein kinase, regulates plant growth, cold tolerance and susceptibility to Botrytis cinerea in tomato. Plant Science, 2020, 301, 110684.	1.7	5

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19	The HD-Zip IV transcription factor SHDZIV8 controls multicellular trichome morphology by regulating the expression of <i>Hairless-2</i> . <i>Journal of Experimental Botany</i> , 2020, 71, 7132-7145.	2.4	20
20	The chaperonin 60 protein SICpn60 \pm 1 modulates photosynthesis and photorespiration in tomato. <i>Journal of Experimental Botany</i> , 2020, 71, 7224-7240.	2.4	6
21	UF, a WOX gene, regulates a novel phenotype of un-fused flower in tomato. <i>Plant Science</i> , 2020, 297, 110523.	1.7	16
22	<i>GREEN STRIPE</i> , encoding methylated TOMATO AGAMOUS-LIKE 1, regulates chloroplast development and Chl synthesis in fruit. <i>New Phytologist</i> , 2020, 228, 302-317.	3.5	36
23	Tomato SD1, encoding a kinase-interacting protein, is a major locus controlling stem development. <i>Journal of Experimental Botany</i> , 2020, 71, 3575-3587.	2.4	12
24	WOOLLY, interacting with MYB transcription factor MYB31, regulates cuticular wax biosynthesis by modulating <i>CER6</i> expression in tomato. <i>Plant Journal</i> , 2020, 103, 323-337.	2.8	44
25	Transcriptomic and functional analyses uncover the regulatory role of lncRNA000170 in tomato multicellular trichome formation. <i>Plant Journal</i> , 2020, 104, 18-29.	2.8	16
26	An allelic variant of GAME9 determines its binding capacity with the GAME17 promoter in the regulation of steroidal glycoalkaloid biosynthesis in tomato. <i>Journal of Experimental Botany</i> , 2020, 71, 2527-2536.	2.4	17
27	Genome-wide analysis of Myo-inositol oxygenase gene family in tomato reveals their involvement in ascorbic acid accumulation. <i>BMC Genomics</i> , 2020, 21, 284.	1.2	39
28	A tomato box protein <i>SlBBX20</i> modulates carotenoid biosynthesis by directly activating <i>PHYTOENE SYNTHASE1</i> , and is targeted for 26S proteasome-mediated degradation. <i>New Phytologist</i> , 2019, 221, 279-294.	3.5	127
29	Knockdown of SINL33 accumulates ascorbate, enhances disease and oxidative stress tolerance in tomato (<i>Solanum lycopersicum</i>). <i>Plant Growth Regulation</i> , 2019, 89, 49-58.	1.8	18
30	Rapid breeding of pink-fruited tomato hybrids using the CRISPR/Cas9 system. <i>Journal of Genetics and Genomics</i> , 2019, 46, 505-508.	1.7	26
31	The tomato WV gene encoding a thioredoxin protein is essential for chloroplast development at low temperature and high light intensity. <i>BMC Plant Biology</i> , 2019, 19, 265.	1.6	8
32	Genome-wide association analysis identifies a natural variation in basic helix-loop-helix transcription factor regulating ascorbate biosynthesis via D-mannose/L-galactose pathway in tomato. <i>PLoS Genetics</i> , 2019, 15, e1008149.	1.5	66
33	Development of a highly specific co-dominant marker for genotyping the Ph-3 (tomato late blight) Tj ETQq1 1 0.784314 rgBT ₄ /Overlook	1.0	
34	Molecular and functional characterization of ShNAC1, an NAC transcription factor from <i>Solanum habrochaites</i> . <i>Plant Science</i> , 2018, 271, 9-19.	1.7	37
35	ShCIGT, a Trihelix family gene, mediates cold and drought tolerance by interacting with SnRK1 in tomato. <i>Plant Science</i> , 2018, 270, 140-149.	1.7	58
36	Silencing <i>GRAS2</i> reduces fruit weight in tomato. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 498-513.	4.1	29

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37	The C2H2 zinc-finger protein SlZFP3 regulates AsA synthesis and salt tolerance by interacting with CSN5B. <i>Plant Biotechnology Journal</i> , 2018, 16, 1201-1213.	4.1	82
38	Tomato LrgB regulates heat tolerance and the assimilation and partitioning of carbon. <i>Plant Science</i> , 2018, 274, 309-319.	1.7	5
39	<i>SlHair</i> , encoding a single C2H2 zinc-finger protein, regulates multicellular trichome formation in tomato. <i>Plant Journal</i> , 2018, 96, 90-102.	2.8	97
40	Fine mapping of BoGL1, a gene controlling the glossy green trait in cabbage (<i>Brassica oleracea</i> L. Var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462	1.6	9
41	The tomato B-type cyclin gene, SlCycB2, plays key roles in reproductive organ development, trichome initiation, terpenoids biosynthesis and <i>Prodenia litura</i> defense. <i>Plant Science</i> , 2017, 262, 103-114.	1.7	71
42	Overexpression of annexin gene AnnSp2, enhances drought and salt tolerance through modulation of ABA synthesis and scavenging ROS in tomato. <i>Scientific Reports</i> , 2017, 7, 12087.	1.6	97
43	An InDel in the Promoter of <i>AI-ACTIVATED MALATE TRANSPORTER9</i> Selected during Tomato Domestication Determines Fruit Malate Contents and Aluminum Tolerance. <i>Plant Cell</i> , 2017, 29, 2249-2268.	3.1	207
44	Cgl2 plays an essential role in cuticular wax biosynthesis in cabbage (<i>Brassica oleracea</i> L. var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462	1.6	20
45	Overexpression of SlRBZ Results in Chlorosis and Dwarfism through Impairing Chlorophyll, Carotenoid, and Gibberellin Biosynthesis in Tomato. <i>Frontiers in Plant Science</i> , 2016, 7, 907.	1.7	12
46	HyPRP1 Gene Suppressed by Multiple Stresses Plays a Negative Role in Abiotic Stress Tolerance in Tomato. <i>Frontiers in Plant Science</i> , 2016, 7, 967.	1.7	26
47	An ATL78-Like RING-H2 Finger Protein Confers Abiotic Stress Tolerance through Interacting with RAV2 and CSN5B in Tomato. <i>Frontiers in Plant Science</i> , 2016, 07, 1305.	1.7	35
48	Expression and diversification analysis reveals transposable elements play important roles in the origin of <i>Lycopersicon</i> -specific <i>lncRNAs</i> in tomato. <i>New Phytologist</i> , 2016, 209, 1442-1455.	3.5	87
49	The transcription factor SlDof22 involved in ascorbate accumulation and salinity stress in tomato. <i>Biochemical and Biophysical Research Communications</i> , 2016, 474, 736-741.	1.0	48
50	The tomato HD-Zip I transcription factor SlHZ24 modulates ascorbate accumulation through positive regulation of the <i>d-mannose</i> / <i>l-galactose</i> pathway. <i>Plant Journal</i> , 2016, 85, 16-29.	2.8	116
51	Fine mapping of the dialytic gene that controls multicellular trichome formation and stamen development in tomato. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1531-1539.	1.8	14
52	Overexpression of calmodulin-like (SlCML44) stress-responsive gene from <i>Solanum habrochaites</i> enhances tolerance to multiple abiotic stresses. <i>Scientific Reports</i> , 2016, 6, 31772.	1.6	95
53	Genome-wide identification, characterization and expression analysis of calmodulin-like (CML) proteins in tomato (<i>Solanum lycopersicum</i>). <i>Plant Physiology and Biochemistry</i> , 2016, 102, 167-179.	2.8	73
54	Transcriptome profile analysis of cell proliferation molecular processes during multicellular trichome formation induced by tomato <i>Wo v</i> gene in tobacco. <i>BMC Genomics</i> , 2015, 16, 868.	1.2	42

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55	Transcriptome Profiling of Tomato Fruit Development Reveals Transcription Factors Associated with Ascorbic Acid, Carotenoid and Flavonoid Biosynthesis. PLoS ONE, 2015, 10, e0130885.	1.1	72
56	Genome-wide identification and expression profiling analysis of trihelix gene family in tomato. Biochemical and Biophysical Research Communications, 2015, 468, 653-659.	1.0	46
57	Transcriptome profile analysis of cell proliferation molecular processes during multicellular trichome formation induced by tomato <i>Wo v</i> gene in tobacco. Genomics Data, 2015, 6, 173-174.	1.3	4
58	Overexpression of ShDHN, a dehydrin gene from <i>Solanum habrochaites</i> enhances tolerance to multiple abiotic stresses in tomato. Plant Science, 2015, 231, 198-211.	1.7	153
59	Ectopic expression of FaGalUR leads to ascorbate accumulation with enhanced oxidative stress, cold, and salt tolerance in tomato. Plant Growth Regulation, 2015, 76, 187-197.	1.8	35
60	Comprehensive analysis and expression profile of the homeodomain leucine zipper IV transcription factor family in tomato. Plant Physiology and Biochemistry, 2015, 96, 141-153.	2.8	27
61	Knockdown of a JmjC domain-containing gene JMJ524 confers altered gibberellin responses by transcriptional regulation of GRAS protein lacking the DELLA domain genes in tomato. Journal of Experimental Botany, 2015, 66, 1413-1426.	2.4	18
62	Members of the tomato FRUITFULL MADS-box family regulate style abscission and fruit ripening. Journal of Experimental Botany, 2014, 65, 3005-3014.	2.4	113
63	Ascorbic Acid Accumulation is Transcriptionally Modulated in High-Pigment-1 Tomato Fruit. Plant Molecular Biology Reporter, 2014, 32, 52-61.	1.0	13
64	Genomic analyses provide insights into the history of tomato breeding. Nature Genetics, 2014, 46, 1220-1226.	9.4	801
65	Genome-wide classification and expression analysis of nucleobase-ascorbate transporter (NAT) gene family in tomato. Plant Growth Regulation, 2014, 73, 19-30.	1.8	26
66	Identification and Expression Pattern of a ZPR1 Gene in Wild Tomato (<i>Solanum Pennellii</i>). Plant Molecular Biology Reporter, 2013, 31, 409-417.	1.0	9
67	Genetic analysis and identification of QTLs for resistance to cucumber mosaic virus in chili pepper (<i>Capsicum annuum</i> L.). Euphytica, 2013, 193, 135-145.	0.6	30
68	A STAYGREEN protein <i>S</i> 1 regulates lycopene and β -carotene accumulation by interacting directly with <i>S</i> 1 and <i>PSY</i> 1 during ripening processes in tomato. New Phytologist, 2013, 198, 442-452.	3.5	149
69	Trichomes as models for studying plant cell differentiation. Cellular and Molecular Life Sciences, 2013, 70, 1937-1948.	2.4	163
70	<i>SlNAC</i> 1, a stress-related transcription factor, is fine-tuned on both the transcriptional and the post-translational level. New Phytologist, 2013, 197, 1214-1224.	3.5	55
71	Differential Modulation of Photosynthesis, Signaling, and Transcriptional Regulation between Tolerant and Sensitive Tomato Genotypes under Cold Stress. PLoS ONE, 2012, 7, e50785.	1.1	91
72	Over-expression of sly-miR156a in tomato results in multiple vegetative and reproductive trait alterations and partial phenocopy of the <i>sft</i> mutant. FEBS Letters, 2011, 585, 435-439.	1.3	174

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73	Fine-mapping of the woolly gene controlling multicellular trichome formation and embryonic development in tomato. <i>Theoretical and Applied Genetics</i> , 2011, 123, 625-633.	1.8	26
74	Manipulation of light signal transduction as a means of modifying fruit nutritional quality in tomato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9897-9902.	3.3	413
75	Critical Roles of Mitochondrial Fatty Acid Synthesis in Tomato Development and Environmental Response. <i>Plant Physiology</i> , 0, , .	2.3	1