Xue-Feng

List of Publications by Year in descending order

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304743 345221 2,479 41 22 36 citations h-index g-index papers 45 45 45 2675 all docs docs citations times ranked citing authors

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#	Article	IF	CITATIONS
1	A Chromosome Bin Map of 16,000 Expressed Sequence Tag Loci and Distribution of Genes Among the Three Genomes of Polyploid Wheat. Genetics, 2004, 168, 701-712.	2.9	369
2	Comparative DNA Sequence Analysis of Wheat and Rice Genomes. Genome Research, 2003, 13, 1818-1827.	5.5	369
3	Genome evolution of allopolyploids: a process of cytological and genetic diploidization. Cytogenetic and Genome Research, 2005, 109, 236-249.	1.1	169
4	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. Nature Genetics, 2021, 53, 564-573.	21.4	138
5	Allopolyploidization-accommodated Genomic Sequence Changes in Triticale. Annals of Botany, 2008, 101, 825-832.	2.9	116
6	Genome-Wide Association Mapping of Seedling Heat Tolerance in Winter Wheat. Frontiers in Plant Science, 2018, 9, 1272.	3.6	103
7	High Resolution Genetic Mapping by Genome Sequencing Reveals Genome Duplication and Tetraploid Genetic Structure of the Diploid Miscanthus sinensis. PLoS ONE, 2012, 7, e33821.	2.5	103
8	Polyploidization-induced genome variation in triticale. Genome, 2004, 47, 839-848.	2.0	95
9	Analysis of Expressed Sequence Tag Loci on Wheat Chromosome Group 4. Genetics, 2004, 168, 651-663.	2.9	90
10	Development of an Expressed Sequence Tag (EST) Resource for Wheat (Triticum aestivum L.). Genetics, 2004, 168, 585-593.	2.9	87
11	Timing and rate of genome variation in triticale following allopolyploidization. Genome, 2006, 49, 950-958.	2.0	86
12	Improving phosphorus acquisition of white clover (Trifolium repens L.) by transgenic expression of plant-derived phytase and acid phosphatase genes. Plant Science, 2009, 176, 479-488.	3.6	81
13	A 2600-Locus Chromosome Bin Map of Wheat Homoeologous Group 2 Reveals Interstitial Gene-Rich Islands and Colinearity With Rice. Genetics, 2004, 168, 625-637.	2.9	78
14	RhizoVision Crown: An Integrated Hardware and Software Platform for Root Crown Phenotyping. Plant Phenomics, 2020, 2020, 3074916.	5.9	74
15	Triticale Improvement for Forage and Cover Crop Uses in the Southern Great Plains of the United States. Frontiers in Plant Science, 2018, 9, 1130.	3.6	59
16	Molecular linkage mapping in rye (Secale cereale L.). Theoretical and Applied Genetics, 2001, 102, 517-523.	3.6	56
17	Comparison of TaqMan, KASP and rhAmp SNP genotyping platforms in hexaploid wheat. PLoS ONE, 2019, 14, e0217222.	2.5	54
18	Transgenic expression of phytase and acid phosphatase genes in alfalfa (Medicago sativa) leads to improved phosphate uptake in natural soils. Molecular Breeding, 2012, 30, 377-391.	2.1	53

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19	A consensus map of rye integrating mapping data from five mapping populations. Theoretical and Applied Genetics, 2009, 118, 793-800.	3.6	46
20	Contrasting geographic patterns of genetic variation for molecular markers vs. phenotypic traits in the energy grass <i>Miscanthus sinensis</i> . GCB Bioenergy, 2013, 5, 562-571.	5.6	28
21	Functional phenomics and genetics of the root economics space in winter wheat using highâ€ŧhroughput phenotyping of respiration and architecture. New Phytologist, 2021, 232, 98-112.	7.3	26
22	Imaging of plant current pathways for non-invasive root Phenotyping using a newly developed electrical current source density approach. Plant and Soil, 2020, 450, 567-584.	3.7	24
23	Genome-Wide Association Mapping of Seedling Drought Tolerance in Winter Wheat. Frontiers in Plant Science, 2020, 11, 573786.	3.6	22
24	Physical mapping of restriction fragment length polymorphism (RFLP) markers in homoeologous groups 1 and 3 chromosomes of wheat by in situ hybridization. Genome, 2001, 44, 401-412.	2.0	21
25	Structural and functional analyses of the wheat genomes based on expressed sequence tags (ESTs) related to abiotic stresses. Genome, 2006, 49, 1324-1340.	2.0	17
26	Threeâ€channel electrical impedance spectroscopy for fieldâ€scale root phenotyping. The Plant Phenome Journal, 2021, 4, e20021.	2.0	10
27	Linkage mapping evidence for a syntenic QTL associated with flowering time in perennial C 4 rhizomatous grasses Miscanthus and switchgrass. GCB Bioenergy, 2021, 13, 98-111.	5.6	8
28	Crop breeding has increased the productivity and leaf wax n-alkane concentration in a series of five winter wheat cultivars developed over the last 60 years. Journal of Plant Physiology, 2019, 243, 153056.	3.5	7
29	Genomic Selection of Forage Quality Traits in Winter Wheat. Crop Science, 2019, 59, 2473-2483.	1.8	7
30	Impoverishing Roots Will Improve Wheat Yield and Profitability Through Increased Water and Nitrogen Use Efficiencies. Journal of Geophysical Research G: Biogeosciences, 2021, 126, e2020JG005829.	3.0	7
31	Characterization of a male sterile mutant from progeny of a transgenic plant containing a leaf senescence-inhibition gene in wheat. Euphytica, 2011, 177, 241-251.	1.2	5
32	Genomic selection of forage agronomic traits in winter wheat. Crop Science, 2021, 61, 410-421.	1.8	5
33	Genotyping-by-sequencing and genomic selection applications in hexaploid triticale. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	5
34	Screening oat germplasm for better adaptation to cold stress in the Southern Great Plains of the United States. Journal of Agronomy and Crop Science, 2019, 205, 213-219.	3.5	4
35	Selection signatures across seven decades of hard winter wheat breeding in the Great Plains of the United States. Plant Genome, 2020, 13, e20032.	2.8	4
36	Improving Dual-Purpose Winter Wheat in the Southern Great Plains of the United States. , 2020, , .		3

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#	Article	IF	CITATIONS
37	Genome-Wide Association Mapping of Seedling Vigor and Regrowth Vigor in Winter Wheat. Crops, 2021, 1, 153-165.	1.4	3
38	Small Grains as Winter Pasture in the Southern Great Plains of the United States. , 0, , .		1
39	Editorial: Genomics-Enabled Triticeae Improvement. Frontiers in Plant Science, 2022, 13, 871816.	3.6	1
40	Biotechnological Improvement of Forage Crops. , 2007, , 333-338.		0
41	Transgenesis in Forage Crops. , 2009, , 335-340.		0