

Chenggen Chu

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

1,555
citations

331670

21
h-index

315739

38
g-index

45
all docs

45
docs citations

45
times ranked

1429
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential proteomic analysis of proteins in wheat spikes induced by <i>Fusarium graminearum</i> . <i>Proteomics</i> , 2005, 5, 4496-4503.	2.2	103
2	Whole genome mapping in a wheat doubled haploid population using SSRs and TRAPs and the identification of QTL for agronomic traits. <i>Molecular Breeding</i> , 2008, 22, 251-266.	2.1	97
3	Development of oligonucleotides and multiplex probes for quick and accurate identification of wheat and <i>Thinopyrum bessarabicum</i> chromosomes. <i>Genome</i> , 2017, 60, 93-103.	2.0	96
4	Chromosomal locations and genetic relationships of tiller and spike characters in wheat. <i>Euphytica</i> , 2002, 125, 357-366.	1.2	89
5	Host-selective toxins produced by <i>Stagonospora nodorum</i> confer disease susceptibility in adult wheat plants under field conditions. <i>Theoretical and Applied Genetics</i> , 2009, 118, 1489-1497.	3.6	87
6	Structural chromosome rearrangements and polymorphisms identified in Chinese wheat cultivars by high-resolution multiplex oligonucleotide FISH. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1967-1986.	3.6	83
7	<i>SnTox5</i> : a novel <i>Stagonospora nodorum</i> effector-wheat gene interaction and its relationship with the <i>SnToxA</i> and <i>Tsn1</i> and <i>SnTox3</i> interactions. <i>Molecular Plant Pathology</i> , 2012, 13, 1101-1109.	4.2	78
8	Identification of novel tan spot resistance loci beyond the known host-selective toxin insensitivity genes in wheat. <i>Theoretical and Applied Genetics</i> , 2008, 117, 873-881.	3.6	77
9	Molecular mapping of hybrid necrosis genes <i>Ne1</i> and <i>Ne2</i> in hexaploid wheat using microsatellite markers. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1374-1381.	3.6	74
10	Genome-wide identification of QTL conferring high-temperature adult-plant (HTAP) resistance to stripe rust (<i>Puccinia striiformis</i> f. sp. <i>tritici</i>) in wheat. <i>Molecular Breeding</i> , 2012, 29, 791-800.	2.1	73
11	A Novel Retrotransposon Inserted in the Dominant <i>Vrn-B1</i> Allele Confers Spring Growth Habit in Tetraploid Wheat (<i>Triticum turgidum</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 637-645.	1.8	72
12	Identification of novel tan spot resistance QTLs using an SSR-based linkage map of tetraploid wheat. <i>Molecular Breeding</i> , 2010, 25, 327-338.	2.1	66
13	Identification and molecular mapping of two QTLs with major effects for resistance to <i>Fusarium</i> head blight in wheat. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1107-1119.	3.6	65
14	Identification of novel QTLs for seedling and adult plant leaf rust resistance in a wheat doubled haploid population. <i>Theoretical and Applied Genetics</i> , 2009, 119, 263-269.	3.6	59
15	Comparison of TaqMan, KASP and rhAmp SNP genotyping platforms in hexaploid wheat. <i>PLoS ONE</i> , 2019, 14, e0217222.	2.5	54
16	Quantitative Trait Loci Analysis for the Effect of <i>Rht-B1</i> Dwarfing Gene on Coleoptile Length and Seedling Root Length and Number of Bread Wheat. <i>Crop Science</i> , 2011, 51, 2561-2568.	1.8	47
17	Genetic analysis of disease susceptibility contributed by the compatible <i>Tsn1-SnToxA</i> and <i>Snn1-SnTox1</i> interactions in the wheat- <i>Stagonospora nodorum</i> pathosystem. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1451-1459.	3.6	42
18	A simple and efficient non-denaturing FISH method for maize chromosome differentiation using single-strand oligonucleotide probes. <i>Genome</i> , 2017, 60, 657-664.	2.0	33

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19	Physical localization of a novel blue-grained gene derived from <i>Thinopyrum bessarabicum</i> . <i>Molecular Breeding</i> , 2013, 31, 195-204.	2.1	28
20	Physical mapping of chromosome 4J of <i>Thinopyrum bessarabicum</i> using gamma radiation-induced aberrations. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1319-1328.	3.6	26
21	Evaluation of Seedling Resistance to Tan Spot and <i>Stagonospora nodorum</i> Blotch in Tetraploid Wheat. <i>Crop Science</i> , 2008, 48, 1107-1116.	1.8	22
22	Seedling Resistance to Tan Spot and <i>Stagonospora nodorum</i> Leaf Blotch in Wild Emmer Wheat (<i>Triticum dicoccoides</i>). <i>Plant Disease</i> , 2008, 92, 1229-1236.	1.4	21
23	RNA-seq analysis reveals different drought tolerance mechanisms in two broadly adapted wheat cultivars TAM 111 and TAM 112. <i>Scientific Reports</i> , 2021, 11, 4301.	3.3	19
24	Genome wide identification of QTL associated with yield and yield components in two popular wheat cultivars TAM 111 and TAM 112. <i>PLoS ONE</i> , 2020, 15, e0237293.	2.5	17
25	Function and evolution of allelic variations of <i>Sr13</i> conferring resistance to stem rust in tetraploid wheat (<i>Triticum turgidum</i> L.). <i>Plant Journal</i> , 2021, 106, 1674-1691.	5.7	15
26	Genetic Dissection of QTL Associated with Grain Yield in Diverse Environments. <i>Agronomy</i> , 2014, 4, 556-578.	3.0	12
27	Population genomics and haplotype analysis in spelt and bread wheat identifies a gene regulating glume color. <i>Communications Biology</i> , 2021, 4, 375.	4.4	11
28	Comparative analysis of genetic background in eight near-isogenic wheat lines with different H genes conferring resistance to Hessian fly. <i>Genome</i> , 2011, 54, 81-89.	2.0	10
29	Chromosome aberrations induced by zebularine in triticale. <i>Genome</i> , 2016, 59, 485-492.	2.0	10
30	RNA-seq facilitates development of chromosome-specific markers and transfer of rye chromatin to wheat. <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	10
31	Genetic dissection of end-use quality traits in two widely adapted wheat cultivars TAM 111 and TAM 112. <i>Crop Science</i> , 2021, 61, 1944-1959.	1.8	9
32	Predominant wheat-alien chromosome translocations in newly developed wheat of China. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	9
33	Frequent variations in tandem repeats pSc200 and pSc119.2 cause rapid chromosome evolution of open-pollinated rye. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	8
34	Physical organization of repetitive sequences and chromosome diversity of barley revealed by fluorescence in situ hybridization (FISH). <i>Genome</i> , 2019, 62, 329-339.	2.0	8
35	Development of the Wheat Practical Haplotype Graph database as a resource for genotyping data storage and genotype imputation. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	7
36	Genome-wide QTL mapping of yield and agronomic traits in two widely adapted winter wheat cultivars from multiple mega-environments. <i>PeerJ</i> , 2021, 9, e12350.	2.0	6

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37	Mechanism of Sugarbeet Seed Germination Enhanced by Hydrogen Peroxide. <i>Frontiers in Plant Science</i> , 2022, 13, 888519.	3.6	5
38	Marker-assisted characterization of durum wheat Langdonâ€™Golden Ball disomic substitution lines. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1575-1585.	3.6	2
39	Chromosome diversity in <i>Dasypyrum villosum</i> , an important genetic and trait resource for hexaploid wheat engineering. <i>Annals of Botany</i> , 2023, 131, 185-198.	2.9	2
40	Newly Developed Sugarbeet Lines with Altered Postharvest Respiration Rates Differ in Transcription Factor and Glycolytic Enzyme Expression. <i>Crop Science</i> , 0, , .	1.8	1
41	A new strategy for using historical imbalanced yield data to conduct genome-wide association studies and develop genomic prediction models for wheat breeding. <i>Molecular Breeding</i> , 2022, 42, 1.	2.1	0
42	Frequent numerical and structural chromosome changes in early generations of synthetic hexaploid wheat. <i>Genome</i> , 2022, 65, 205-217.	2.0	0