

Yong Jiang

List of Publications by Year in descending order

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37
papers

2,210
citations

430874

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330143

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docs citations

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citing authors

#	ARTICLE	IF	CITATIONS
1	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	17.5	356
2	Genebank genomics highlights the diversity of a global barley collection. <i>Nature Genetics</i> , 2019, 51, 319-326.	21.4	322
3	Modeling Epistasis in Genomic Selection. <i>Genetics</i> , 2015, 201, 759-768.	2.9	210
4	Modelling the genetic architecture of flowering time control in barley through nested association mapping. <i>BMC Genomics</i> , 2015, 16, 290.	2.8	192
5	Genome-based establishment of a high-yielding heterotic pattern for hybrid wheat breeding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15624-15629.	7.1	178
6	A quantitative genetic framework highlights the role of epistatic effects for grain-yield heterosis in bread wheat. <i>Nature Genetics</i> , 2017, 49, 1741-1746.	21.4	144
7	Genomic selection in a commercial winter wheat population. <i>Theoretical and Applied Genetics</i> , 2016, 129, 641-651.	3.6	129
8	Potential and limits of whole genome prediction of resistance to <i>Fusarium</i> head blight and <i>Septoria tritici</i> blotch in a vast Central European elite winter wheat population. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2471-2481.	3.6	92
9	The roles of pleiotropy and close linkage as revealed by association mapping of yield and correlated traits of wheat (<i>Triticum aestivum</i> L.). <i>Journal of Experimental Botany</i> , 2017, 68, 4089-4101.	4.8	61
10	Haplotype-Based Genome-Wide Prediction Models Exploit Local Epistatic Interactions Among Markers. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1687-1699.	1.8	50
11	Validating the prediction accuracies of marker-assisted and genomic selection of <i>Fusarium</i> head blight resistance in wheat using an independent sample. <i>Theoretical and Applied Genetics</i> , 2017, 130, 471-482.	3.6	49
12	Potential of marker selection to increase prediction accuracy of genomic selection in soybean (<i>Glycine max</i> L.). <i>Molecular Breeding</i> , 2016, 36, 113.	2.1	46
13	Negative dominance and dominance-by-dominance epistatic effects reduce grain-yield heterosis in wide crosses in wheat. <i>Science Advances</i> , 2020, 6, eaay4897.	10.3	40
14	Genome-wide metabolite associations revealed low heritability, high genetic complexity, and causal relations for leaf metabolites in winter wheat (<i>Triticum aestivum</i> L.). <i>Journal of Experimental Botany</i> , 2017, 68, erw441.	4.8	33
15	Reciprocal recurrent genomic selection: an attractive tool to leverage hybrid wheat breeding. <i>Theoretical and Applied Genetics</i> , 2019, 132, 687-698.	3.6	33
16	Genome-wide mapping and prediction suggests presence of local epistasis in a vast elite winter wheat populations adapted to Central Europe. <i>Theoretical and Applied Genetics</i> , 2017, 130, 635-647.	3.6	32
17	Prospects and limits of marker imputation in quantitative genetic studies in European elite wheat (<i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2015, 16, 168.	2.8	30
18	Identification of QTL hot spots for malting quality in two elite breeding lines with distinct tolerance to abiotic stress. <i>BMC Plant Biology</i> , 2018, 18, 106.	3.6	25

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19	Unlocking big data doubled the accuracy in predicting the grain yield in hybrid wheat. <i>Science Advances</i> , 2021, 7, .	10.3	22
20	Selecting Closely-Linked SNPs Based on Local Epistatic Effects for Haplotype Construction Improves Power of Association Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 4115-4126.	1.8	17
21	Can metabolic prediction be an alternative to genomic prediction in barley?. <i>PLoS ONE</i> , 2020, 15, e0234052.	2.5	17
22	Efficient Algorithms for Calculating Epistatic Genomic Relationship Matrices. <i>Genetics</i> , 2020, 216, 651-669.	2.9	15
23	Genetic Dissection of Hybrid Performance and Heterosis for Yield-Related Traits in Maize. <i>Frontiers in Plant Science</i> , 2021, 12, 774478.	3.6	15
24	The Hall algebra approach to Drinfeld's presentation of quantum loop algebras. <i>Advances in Mathematics</i> , 2012, 231, 2593-2625.	1.1	13
25	Exome association analysis sheds light onto leaf rust (<i>Puccinia triticina</i>) resistance genes currently used in wheat breeding (<i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2020, 18, 1396-1408.	8.3	13
26	Haplotype-based genome-wide association increases the predictability of leaf rust (<i>Puccinia</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 46</i>	4.8	13
27	On the use of GBLUP and its extension for GWAS with additive and epistatic effects. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	9
28	A SNP-based GWAS and functional haplotype-based GWAS of flag leaf-related traits and their influence on the yield of bread wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 3895-3909.	3.6	8
29	Using Genome-Wide Predictions to Assess the Phenotypic Variation of a Barley (<i>Hordeum</i> sp.) Gene Bank Collection for Important Agronomic Traits and Passport Information. <i>Frontiers in Plant Science</i> , 2020, 11, 604781.	3.6	7
30	Characterization of heterosis and genomic prediction-based establishment of heterotic patterns for developing better hybrids in pigeonpea. <i>Plant Genome</i> , 2021, 14, e20125.	2.8	6
31	Genome-wide prediction for hybrids between parents with distinguished difference on exotic introgressions in <i>Brassica napus</i> . <i>Crop Journal</i> , 2021, 9, 1169-1178.	5.2	6
32	Genomic prediction models trained with historical records enable populating the German ex situ genebank bio-digital resource center of barley (<i>Hordeum</i> sp.) with information on resistances to soilborne barley mosaic viruses. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2181-2196.	3.6	5
33	The elements in crystal bases corresponding to exceptional modules. <i>Chinese Annals of Mathematics Series B</i> , 2010, 31, 1-20.	0.4	4
34	Improving Selection Efficiency of Crop Breeding With Genomic Prediction Aided Sparse Phenotyping. <i>Frontiers in Plant Science</i> , 2021, 12, 735285.	3.6	4
35	An insight into the description of the crystal structure for Mirkovič-Vilonen polytopes. <i>Transactions of the American Mathematical Society</i> , 2017, 369, 6407-6427.	0.9	3
36	Parametrizations of Canonical Bases and Irreducible Components of Nilpotent Varieties. <i>International Mathematics Research Notices</i> , 2014, 2014, 3263-3278.	1.0	2

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37	Tame Quivers and Affine Enveloping Algebras. Pure and Applied Mathematics Quarterly, 2012, 8, 609-652.	0.4	0