

# Xueqiang Zhao

## List of Publications by Year in descending order

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22  
papers

1,678  
citations

394421

19  
h-index

677142

22  
g-index

26  
all docs

26  
docs citations

26  
times ranked

1789  
citing authors

#	ARTICLE	IF	CITATIONS
1	A wheat transcription factor positively sets seed vigour by regulating the grain nitrate signal. <i>New Phytologist</i> , 2020, 225, 1667-1680.	7.3	43
2	Dissection of Pleiotropic QTL Regions Controlling Wheat Spike Characteristics Under Different Nitrogen Treatments Using Traditional and Conditional QTL Mapping. <i>Frontiers in Plant Science</i> , 2019, 10, 187.	3.6	56
3	Reducing expression of a nitrate-responsive <i>ZIP</i> transcription factor increases grain yield and N use in wheat. <i>Plant Biotechnology Journal</i> , 2019, 17, 1823-1833.	8.3	48
4	A wheat/rye polymorphism affects seminal root length and yield across different irrigation regimes. <i>Journal of Experimental Botany</i> , 2019, 70, 4027-4037.	4.8	27
5	Transgenic expression of plastidic glutamine synthetase increases nitrogen uptake and yield in wheat. <i>Plant Biotechnology Journal</i> , 2018, 16, 1858-1867.	8.3	101
6	QTL Detection for Kernel Size and Weight in Bread Wheat ( <i>Triticum aestivum</i> L.) Using a High-Density SNP and SSR-Based Linkage Map. <i>Frontiers in Plant Science</i> , 2018, 9, 1484.	3.6	78
7	Characterization of the temporal and spatial expression of wheat ( <i>Triticum aestivum</i> L.) plant height at the QTL level and their influence on yield-related traits. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1235-1252.	3.6	68
8	The Auxin Biosynthetic <i>TRYPTOPHAN AMINOTRANSFERASE RELATED TaTAR2.1-3A</i> Increases Grain Yield of Wheat. <i>Plant Physiology</i> , 2017, 174, 2274-2288.	4.8	81
9	Characterization of QTLs for Root Traits of Wheat Grown under Different Nitrogen and Phosphorus Supply Levels. <i>Frontiers in Plant Science</i> , 2017, 8, 2096.	3.6	50
10	Knock out of the PHOSPHATE 2 Gene <i>TaPHO2-A1</i> Improves Phosphorus Uptake and Grain Yield under Low Phosphorus Conditions in Common Wheat. <i>Scientific Reports</i> , 2016, 6, 29850.	3.3	50
11	QTL detection for wheat kernel size and quality and the responses of these traits to low nitrogen stress. <i>Theoretical and Applied Genetics</i> , 2016, 129, 469-484.	3.6	100
12	The nitrate inducible NAC transcription factor <i>TaNAC2-5A</i> controls nitrate response and increases wheat yield. <i>Plant Physiology</i> , 2015, 169, pp.00568.2015.	4.8	146
13	QTLs for flag leaf size and their influence on yield-related traits in wheat ( <i>Triticum aestivum</i> L.). <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	91
14	A Wheat CCAAT Box-Binding Transcription Factor Increases the Grain Yield of Wheat with Less Fertilizer Input. <i>Plant Physiology</i> , 2015, 167, 411-423.	4.8	162
15	Further genetic analysis of a major quantitative trait locus controlling root length and related traits in common wheat. <i>Molecular Breeding</i> , 2014, 33, 975-985.	2.1	31
16	Auxin biosynthetic gene <i>TAR2</i> is involved in low nitrogen-mediated reprogramming of root architecture in <i>A. trichodes</i> . <i>Plant Journal</i> , 2014, 78, 70-79.	5.7	193
17	A genotypic difference in primary root length is associated with the inhibitory role of transforming growth factor- $\beta$ receptor-interacting protein-1 on root meristem size in wheat. <i>Plant Journal</i> , 2014, 77, 931-943.	5.7	33
18	A phosphate starvation response regulator <i>Ta-PHR1</i> is involved in phosphate signalling and increases grain yield in wheat. <i>Annals of Botany</i> , 2013, 111, 1139-1153.	2.9	139

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19	Major quantitative trait loci for seminal root morphology of wheat seedlings. <i>Molecular Breeding</i> , 2012, 30, 139-148.	2.1	123
20	Functional characterization of the trans-membrane domain interactions of the Sec61 protein translocation complex beta-subunit. <i>BMC Cell Biology</i> , 2009, 10, 76.	3.0	18
21	Use of Bimolecular Fluorescence Complementation in Yeast <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2008, 457, 165-175.	0.9	11
22	The Transmembrane Domain Is Sufficient for Sbh1p Function, Its Association with the Sec61 Complex, and Interaction with Rtn1p. <i>Journal of Biological Chemistry</i> , 2007, 282, 30618-30628.	3.4	21