

# Keyan Zhao

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

22  
papers

5,341  
citations

20  
h-index

22  
g-index

22  
ext. papers

6,145  
ext. citations

7.8  
avg, IF

4.37  
L-index

#	Paper	IF	Citations
22	Genome-wide association mapping reveals a rich genetic architecture of complex traits in <i>Oryza sativa</i> . <i>Nature Communications</i> , <b>2011</b> , 2, 467	17.4	875
21	The pattern of polymorphism in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , <b>2005</b> , 3, e196	9.7	764
20	An <i>Arabidopsis</i> example of association mapping in structured samples. <i>PLoS Genetics</i> , <b>2007</b> , 3, e4	6	537
19	Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 12273-8	11.5	499
18	A single IGF1 allele is a major determinant of small size in dogs. <i>Science</i> , <b>2007</b> , 316, 112-5	33.3	472
17	Genome-wide association mapping in <i>Arabidopsis</i> identifies previously known flowering time and pathogen resistance genes. <i>PLoS Genetics</i> , <b>2005</b> , 1, e60	6	337
16	A simple genetic architecture underlies morphological variation in dogs. <i>PLoS Biology</i> , <b>2010</b> , 8, e1000451	9.7	331
15	Genetic architecture of aluminum tolerance in rice ( <i>Oryza sativa</i> ) determined through genome-wide association analysis and QTL mapping. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002221	6	278
14	Genomic diversity and introgression in <i>O. sativa</i> reveal the impact of domestication and breeding on the rice genome. <i>PLoS ONE</i> , <b>2010</b> , 5, e10780	3.7	209
13	Variation in molybdenum content across broadly distributed populations of <i>Arabidopsis thaliana</i> is controlled by a mitochondrial molybdenum transporter (MOT1). <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000004	6	192
12	Development of genome-wide SNP assays for rice. <i>Breeding Science</i> , <b>2010</b> , 60, 524-535	2	149
11	High-throughput two-dimensional root system phenotyping platform facilitates genetic analysis of root growth and development. <i>Plant, Cell and Environment</i> , <b>2013</b> , 36, 454-66	8.4	133
10	High-throughput single nucleotide polymorphism genotyping for breeding applications in rice using the BeadXpress platform. <i>Molecular Breeding</i> , <b>2012</b> , 29, 875-886	3.4	117
9	A nonparametric test reveals selection for rapid flowering in the <i>Arabidopsis</i> genome. <i>PLoS Biology</i> , <b>2006</b> , 4, e137	9.7	108
8	Genome-wide survey of <i>Arabidopsis</i> natural variation in downy mildew resistance using combined association and linkage mapping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 10302-7	11.5	94
7	Haplotype structure and phenotypic associations in the chromosomal regions surrounding two <i>Arabidopsis thaliana</i> flowering time loci. <i>Genetics</i> , <b>2004</b> , 168, 1627-38	4	63
6	Development of a Research Platform for Dissecting Phenotype-Genotype Associations in Rice ( <i>Oryza</i> spp.). <i>Rice</i> , <b>2010</b> , 3, 205-217	5.8	62

5	ALCHEMY: a reliable method for automated SNP genotype calling for small batch sizes and highly homozygous populations. <i>Bioinformatics</i> , <b>2010</b> , 26, 2952-60	7.2	45
4	Differential genetic regulation of canine hip dysplasia and osteoarthritis. <i>PLoS ONE</i> , <b>2010</b> , 5, e13219	3.7	43
3	Association mapping with single-feature polymorphisms. <i>Genetics</i> , <b>2006</b> , 173, 1125-33	4	28
2	Genome-wide association mapping using mixed-models: application to GAW15 Problem 3. <i>BMC Proceedings</i> , <b>2007</b> , 1 Suppl 1, S164	2.3	4
1	Genome-wide association mapping in <i>Arabidopsis thaliana</i> identifies previously known genes responsible for variation in flowering time and pathogen resistance. <i>PLoS Genetics</i> , <b>2005</b> , preprint, e60	6	1