

# Xiangchao Gan

## 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.

35  
papers

4,553  
citations

19  
h-index

43  
g-index

43  
ext. papers

5,957  
ext. citations

19.3  
avg, IF

5.67  
L-index

#	Paper	IF	Citations
35	Mouse genomic variation and its effect on phenotypes and gene regulation. <i>Nature</i> , <b>2011</b> , 477, 289-94	50.4	1087
34	1,135 Genomes Reveal the Global Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>Cell</i> , <b>2016</b> , 166, 481-491	40.1	620
33	Sparse whole-genome sequencing identifies two loci for major depressive disorder. <i>Nature</i> , <b>2015</b> , 523, 588-91	50.4	584
32	Multiple reference genomes and transcriptomes for <i>Arabidopsis thaliana</i> . <i>Nature</i> , <b>2011</b> , 477, 419-23	50.4	495
31	Epigenomic Diversity in a Global Collection of <i>Arabidopsis thaliana</i> Accessions. <i>Cell</i> , <b>2016</b> , 166, 492-505	56.2	353
30	Sequence-based characterization of structural variation in the mouse genome. <i>Nature</i> , <b>2011</b> , 477, 326-9	50.4	230
29	Leaf shape evolution through duplication, regulatory diversification, and loss of a homeobox gene. <i>Science</i> , <b>2014</b> , 343, 780-3	33.3	188
28	Molecular signatures of major depression. <i>Current Biology</i> , <b>2015</b> , 25, 1146-56	6.3	162
27	Commercially available outbred mice for genome-wide association studies. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001085	10.85	102
26	Genome-wide analysis of mutations in mutant lineages selected following fast-neutron irradiation mutagenesis of <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , <b>2012</b> , 22, 1306-15	9.7	87
25	Morphomechanical Innovation Drives Explosive Seed Dispersal. <i>Cell</i> , <b>2016</b> , 166, 222-33	56.2	86
24	Microarray missing data imputation based on a set theoretic framework and biological knowledge. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 1608-19	20.1	79
23	Regenerant <i>Arabidopsis</i> lineages display a distinct genome-wide spectrum of mutations conferring variant phenotypes. <i>Current Biology</i> , <b>2011</b> , 21, 1385-90	6.3	65
22	Resolving the backbone of the Brassicaceae phylogeny for investigating trait diversity. <i>New Phytologist</i> , <b>2019</b> , 222, 1638-1651	9.8	62
21	<i>Cardamine hirsuta</i> : a versatile genetic system for comparative studies. <i>Plant Journal</i> , <b>2014</b> , 78, 1-15	6.9	61
20	The architecture of parent-of-origin effects in mice. <i>Cell</i> , <b>2014</b> , 156, 332-42	56.2	59
19	Discovering biclusters in gene expression data based on high-dimensional linear geometries. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 209	3.6	59

18	The Cardamine <i>hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , <b>2016</b> , 2, 16167	11.5	56
17	A WOX/Auxin Biosynthesis Module Controls Growth to Shape Leaf Form. <i>Current Biology</i> , <b>2020</b> , 30, 4857-4868.e6	11.6	12
16	Genomic Rearrangements in Considered as Quantitative Traits. <i>Genetics</i> , <b>2017</b> , 205, 1425-1441	4	15
15	LMI1 homeodomain protein regulates organ proportions by spatial modulation of endoreduplication. <i>Genes and Development</i> , <b>2018</b> , 32, 1361-1366	12.6	15
14	Photoreceptor Activity Contributes to Contrasting Responses to Shade in Cardamine and Arabidopsis Seedlings. <i>Plant Cell</i> , <b>2019</b> , 31, 2649-2663	11.6	12
13	Autoregulation of RCO by Low-Affinity Binding Modulates Cytokinin Action and Shapes Leaf Diversity. <i>Current Biology</i> , <b>2019</b> , 29, 4183-4192.e6	6.3	10
12	Extending the model of Arabidopsis telomere length and composition across Brassicaceae. <i>Chromosome Research</i> , <b>2014</b> , 22, 153-66	4.4	8
11	Gene expression evolution in pattern-triggered immunity within Arabidopsis thaliana and across Brassicaceae species. <i>Plant Cell</i> , <b>2021</b> ,	11.6	8
10	Blocking artifact reduction in compressed images based on edge-adaptive quadrangle meshes. <i>Journal of Visual Communication and Image Representation</i> , <b>2003</b> , 14, 492-507	2.7	5
9	Microarray-based ultra-high resolution discovery of genomic deletion mutations. <i>BMC Genomics</i> , <b>2014</b> , 15, 224	4.5	4
8	Microarray-based optimization to detect genomic deletion mutations. <i>Genomics Data</i> , <b>2014</b> , 2, 53-54		4
7	Beyond flowering time: diverse roles of an APETALA2-like transcription factor in shoot architecture and perennial traits. <i>New Phytologist</i> , <b>2021</b> , 229, 444-459	9.8	4
6	Complement Genome Annotation Lift Over Using a Weighted Sequence Alignment Strategy. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1046	4.5	3
5	Recovery of novel association loci in Arabidopsis thaliana and Drosophila melanogaster through leveraging INDELs association and integrated burden test. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007699	6	3
4	Gene expression evolution in pattern-triggered immunity within Arabidopsis thaliana and across Brassicaceae species		2
3	Fine-scale empirical data on niche divergence and homeolog expression patterns in an allopolyploid and its diploid progenitor species. <i>New Phytologist</i> , <b>2021</b> , 229, 3587-3601	9.8	2
2	Bicluster Analysis for Coherent Pattern Discovery <b>2015</b> , 1665-1674		1
1	Microarray Gene Expression Data Analysis <b>2010</b> , 623-650		0

