

# Xiaosen Guo

## List of Publications by Year in Descending Order

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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.

16  
papers

12,675  
citations

15  
h-index

17  
g-index

17  
ext. papers

17,004  
ext. citations

27.7  
avg, IF

3.49  
L-index

#	Paper	IF	Citations
16	Balanced Chromosomal Rearrangement Detection by Low-Pass Whole-Genome Sequencing. <i>Current Protocols in Human Genetics</i> , <b>2018</b> , 96, 8.18.1-8.18.16	3.2	7
15	Identification of balanced chromosomal rearrangements previously unknown among participants in the 1000 Genomes Project: implications for interpretation of structural variation in genomes and the future of clinical cytogenetics. <i>Genetics in Medicine</i> , <b>2018</b> , 20, 697-707	8.1	36
14	Whole-genome sequencing of 175 Mongolians uncovers population-specific genetic architecture and gene flow throughout North and East Asia. <i>Nature Genetics</i> , <b>2018</b> , 50, 1696-1704	36.3	27
13	Deep whole-genome sequencing of 90 Han Chinese genomes. <i>GigaScience</i> , <b>2017</b> , 6, 1-7	7.6	22
12	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , <b>2017</b> , 548, 87-91	50.4	87
11	A Genetic Mechanism for Convergent Skin Lightening during Recent Human Evolution. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 1177-87	8.3	28
10	A global reference for human genetic variation. <i>Nature</i> , <b>2015</b> , 526, 68-74	50.4	8599
9	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , <b>2015</b> , 526, 82-90	50.4	776
8	Association Analysis of Genetic Variants with Type 2 Diabetes in a Mongolian Population in China. <i>Journal of Diabetes Research</i> , <b>2015</b> , 2015, 613236	3.9	18
7	The genome of a Mongolian individual reveals the genetic imprints of Mongolians on modern human populations. <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 3122-36	3.9	19
6	The draft genome of watermelon ( <i>Citrullus lanatus</i> ) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , <b>2013</b> , 45, 51-8	36.3	503
5	Whole-genome sequencing of giant pandas provides insights into demographic history and local adaptation. <i>Nature Genetics</i> , <b>2013</b> , 45, 67-71	36.3	219
4	An Aboriginal Australian genome reveals separate human dispersals into Asia. <i>Science</i> , <b>2011</b> , 334, 94-8	33.3	528
3	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , <b>2010</b> , 463, 311-7	50.4	864
2	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , <b>2010</b> , 463, 757-62	50.4	567
1	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , <b>2010</b> , 42, 1027-30	36.3	365