

# Wei-Ming He

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7412153/publications.pdf>

Version: 2024-02-01

10  
papers

5,268  
citations

1040056

9  
h-index

1372567

10  
g-index

10  
all docs

10  
docs citations

10  
times ranked

8568  
citing authors

#	ARTICLE	IF	CITATIONS
1	LDBlockShow: a fast and convenient tool for visualizing linkage disequilibrium and haplotype blocks based on variant call format files. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	177
2	Whole genome sequence analysis reveals genetic structure and X-chromosome haplotype structure in indigenous Chinese pigs. <i>Scientific Reports</i> , 2020, 10, 9433.	3.3	11
3	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. <i>Nature Genetics</i> , 2019, 51, 857-864.	21.4	219
4	Recent breeding programs enhanced genetic diversity in both desi and kabuli varieties of chickpea ( <i>Cicer arietinum</i> L.). <i>Scientific Reports</i> , 2016, 6, 38636.	3.3	77
5	Adaptation and possible ancient interspecies introgression in pigs identified by whole-genome sequencing. <i>Nature Genetics</i> , 2015, 47, 217-225.	21.4	288
6	Draft genome sequence of chickpea ( <i>Cicer arietinum</i> ) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	17.5	1,049
7	Whole-genome sequencing of giant pandas provides insights into demographic history and local adaptation. <i>Nature Genetics</i> , 2013, 45, 67-71.	21.4	303
8	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2012, 30, 105-111.	17.5	818
9	Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. <i>Science</i> , 2010, 329, 75-78.	12.6	1,339
10	Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. <i>Nature Genetics</i> , 2010, 42, 1053-1059.	21.4	987