

# Binghang Liu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11346389/publications.pdf>

Version: 2024-02-01

13  
papers

13,006  
citations

623188

14  
h-index

996533

15  
g-index

15  
all docs

15  
docs citations

15  
times ranked

19327  
citing authors

#	ARTICLE	IF	CITATIONS
1	SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. <i>GigaScience</i> , 2012, 1, 18.	3.3	4,510
2	The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 2012, 490, 49-54.	13.7	1,966
3	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
4	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
5	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	13.7	1,058
6	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582
7	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443
8	Insights into salt tolerance from the genome of <i>Thellungiella salsuginea</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12219-12224.	3.3	272
9	Comparison of the two major classes of assembly algorithms: overlap-layout-consensus and de-bruijn-graph. <i>Briefings in Functional Genomics</i> , 2012, 11, 25-37.	1.3	195
10	COPE: an accurate <i>k</i> -mer-based pair-end reads connection tool to facilitate genome assembly. <i>Bioinformatics</i> , 2012, 28, 2870-2874.	1.8	145
11	De novo assembly of a haplotype-resolved human genome. <i>Nature Biotechnology</i> , 2015, 33, 617-622.	9.4	73
12	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014, 3, 27.	3.3	72
13	BASE: a practical de novo assembler for large genomes using long NGS reads. <i>BMC Genomics</i> , 2016, 17, 499.	1.2	6