

Binghang Liu

List of Publications by Year in descending order

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

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