

Chang Yu

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.

19
papers

17,494
citations

18
h-index

22
g-index

22
ext. papers

20,972
ext. citations

21
avg, IF

5.14
L-index

#	Paper	IF	Citations
19	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010 , 464, 59-65	50.4	7044
18	SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. <i>GigaScience</i> , 2012 , 1, 18	7.6	3152
17	SOAP2: an improved ultrafast tool for short read alignment. <i>Bioinformatics</i> , 2009 , 25, 1966-7	7.2	2784
16	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010 , 463, 311-7	50.4	864
15	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008 , 456, 60-5	50.4	744
14	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2011 , 30, 105-11	44.5	635
13	Single-cell exome sequencing and monoclonal evolution of a JAK2-negative myeloproliferative neoplasm. <i>Cell</i> , 2012 , 148, 873-85	56.2	431
12	Historical variations in mutation rate in an epidemic pathogen, <i>Yersinia pestis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 577-82	11.5	284
11	Complete resequencing of 40 genomes reveals domestication events and genes in silkworm (<i>Bombyx</i>). <i>Science</i> , 2009 , 326, 433-6	33.3	277
10	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. <i>Nature Genetics</i> , 2010 , 42, 969-72	36.3	264
9	The DNA methylome of human peripheral blood mononuclear cells. <i>PLoS Biology</i> , 2010 , 8, e1000533	9.7	256
8	Single-base resolution maps of cultivated and wild rice methylomes and regulatory roles of DNA methylation in plant gene expression. <i>BMC Genomics</i> , 2012 , 13, 300	4.5	202
7	SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. <i>Bioinformatics</i> , 2012 , 28, 878-9	7.2	158
6	Discovery of biclonal origin and a novel oncogene SLC12A5 in colon cancer by single-cell sequencing. <i>Cell Research</i> , 2014 , 24, 701-12	24.7	99
5	Single-cell sequencing analysis characterizes common and cell-lineage-specific mutations in a muscle-invasive bladder cancer. <i>GigaScience</i> , 2012 , 1, 12	7.6	82
4	SOAP3-dp: fast, accurate and sensitive GPU-based short read aligner. <i>PLoS ONE</i> , 2013 , 8, e65632	3.7	76
3	PSCC: sensitive and reliable population-scale copy number variation detection method based on low coverage sequencing. <i>PLoS ONE</i> , 2014 , 9, e85096	3.7	21

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| 2 | Two-step source tracing strategy of <i>Yersinia pestis</i> and its historical epidemiology in a specific region. <i>PLoS ONE</i> , 2014 , 9, e85374 | 3.7 | 9 |
| 1 | MICA: A fast short-read aligner that takes full advantage of Many Integrated Core Architecture (MIC). <i>BMC Bioinformatics</i> , 2015 , 16 Suppl 7, S10 | 3.6 | 7 |