

Chang Yu

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.

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	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
18	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
17	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
16	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
15	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
14	SOAP3-dp: fast, accurate and sensitive GPU-based short read aligner. <i>PLoS ONE</i> , 2013 , 8, e65632	3.7	76
13	SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. <i>Bioinformatics</i> , 2012 , 28, 878-9	7.2	158
12	Single-cell exome sequencing and monoclonal evolution of a JAK2-negative myeloproliferative neoplasm. <i>Cell</i> , 2012 , 148, 873-85	56.2	431
11	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
10	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
9	SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. <i>GigaScience</i> , 2012 , 1, 18	7.6	3152
8	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
7	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010 , 463, 311-7	50.4	864
6	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010 , 464, 59-65	50.4	7044
5	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
4	The DNA methylome of human peripheral blood mononuclear cells. <i>PLoS Biology</i> , 2010 , 8, e1000533	9.7	256
3	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

- 2 SOAP2: an improved ultrafast tool for short read alignment. *Bioinformatics*, **2009**, 25, 1966-7 7.2 2784
- 1 The diploid genome sequence of an Asian individual. *Nature*, **2008**, 456, 60-5 50.4 744