Chang Yu

List of Publications by Year
in descending order

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Version: 2024-02-01

20
papers

22,749
citations

394286
19
h-index

713332
21
g-index

22
all docs

22
docs citations

22
times ranked

34609
citing authors

#	Article	IF	Citations
1	MICA: A fast short-read aligner that takes full advantage of Many Integrated Core Architecture (MIC). BMC Bioinformatics, 2015, 16, S10.	1.2	14
2	Discovery of biclonal origin and a novel oncogene SLC12A5 in colon cancer by single-cell sequencing. Cell Research, 2014, 24, 701-712.	5.7	123
3	PSCC: Sensitive and Reliable Population-Scale Copy Number Variation Detection Method Based on Low Coverage Sequencing. PLoS ONE, 2014, 9, e85096.	1.1	30
4	Two-Step Source Tracing Strategy of Yersinia pestis and Its Historical Epidemiology in a Specific Region. PLoS ONE, 2014, 9, e85374.	1.1	9
5	Historical variations in mutation rate in an epidemic pathogen, <i>Yersinia pestis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 577-582.	3.3	373
6	SOAP3-dp: Fast, Accurate and Sensitive GPU-Based Short Read Aligner. PLoS ONE, 2013, 8, e65632.	1.1	104
7	Efficient SNP-sensitive alignment and database-assisted SNP calling for low coverage samples. , 2012, , .		0
8	SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. Bioinformatics, 2012, 28, 878-879.	1.8	200
9	Single-Cell Exome Sequencing and Monoclonal Evolution of a JAK2-Negative Myeloproliferative Neoplasm. Cell, 2012, 148, 873-885.	13.5	503
10	Single-base resolution maps of cultivated and wild rice methylomes and regulatory roles of DNA methylation in plant gene expression. BMC Genomics, 2012, 13, 300.	1.2	266
11	Single-cell sequencing analysis characterizes common and cell-lineage-specific mutations in a muscle-invasive bladder cancer. GigaScience, 2012, 1, 12.	3.3	99
12	SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. GigaScience, 2012, 1, 18.	3.3	4,510
13	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. Nature Biotechnology, 2012, 30, 105-111.	9.4	818
14	The sequence and de novo assembly of the giant panda genome. Nature, 2010, 463, 311-317.	13.7	1,058
15	A human gut microbial gene catalogue established by metagenomic sequencing. Nature, 2010, 464, 59-65.	13.7	9,342
16	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. Nature Genetics, 2010, 42, 969-972.	9.4	297
17	The DNA Methylome of Human Peripheral Blood Mononuclear Cells. PLoS Biology, 2010, 8, e1000533.	2.6	290
18	Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	6.0	342

#	ARTICLE	IF	CITATIONS
19	SOAP2: an improved ultrafast tool for short read alignment. Bioinformatics, 2009, 25, 1966-1967.	1.8	3,329
20	The diploid genome sequence of an Asian individual. Nature, 2008, 456, 60-65.	13.7	834