

# Chang Yu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12131784/publications.pdf>

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	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342
2	SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. <i>GigaScience</i> , 2012, 1, 18.	3.3	4,510
3	SOAP2: an improved ultrafast tool for short read alignment. <i>Bioinformatics</i> , 2009, 25, 1966-1967.	1.8	3,329
4	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	13.7	1,058
5	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008, 456, 60-65.	13.7	834
6	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2012, 30, 105-111.	9.4	818
7	Single-Cell Exome Sequencing and Monoclonal Evolution of a JAK2-Negative Myeloproliferative Neoplasm. <i>Cell</i> , 2012, 148, 873-885.	13.5	503
8	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, 577-582.	3.3	373
9	Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm ( <i>Bombyx mori</i> ). <i>PLoS ONE</i> , 2014, 9, e107431.	6.0	342
10	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. <i>Nature Genetics</i> , 2010, 42, 969-972.	9.4	297
11	The DNA Methylome of Human Peripheral Blood Mononuclear Cells. <i>PLoS Biology</i> , 2010, 8, e1000533.	2.6	290
12	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.	1.2	266
13	SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. <i>Bioinformatics</i> , 2012, 28, 878-879.	1.8	200
14	Discovery of biclonal origin and a novel oncogene SLC12A5 in colon cancer by single-cell sequencing. <i>Cell Research</i> , 2014, 24, 701-712.	5.7	123
15	SOAP3-dp: Fast, Accurate and Sensitive GPU-Based Short Read Aligner. <i>PLoS ONE</i> , 2013, 8, e65632.	1.1	104
16	Single-cell sequencing analysis characterizes common and cell-lineage-specific mutations in a muscle-invasive bladder cancer. <i>GigaScience</i> , 2012, 1, 12.	3.3	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.	1.1	30
18	MICA: A fast short-read aligner that takes full advantage of Many Integrated Core Architecture (MIC). <i>BMC Bioinformatics</i> , 2015, 16, S10.	1.2	14

#	ARTICLE	IF	CITATIONS
19	Two-Step Source Tracing Strategy of <i>Yersinia pestis</i> and Its Historical Epidemiology in a Specific Region. PLoS ONE, 2014, 9, e85374.	1.1	9
20	Efficient SNP-sensitive alignment and database-assisted SNP calling for low coverage samples. , 2012, , .		0