

Chen-Shan Chin

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

17,688
citations

126907

33
h-index

243625

44
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67
all docs

67
docs citations

67
times ranked

23257
citing authors

#	ARTICLE	IF	CITATIONS
1	Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. <i>Nature Methods</i> , 2013, 10, 563-569.	19.0	4,029
2	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016, 13, 1050-1054.	19.0	1,658
3	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
4	Improved maize reference genome with single-molecule technologies. <i>Nature</i> , 2017, 546, 524-527.	27.8	1,113
5	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , 2019, 37, 1155-1162.	17.5	1,010
6	Assembling large genomes with single-molecule sequencing and locality-sensitive hashing. <i>Nature Biotechnology</i> , 2015, 33, 623-630.	17.5	877
7	Origins of the <i>E. coli</i> Strain Causing an Outbreak of Hemolytic Uremic Syndrome in Germany. <i>New England Journal of Medicine</i> , 2011, 365, 709-717.	27.0	778
8	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. <i>Genome Research</i> , 2017, 27, 849-864.	5.5	728
9	The Origin of the Haitian Cholera Outbreak Strain. <i>New England Journal of Medicine</i> , 2011, 364, 33-42.	27.0	676
10	Validation of ITD mutations in FLT3 as a therapeutic target in human acute myeloid leukaemia. <i>Nature</i> , 2012, 485, 260-263.	27.8	641
11	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	12.8	636
12	Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , 2015, 12, 780-786.	19.0	465
13	Comparing genomic expression patterns across species identifies shared transcriptional profile in aging. <i>Nature Genetics</i> , 2004, 36, 197-204.	21.4	434
14	A flexible and efficient template format for circular consensus sequencing and SNP detection. <i>Nucleic Acids Research</i> , 2010, 38, e159-e159.	14.5	377
15	Long-read sequence assembly of the gorilla genome. <i>Science</i> , 2016, 352, aae0344.	12.6	368
16	Scaffolding of long read assemblies using long range contact information. <i>BMC Genomics</i> , 2017, 18, 527.	2.8	194
17	A hybrid approach for the automated finishing of bacterial genomes. <i>Nature Biotechnology</i> , 2012, 30, 701-707.	17.5	178
18	De novo PacBio long-read and phased avian genome assemblies correct and add to reference genes generated with intermediate and short reads. <i>GigaScience</i> , 2017, 6, 1-16.	6.4	165

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19	A complete reference genome improves analysis of human genetic variation. <i>Science</i> , 2022, 376, eabl3533.	12.6	144
20	Heterogeneous resistance to quizartinib in acute myeloid leukemia revealed by single-cell analysis. <i>Blood</i> , 2017, 130, 48-58.	1.4	143
21	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line. <i>Genome Research</i> , 2018, 28, 1126-1135.	5.5	142
22	Extending reference assembly models. <i>Genome Biology</i> , 2015, 16, 13.	8.8	139
23	Long-read, whole-genome shotgun sequence data for five model organisms. <i>Scientific Data</i> , 2014, 1, 140045.	5.3	138
24	HLA Typing for the Next Generation. <i>PLoS ONE</i> , 2015, 10, e0127153.	2.5	125
25	Chromosome-scale, haplotype-resolved assembly of human genomes. <i>Nature Biotechnology</i> , 2021, 39, 309-312.	17.5	109
26	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. <i>PLoS Genetics</i> , 2016, 12, e1005954.	3.5	105
27	Curated variation benchmarks for challenging medically relevant autosomal genes. <i>Nature Biotechnology</i> , 2022, 40, 672-680.	17.5	90
28	Benchmarking challenging small variants with linked and long reads. <i>Cell Genomics</i> , 2022, 2, 100128.	6.5	77
29	Global identification of noncoding RNAs in <i>Saccharomyces cerevisiae</i> by modulating an essential RNA processing pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4192-4197.	7.1	69
30	A diploid assembly-based benchmark for variants in the major histocompatibility complex. <i>Nature Communications</i> , 2020, 11, 4794.	12.8	56
31	Genome-wide regulatory complexity in yeast promoters: Separation of functionally conserved and neutral sequence. <i>Genome Research</i> , 2005, 15, 205-213.	5.5	43
32	Dynamics and Design Principles of a Basic Regulatory Architecture Controlling Metabolic Pathways. <i>PLoS Biology</i> , 2008, 6, e146.	5.6	43
33	Stationary-state skewness in two-dimensional Kardar-Parisi-Zhang type growth. <i>Physical Review E</i> , 1999, 59, 2633-2641.	2.1	40
34	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. <i>Nature Communications</i> , 2020, 11, 2288.	12.8	39
35	Amplification-free long-read sequencing reveals unforeseen CRISPR-Cas9 off-target activity. <i>Genome Biology</i> , 2020, 21, 290.	8.8	35
36	Passive random walkers and riverlike networks on growing surfaces. <i>Physical Review E</i> , 2002, 66, 021104.	2.1	22

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37	Comprehensive analysis of single molecule sequencing-derived complete genome and whole transcriptome of <i>Hyposidra talaca</i> nuclear polyhedrosis virus. <i>Scientific Reports</i> , 2018, 8, 8924.	3.3	8
38	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. <i>F1000Research</i> , 2021, 10, 246.	1.6	3
39	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. <i>F1000Research</i> , 2021, 10, 246.	1.6	2
40	Reconstructed rough growing interfaces: Ridge-line trapping of domain walls. <i>Physical Review E</i> , 2001, 64, 031606.	2.1	1
41	A draft sequence reference of the <i>Psilocybe cubensis</i> genome. <i>F1000Research</i> , 2021, 10, 281.	1.6	1
42	A draft reference assembly of the <i>Psilocybe cubensis</i> genome. <i>F1000Research</i> , 2021, 10, 281.	1.6	1
43	Ten simple rules for large-scale data processing. <i>PLoS Computational Biology</i> , 2022, 18, e1009757.	3.2	1