

Chen-Shan Chin

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.

62

papers

11,016

citations

31

h-index

67

g-index

67

ext. papers

15,032

ext. citations

19.9

avg, IF

5.63

L-index

#	Paper	IF	Citations
62	Curated variation benchmarks for challenging medically relevant autosomal genes.. <i>Nature Biotechnology</i> , 2022 ,	44.5	12
61	A complete reference genome improves analysis of human genetic variation.. <i>Science</i> , 2022 , 376, eabl3533	33.3	12
60	The complete sequence of a human genome.. <i>Science</i> , 2022 , 376, 44-53	33.3	107
59	Benchmarking challenging small variants with linked and long reads. <i>Cell Genomics</i> , 2022 , 2, 100128		2
58	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	3.6	2
57	A draft sequence reference of the genome. <i>F1000Research</i> , 2021 , 10, 281	3.6	0
56	A draft reference assembly of the <i>Psilocybe cubensis</i> genome. <i>F1000Research</i> , 2021 , 10, 281	3.6	
55	Chromosome-scale, haplotype-resolved assembly of human genomes. <i>Nature Biotechnology</i> , 2021 , 39, 309-312	44.5	44
54	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	3.6	1
53	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. <i>Nature Communications</i> , 2020 , 11, 2288	17.4	21
52	Amplification-free long-read sequencing reveals unforeseen CRISPR-Cas9 off-target activity. <i>Genome Biology</i> , 2020 , 21, 290	18.3	12
51	A diploid assembly-based benchmark for variants in the major histocompatibility complex. <i>Nature Communications</i> , 2020 , 11, 4794	17.4	22
50	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019 , 10, 1784	17.4	346
49	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , 2019 , 37, 1155-1162	44.5	427
48	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	4.9	6
47	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	9.7	74
46	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	9.7	365

45	Heterogeneous resistance to quizartinib in acute myeloid leukemia revealed by single-cell analysis. <i>Blood</i> , 2017 , 130, 48-58	2.2	100
44	Improved maize reference genome with single-molecule technologies. <i>Nature</i> , 2017 , 546, 524-527	50.4	643
43	Scaffolding of long read assemblies using long range contact information. <i>BMC Genomics</i> , 2017 , 18, 527	4.5	90
42	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	7.6	97
41	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016 , 13, 1050-1054	21.6	1015
40	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. <i>PLoS Genetics</i> , 2016 , 12, e1005954	6	77
39	Long-read sequence assembly of the gorilla genome. <i>Science</i> , 2016 , 352, aae0344	33.3	282
38	Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , 2015 , 12, 780-6	21.6	383
37	Extending reference assembly models. <i>Genome Biology</i> , 2015 , 16, 13	18.3	107
36	HLA Typing for the Next Generation. <i>PLoS ONE</i> , 2015 , 10, e0127153	3.7	95
35	Assembling large genomes with single-molecule sequencing and locality-sensitive hashing. <i>Nature Biotechnology</i> , 2015 , 33, 623-30	44.5	650
34	Long-read, whole-genome shotgun sequence data for five model organisms. <i>Scientific Data</i> , 2014 , 1, 140045	8.2	106
33	Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. <i>Nature Methods</i> , 2013 , 10, 563-9	21.6	2823
32	A hybrid approach for the automated finishing of bacterial genomes. <i>Nature Biotechnology</i> , 2012 , 30, 701-707	44.5	157
31	Validation of ITD mutations in FLT3 as a therapeutic target in human acute myeloid leukaemia. <i>Nature</i> , 2012 , 485, 260-3	50.4	525
30	Origins of the E. coli strain causing an outbreak of hemolytic-uremic syndrome in Germany. <i>New England Journal of Medicine</i> , 2011 , 365, 709-17	59.2	658
29	The origin of the Haitian cholera outbreak strain. <i>New England Journal of Medicine</i> , 2011 , 364, 33-42	59.2	559
28	A flexible and efficient template format for circular consensus sequencing and SNP detection. <i>Nucleic Acids Research</i> , 2010 , 38, e159	20.1	292

27	Dynamics and design principles of a basic regulatory architecture controlling metabolic pathways. <i>PLoS Biology</i> , 2008 , 6, e146	9.7	39
26	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, 4192-7	11.5	66
25	Genome-wide regulatory complexity in yeast promoters: separation of functionally conserved and neutral sequence. <i>Genome Research</i> , 2005 , 15, 205-13	9.7	39
24	Comparing genomic expression patterns across species identifies shared transcriptional profile in aging. <i>Nature Genetics</i> , 2004 , 36, 197-204	36.3	362
23	Passive random walkers and riverlike networks on growing surfaces. <i>Physical Review E</i> , 2002 , 66, 021104	2.4	17
22	Reconstructed rough growing interfaces: ridge-line trapping of domain walls. <i>Physical Review E</i> , 2001 , 64, 031606	2.4	1
21	Stationary-state skewness in two-dimensional Kardar-Parisi-Zhang type growth. <i>Physical Review E</i> , 1999 , 59, 2633-2641	2.4	35
20	Assembling Large Genomes with Single-Molecule Sequencing and Locality Sensitive Hashing		10
19	Phased Diploid Genome Assembly with Single Molecule Real-Time Sequencing		16
18	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly		13
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16	Ribbon: Visualizing complex genome alignments and structural variation		29
15	Scaffolding of long read assemblies using long range contact information		1
14	De Novo PacBio long-read and phased avian genome assemblies correct and add to genes important in neuroscience research		8
13	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line		6
12	Multi-platform discovery of haplotype-resolved structural variation in human genomes		26
11	Amplification-free long read sequencing reveals unforeseen CRISPR-Cas9 off-target activity		5
10	Benchmarking challenging small variants with linked and long reads		26

9	Highly-accurate long-read sequencing improves variant detection and assembly of a human genome	29
8	Human Genome Assembly in 100 Minutes	40
7	Accurate chromosome-scale haplotype-resolved assembly of human genomes	18
6	A Diploid Assembly-based Benchmark for Variants in the Major Histocompatibility Complex	4
5	Effect of Sequence Depth and Length in Long-read Assembly of the Maize Inbred NC358	5
4	Long-read whole genome analysis of human single cells	3
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1	Automated assembly of high-quality diploid human reference genomes	3