

# Chen-Shan Chin

## List of Publications by Citations

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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	Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. <i>Nature Methods</i> , <b>2013</b> , 10, 563-9	21.6	2823
61	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , <b>2016</b> , 13, 1050-1054	21.6	1015
60	Origins of the E. coli strain causing an outbreak of hemolytic-uremic syndrome in Germany. <i>New England Journal of Medicine</i> , <b>2011</b> , 365, 709-17	59.2	658
59	Assembling large genomes with single-molecule sequencing and locality-sensitive hashing. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 623-30	44.5	650
58	Improved maize reference genome with single-molecule technologies. <i>Nature</i> , <b>2017</b> , 546, 524-527	50.4	643
57	The origin of the Haitian cholera outbreak strain. <i>New England Journal of Medicine</i> , <b>2011</b> , 364, 33-42	59.2	559
56	Validation of ITD mutations in FLT3 as a therapeutic target in human acute myeloid leukaemia. <i>Nature</i> , <b>2012</b> , 485, 260-3	50.4	525
55	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 1155-1162	44.5	427
54	Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , <b>2015</b> , 12, 780-6	21.6	383
53	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. <i>Genome Research</i> , <b>2017</b> , 27, 849-864	9.7	365
52	Comparing genomic expression patterns across species identifies shared transcriptional profile in aging. <i>Nature Genetics</i> , <b>2004</b> , 36, 197-204	36.3	362
51	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , <b>2019</b> , 10, 1784	17.4	346
50	A flexible and efficient template format for circular consensus sequencing and SNP detection. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, e159	20.1	292
49	Long-read sequence assembly of the gorilla genome. <i>Science</i> , <b>2016</b> , 352, aae0344	33.3	282
48	A hybrid approach for the automated finishing of bacterial genomes. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 701-707	44.5	157
47	Extending reference assembly models. <i>Genome Biology</i> , <b>2015</b> , 16, 13	18.3	107
46	The complete sequence of a human genome.. <i>Science</i> , <b>2022</b> , 376, 44-53	33.3	107

45	Long-read, whole-genome shotgun sequence data for five model organisms. <i>Scientific Data</i> , <b>2014</b> , 1, 140045	8.2	106
44	Heterogeneous resistance to quizartinib in acute myeloid leukemia revealed by single-cell analysis. <i>Blood</i> , <b>2017</b> , 130, 48-58	2.2	100
43	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> , <b>2017</b> , 6, 1-16	7.6	97
42	HLA Typing for the Next Generation. <i>PLoS ONE</i> , <b>2015</b> , 10, e0127153	3.7	95
41	Scaffolding of long read assemblies using long range contact information. <i>BMC Genomics</i> , <b>2017</b> , 18, 527	4.5	90
40	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1005954	6	77
39	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line. <i>Genome Research</i> , <b>2018</b> , 28, 1126-1135	9.7	74
38	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> , <b>2006</b> , 103, 4192-7	11.5	66
37	The complete sequence of a human genome		58
36	Chromosome-scale, haplotype-resolved assembly of human genomes. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 309-312	44.5	44
35	Human Genome Assembly in 100 Minutes		40
34	Dynamics and design principles of a basic regulatory architecture controlling metabolic pathways. <i>PLoS Biology</i> , <b>2008</b> , 6, e146	9.7	39
33	Genome-wide regulatory complexity in yeast promoters: separation of functionally conserved and neutral sequence. <i>Genome Research</i> , <b>2005</b> , 15, 205-13	9.7	39
32	Stationary-state skewness in two-dimensional Kardar-Parisi-Zhang type growth. <i>Physical Review E</i> , <b>1999</b> , 59, 2633-2641	2.4	35
31	Ribbon: Visualizing complex genome alignments and structural variation		29
30	Highly-accurate long-read sequencing improves variant detection and assembly of a human genome		29
29	Multi-platform discovery of haplotype-resolved structural variation in human genomes		26
28	Benchmarking challenging small variants with linked and long reads		26

27	A diploid assembly-based benchmark for variants in the major histocompatibility complex. <i>Nature Communications</i> , <b>2020</b> , 11, 4794	17.4	22
26	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. <i>Nature Communications</i> , <b>2020</b> , 11, 2288	17.4	21
25	Accurate chromosome-scale haplotype-resolved assembly of human genomes		18
24	Passive random walkers and riverlike networks on growing surfaces. <i>Physical Review E</i> , <b>2002</b> , 66, 021104	2.4	17
23	Phased Diploid Genome Assembly with Single Molecule Real-Time Sequencing		16
22	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly		13
21	Curated variation benchmarks for challenging medically relevant autosomal genes.. <i>Nature Biotechnology</i> , <b>2022</b> ,	44.5	12
20	Amplification-free long-read sequencing reveals unforeseen CRISPR-Cas9 off-target activity. <i>Genome Biology</i> , <b>2020</b> , 21, 290	18.3	12
19	A complete reference genome improves analysis of human genetic variation.. <i>Science</i> , <b>2022</b> , 376, eabl3533	33.3	12
18	Assembling Large Genomes with Single-Molecule Sequencing and Locality Sensitive Hashing		10
17	Improved maize reference genome with single molecule technologies		10
16	A complete reference genome improves analysis of human genetic variation		9
15	De Novo PacBio long-read and phased avian genome assemblies correct and add to genes important in neuroscience research		8
14	Comprehensive analysis of single molecule sequencing-derived complete genome and whole transcriptome of <i>Hyposidra talaca</i> nuclear polyhedrosis virus. <i>Scientific Reports</i> , <b>2018</b> , 8, 8924	4.9	6
13	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line		6
12	Amplification-free long read sequencing reveals unforeseen CRISPR-Cas9 off-target activity		5
11	Effect of Sequence Depth and Length in Long-read Assembly of the Maize Inbred NC358		5
10	A Diploid Assembly-based Benchmark for Variants in the Major Histocompatibility Complex		4

9	Long-read whole genome analysis of human single cells		3
8	Automated assembly of high-quality diploid human reference genomes		3
7	An International Virtual Hackathon to Build Tools for the Analysis of Structural Variants within Species Ranging from Coronaviruses to Vertebrates. <i>F1000Research</i> , <b>2021</b> , 10, 246	3.6	2
6	Benchmarking challenging small variants with linked and long reads. <i>Cell Genomics</i> , <b>2022</b> , 2, 100128		2
5	Reconstructed rough growing interfaces: ridge-line trapping of domain walls. <i>Physical Review E</i> , <b>2001</b> , 64, 031606	2.4	1
4	Scaffolding of long read assemblies using long range contact information		1
3	An International Virtual Hackathon to Build Tools for the Analysis of Structural Variants within Species Ranging from Coronaviruses to Vertebrates. <i>F1000Research</i> , <b>2021</b> , 10, 246	3.6	1
2	A draft sequence reference of the genome. <i>F1000Research</i> , <b>2021</b> , 10, 281	3.6	0
1	A draft reference assembly of the <i>Psilocybe cubensis</i> genome. <i>F1000Research</i> , <b>2021</b> , 10, 281	3.6	