

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
g-index

67
all docs

67
docs citations

67
times ranked

23257
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Curated variation benchmarks for challenging medically relevant autosomal genes. <i>Nature Biotechnology</i> , 2022, 40, 672-680. | 17.5 | 90 |
| 2 | Ten simple rules for large-scale data processing. <i>PLoS Computational Biology</i> , 2022, 18, e1009757. | 3.2 | 1 |
| 3 | A complete reference genome improves analysis of human genetic variation. <i>Science</i> , 2022, 376, eabl3533. | 12.6 | 144 |
| 4 | The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53. | 12.6 | 1,222 |
| 5 | Benchmarking challenging small variants with linked and long reads. <i>Cell Genomics</i> , 2022, 2, 100128. | 6.5 | 77 |
| 6 | Chromosome-scale, haplotype-resolved assembly of human genomes. <i>Nature Biotechnology</i> , 2021, 39, 309-312. | 17.5 | 109 |
| 7 | 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 |
| 8 | A draft sequence reference of the <i>Psilocybe cubensis</i> genome. <i>F1000Research</i> , 2021, 10, 281. | 1.6 | 1 |
| 9 | A draft reference assembly of the <i>Psilocybe cubensis</i> genome. <i>F1000Research</i> , 2021, 10, 281. | 1.6 | 1 |
| 10 | 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 |
| 11 | Amplification-free long-read sequencing reveals unforeseen CRISPR-Cas9 off-target activity. <i>Genome Biology</i> , 2020, 21, 290. | 8.8 | 35 |
| 12 | A diploid assembly-based benchmark for variants in the major histocompatibility complex. <i>Nature Communications</i> , 2020, 11, 4794. | 12.8 | 56 |
| 13 | 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 |
| 14 | 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 |
| 15 | Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784. | 12.8 | 636 |
| 16 | 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 |
| 17 | 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 |
| 18 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Heterogeneous resistance to quizartinib in acute myeloid leukemia revealed by single-cell analysis. <i>Blood</i> , 2017, 130, 48-58. | 1.4 | 143 |
| 20 | Improved maize reference genome with single-molecule technologies. <i>Nature</i> , 2017, 546, 524-527. | 27.8 | 1,113 |
| 21 | 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 |
| 22 | Scaffolding of long read assemblies using long range contact information. <i>BMC Genomics</i> , 2017, 18, 527. | 2.8 | 194 |
| 23 | 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 |
| 24 | Long-read sequence assembly of the gorilla genome. <i>Science</i> , 2016, 352, aae0344. | 12.6 | 368 |
| 25 | Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016, 13, 1050-1054. | 19.0 | 1,658 |
| 26 | HLA Typing for the Next Generation. <i>PLoS ONE</i> , 2015, 10, e0127153. | 2.5 | 125 |
| 27 | Assembling large genomes with single-molecule sequencing and locality-sensitive hashing. <i>Nature Biotechnology</i> , 2015, 33, 623-630. | 17.5 | 877 |
| 28 | Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , 2015, 12, 780-786. | 19.0 | 465 |
| 29 | Extending reference assembly models. <i>Genome Biology</i> , 2015, 16, 13. | 8.8 | 139 |
| 30 | Long-read, whole-genome shotgun sequence data for five model organisms. <i>Scientific Data</i> , 2014, 1, 140045. | 5.3 | 138 |
| 31 | Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. <i>Nature Methods</i> , 2013, 10, 563-569. | 19.0 | 4,029 |
| 32 | A hybrid approach for the automated finishing of bacterial genomes. <i>Nature Biotechnology</i> , 2012, 30, 701-707. | 17.5 | 178 |
| 33 | 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 |
| 34 | 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 |
| 35 | The Origin of the Haitian Cholera Outbreak Strain. <i>New England Journal of Medicine</i> , 2011, 364, 33-42. | 27.0 | 676 |
| 36 | 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 |

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|----|--|------|-----------|
| 37 | Dynamics and Design Principles of a Basic Regulatory Architecture Controlling Metabolic Pathways. PLoS Biology, 2008, 6, e146. | 5.6 | 43 |
| 38 | Global identification of noncoding RNAs in <i>Saccharomyces cerevisiae</i> by modulating an essential RNA processing pathway. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4192-4197. | 7.1 | 69 |
| 39 | Genome-wide regulatory complexity in yeast promoters: Separation of functionally conserved and neutral sequence. Genome Research, 2005, 15, 205-213. | 5.5 | 43 |
| 40 | Comparing genomic expression patterns across species identifies shared transcriptional profile in aging. Nature Genetics, 2004, 36, 197-204. | 21.4 | 434 |
| 41 | Passive random walkers and riverlike networks on growing surfaces. Physical Review E, 2002, 66, 021104. | 2.1 | 22 |
| 42 | Reconstructed rough growing interfaces: Ridge-line trapping of domain walls. Physical Review E, 2001, 64, 031606. | 2.1 | 1 |
| 43 | Stationary-state skewness in two-dimensional Kardar-Parisi-Zhang type growth. Physical Review E, 1999, 59, 2633-2641. | 2.1 | 40 |