## Wan-Ping Lee

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	JAX-CNV: A Whole-genome Sequencing-based Algorithm for Copy Number Detection at Clinical Grade Level. Genomics, Proteomics and Bioinformatics, 2022, 20, 1197-1206.	6.9	3
2	Comprehensive Analysis of Alternative Splicing in Gastric Cancer Identifies Epithelial–Mesenchymal Transition Subtypes Associated with Survival. Cancer Research, 2022, 82, 543-555.	0.9	12
3	Polygenic Risk Scores in Alzheimer's Disease Genetics: Methodology, Applications, Inclusion, and Diversity. Journal of Alzheimer's Disease, 2022, 89, 1-12.	2.6	17
4	Expectations and blind spots for structural variation detection from long-read assemblies and short-read genome sequencing technologies. American Journal of Human Genetics, 2021, 108, 919-928.	6.2	72
5	SEAGLE: A Scalable Exact Algorithm for Large-Scale Set-Based Gene-Environment Interaction Tests in Biobank Data. Frontiers in Genetics, 2021, 12, 710055.	2.3	2
6	Copy Number Variation Identification on 3,800 Alzheimer's Disease Whole Genome Sequencing Data from the Alzheimer's Disease Sequencing Project. Frontiers in Genetics, 2021, 12, 752390.	2.3	4
7	NIA genetics of Alzheimer's disease data storage site (NIAGADS): 2021 update Alzheimer's and Dementia, 2021, 17 Suppl 3, e052258.	0.8	0
8	Copy number variation (CNV) identification and association study on 3,928 Alzheimer's disease whole genome sequencing data from the Alzheimer's Disease Sequencing Project (ADSP) Alzheimer's and Dementia, 2021, 17 Suppl 3, e052721.	0.8	0
9	One reference genome is not enough. Genome Biology, 2019, 20, 104.	8.8	58
10	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
11	Fast and accurate genomic analyses using genome graphs. Nature Genetics, 2019, 51, 354-362.	21.4	167
12	FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods. Genome Biology, 2018, 19, 38.	8.8	46
13	Toolbox for Mobile-Element Insertion Detection on Cancer Genomes. Cancer Informatics, 2015, 14s1, CIN.S24657.	1.9	4
14	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
15	MOSAIK: A Hash-Based Algorithm for Accurate Next-Generation Sequencing Short-Read Mapping. PLoS ONE, 2014, 9, e90581.	2.5	249
16	Toolbox for Mobile-Element Insertion Detection on Cancer Genomes. Cancer Informatics, 2014, 13s4, CIN.S13979.	1.9	4
17	Tangram: a comprehensive toolbox for mobile element insertion detection. BMC Genomics, 2014, 15, 795.	2.8	54
18	SSW Library: An SIMD Smith-Waterman C/C++ Library for Use in Genomic Applications. PLoS ONE, 2013, 8, e82138.	2.5	175

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19	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
20	A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. PLoS Genetics, 2011, 7, e1002236.	3.5	278
21	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	27.8	7,209
22	Voltage-Island Partitioning and Floorplanning Under Timing Constraints. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2009, 28, 690-702.	2.7	13
23	Post-floorplanning power/ground ring synthesis for multiple-supply-voltage designs. , 2009, , .		9
24	Sensitivity-based multiple-Vt cell swapping for leakage power reduction. , 2008, , .		1
25	An ILP algorithm for post-floorplanning voltage-island generation considering power-network planning. IEEE/ACM International Conference on Computer-Aided Design, Digest of Technical Papers, 2007, , .	0.0	2
26	Voltage Island Aware Floorplanning for Power and Timing Optimization. IEEE/ACM International Conference on Computer-Aided Design, Digest of Technical Papers, 2006, , .	0.0	10