

# Hayan Lee

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7454336/publications.pdf>

Version: 2024-02-01

17  
papers

2,359  
citations

687363

13  
h-index

996975

15  
g-index

22  
all docs

22  
docs citations

22  
times ranked

4589  
citing authors

#	ARTICLE	IF	CITATIONS
1	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	21.4	472
2	Piercing the dark matter: bioinformatics of long-range sequencing and mapping. <i>Nature Reviews Genetics</i> , 2018, 19, 329-346.	16.3	395
3	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	28.9	334
4	Whole genome de novo assemblies of three divergent strains of rice, <i>Oryza sativa</i> , document novel gene space of aus and indica. <i>Genome Biology</i> , 2014, 15, 506.	8.8	228
5	Whole genome de novo assemblies of three divergent strains of rice, <i>Oryza sativa</i> , document novel gene space of aus and indica. <i>Genome Biology</i> , 2014, 15, 506.	9.6	123
6	Genomic dark matter: the reliability of short read mapping illustrated by the genome mappability score. <i>Bioinformatics</i> , 2012, 28, 2097-2105.	4.1	116
7	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. <i>GigaScience</i> , 2019, 8, .	6.4	106
8	SplitMEM: a graphical algorithm for pan-genome analysis with suffix skips. <i>Bioinformatics</i> , 2014, 30, 3476-3483.	4.1	102
9	Lifelong physical activity is associated with promoter hypomethylation of genes involved in metabolism, myogenesis, contractile properties and oxidative stress resistance in aged human skeletal muscle. <i>Scientific Reports</i> , 2019, 9, 3272.	3.3	63
10	Multi-faceted epigenetic dysregulation of gene expression promotes esophageal squamous cell carcinoma. <i>Nature Communications</i> , 2020, 11, 3675.	12.8	63
11	Virmid: accurate detection of somatic mutations with sample impurity inference. <i>Genome Biology</i> , 2013, 14, R90.	9.6	58
12	Longitudinal linked-read sequencing reveals ecological and evolutionary responses of a human gut microbiome during antibiotic treatment. <i>Genome Research</i> , 2021, 31, 1433-1446.	5.5	55
13	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	2.8	51
14	On the Security of Intra-Car Wireless Sensor Networks. , 2009, , .		11
15	Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding. <i>GigaScience</i> , 2020, 9, .	6.4	6
16	Candidate variants in TUB are associated with familial tremor. <i>PLoS Genetics</i> , 2020, 16, e1009010.	3.5	3
17	Predictive Signatures for Lung Adenocarcinoma Prognostic Trajectory by Multiomics Data Integration and Ensemble Learning. <i>Lecture Notes in Computer Science</i> , 2021, , 9-23.	1.3	0