Hayan Lee

List of Publications by Year
in descending order

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