Soohyun Lee

List of Publications by Year
in descending order

32 papers	6,065 citations	279798 23 h-index	414414 32 g-index
39 all docs	39 docs citations	39 times ranked	9702 citing authors

#	Article	IF	Citations
1	HiGlass: web-based visual exploration and analysis of genome interaction maps. Genome Biology, 2018, 19, 125.	8.8	950
2	Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33.	1.6	642
3	Endogenous siRNAs Derived from Transposons and mRNAs in Drosophila Somatic Cells. Science, 2008, 320, 1077-1081.	12.6	594
4	Global mapping of translation initiation sites in mammalian cells at single-nucleotide resolution. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2424-32.	7.1	534
5	Collapse of Germline piRNAs in the Absence of Argonaute3 Reveals Somatic piRNAs in Flies. Cell, 2009, 137, 509-521.	28.9	503
6	Somatic mutation in single human neurons tracks developmental and transcriptional history. Science, 2015, 350, 94-98.	12.6	486
7	The Drosophila HP1 Homolog Rhino Is Required for Transposon Silencing and piRNA Production by Dual-Strand Clusters. Cell, 2009, 138, 1137-1149.	28.9	382
8	Comparative analysis of metazoan chromatin organization. Nature, 2014, 512, 449-452.	27.8	363
9	Hallmarks of pluripotency. Nature, 2015, 525, 469-478.	27.8	338
10	A comparison of genetically matched cell lines reveals the equivalence of human iPSCs and ESCs. Nature Biotechnology, 2015, 33, 1173-1181.	17.5	235
11	Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33.	1.6	188
12	Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. Genome Research, 2018, 28, 1217-1227.	5.5	172
13	Accurate quantification of transcriptome from RNA-Seq data by effective length normalization. Nucleic Acids Research, 2011, 39, e9-e9.	14.5	101
14	NGSCheckMate: software for validating sample identity in next-generation sequencing studies within and across data types. Nucleic Acids Research, 2017, 45, e103-e103.	14.5	95
15	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. Cell Stem Cell, 2017, 20, 706-719.e7.	11.1	63
16	HiNT: a computational method for detecting copy number variations and translocations from Hi-C data. Genome Biology, 2020, 21, 73.	8.8	56
17	The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data. Nature Communications, 2022, 13, 2365.	12.8	49
18	Relative Codon Adaptation Index, a Sensitive Measure of Codon Usage Bias. Evolutionary Bioinformatics, 2010, 6, EBO.S4608.	1.2	46

#	Article	IF	Citations
19	Comprehensive identification of transposable element insertions using multiple sequencing technologies. Nature Communications, 2021, 12, 3836.	12.8	44
20	Failure to replicate the STAP cell phenomenon. Nature, 2015, 525, E6-E9.	27.8	41
21	Quantitative Analysis of Single Nucleotide Polymorphisms within Copy Number Variation. PLoS ONE, 2008, 3, e3906.	2.5	34
22	Analyzing Somatic Genome Rearrangements in Human Cancers by Using Whole-Exome Sequencing. American Journal of Human Genetics, 2016, 98, 843-856.	6.2	33
23	Genes involved in complex adaptive processes tend to have highly conserved upstream regions in mammalian genomes. BMC Genomics, 2005, 6, 168.	2.8	26
24	EMSAR: estimation of transcript abundance from RNA-seq data by mappability-based segmentation and reclustering. BMC Bioinformatics, 2015, 16, 278.	2.6	18
25	Whole-genome analysis reveals the contribution of non-coding de novo transposon insertions to autism spectrum disorder. Mobile DNA, 2021, 12, 28.	3.6	17
26	Tibanna: software for scalable execution of portable pipelines on the cloud. Bioinformatics, 2019, 35, 4424-4426.	4.1	11
27	Pairs and Pairix: a file format and a tool for efficient storage and retrieval for Hi-C read pairs. Bioinformatics, 2022, 38, 1729-1731.	4.1	7
28	BamSnap: a lightweight viewer for sequencing reads in BAM files. Bioinformatics, 2021, 37, 263-264.	4.1	5
29	CHOISS for selection of single nucleotide polymorphism markers on interval regularity. Bioinformatics, 2004, 20, 581-582.	4.1	4
30	The complete genome sequence of a dog: a perspective. BioEssays, 2006, 28, 569-573.	2.5	3
31	HiTea: a computational pipeline to identify non-reference transposable element insertions in Hi-C data. Bioinformatics, 2021, 37, 1045-1051.	4.1	3
32	Hi-C Data Formats. Methods in Molecular Biology, 2022, 2301, 133-141.	0.9	0