Kasper D Hansen

List of Publications by Year
in descending order

23 papers	9,266 citations	331670 21 h-index	642732 23 g-index
33 all docs	33 docs citations	33 times ranked	21018 citing authors

#	Article	IF	Citations
1	Orchestrating high-throughput genomic analysis with Bioconductor. Nature Methods, 2015, 12, 115-121.	19.0	3,070
2	Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments. BMC Bioinformatics, 2010, 11, 94.	2.6	1,421
3	BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions. Genome Biology, 2012, 13, R83.	9.6	650
4	Preprocessing, normalization and integration of the Illumina HumanMethylationEPIC array with minfi. Bioinformatics, 2017, 33, 558-560.	4.1	583
5	Biases in Illumina transcriptome sequencing caused by random hexamer priming. Nucleic Acids Research, 2010, 38, e131-e131.	14.5	573
6	Removing technical variability in RNA-seq data using conditional quantile normalization. Biostatistics, 2012, 13, 204-216.	1.5	532
7	Reproducible RNA-seq analysis using recount2. Nature Biotechnology, 2017, 35, 319-321.	17.5	395
8	Cloud-scale RNA-sequencing differential expression analysis with Myrna. Genome Biology, 2010, 11, R83.	9.6	268
9	Social environment is associated with gene regulatory variation in the rhesus macaque immune system. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6490-6495.	7.1	257
10	Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. Nature Methods, 2015, 12, 230-232.	19.0	248
11	Reconstructing A/B compartments as revealed by Hi-C using long-range correlations in epigenetic data. Genome Biology, 2015, 16, 180.	8.8	232
12	Sequencing technology does not eliminate biological variability. Nature Biotechnology, 2011, 29, 572-573.	17.5	193
13	Large-scale hypomethylated blocks associated with Epstein-Barr virus–induced B-cell immortalization. Genome Research, 2014, 24, 177-184.	5.5	130
14	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. Nature Neuroscience, 2019, 22, 307-316.	14.8	120
15	recount3: summaries and queries for large-scale RNA-seq expression and splicing. Genome Biology, 2021, 22, 323.	8.8	103
16	A ketogenic diet rescues hippocampal memory defects in a mouse model of Kabuki syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 125-130.	7.1	102
17	Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. Genome Biology, 2016, 17, 266.	8.8	94
18	Software for the Integration of Multiomics Experiments in Bioconductor. Cancer Research, 2017, 77, e39-e42.	0.9	80

#	Article	IF	Citations
19	Differential expression analysis of RNA-seq data at single-base resolution. Biostatistics, 2014, 15, 413-426.	1.5	56
20	Public data and open source tools for multi-assay genomic investigation of disease. Briefings in Bioinformatics, 2016, 17, 603-615.	6.5	46
21	DNA methylation is stable during replication and cell cycle arrest. Scientific Reports, 2016, 5, 17911.	3.3	44
22	Human methylome variation across Infinium 450K data on the Gene Expression Omnibus. NAR Genomics and Bioinformatics, 2021, 3, lqab025.	3.2	12
23	Rail-dbGaP: analyzing dbGaP-protected data in the cloud with Amazon Elastic MapReduce. Bioinformatics, 2016, 32, 2551-2553.	4.1	5