

Kasper D. Hansen

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

17,963
citations

81743

39
h-index

128067

60
g-index

91
all docs

91
docs citations

91
times ranked

34171
citing authors

#	ARTICLE	IF	CITATIONS
1	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. <i>Bioinformatics</i> , 2014, 30, 1363-1369.	1.8	3,192
2	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	9.0	3,070
3	Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments. <i>BMC Bioinformatics</i> , 2010, 11, 94.	1.2	1,421
4	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	6.0	1,124
5	Increased methylation variation in epigenetic domains across cancer types. <i>Nature Genetics</i> , 2011, 43, 768-775.	9.4	968
6	Functional normalization of 450k methylation array data improves replication in large cancer studies. <i>Genome Biology</i> , 2014, 15, 503.	3.8	665
7	BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions. <i>Genome Biology</i> , 2012, 13, R83.	13.9	650
8	Preprocessing, normalization and integration of the Illumina HumanMethylationEPIC array with minfi. <i>Bioinformatics</i> , 2017, 33, 558-560.	1.8	583
9	Biases in Illumina transcriptome sequencing caused by random hexamer priming. <i>Nucleic Acids Research</i> , 2010, 38, e131-e131.	6.5	573
10	Removing technical variability in RNA-seq data using conditional quantile normalization. <i>Biostatistics</i> , 2012, 13, 204-216.	0.9	532
11	Reproducible RNA-seq analysis using recount2. <i>Nature Biotechnology</i> , 2017, 35, 319-321.	9.4	395
12	Linear models enable powerful differential activity analysis in massively parallel reporter assays. <i>BMC Genomics</i> , 2019, 20, 209.	1.2	322
13	Reversible switching between epigenetic states in honeybee behavioral subcastes. <i>Nature Neuroscience</i> , 2012, 15, 1371-1373.	7.1	305
14	Cloud-scale RNA-sequencing differential expression analysis with Myrna. <i>Genome Biology</i> , 2010, 11, R83.	13.9	268
15	Social environment is associated with gene regulatory variation in the rhesus macaque immune system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6490-6495.	3.3	257
16	Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. <i>Nature Methods</i> , 2015, 12, 230-232.	9.0	248
17	Reconstructing A/B compartments as revealed by Hi-C using long-range correlations in epigenetic data. <i>Genome Biology</i> , 2015, 16, 180.	3.8	232
18	Conservation of an RNA regulatory map between <i>Drosophila</i> and mammals. <i>Genome Research</i> , 2011, 21, 193-202.	2.4	208

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19	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015, 25, 1801-1811.	2.4	195
20	Sequencing technology does not eliminate biological variability. <i>Nature Biotechnology</i> , 2011, 29, 572-573.	9.4	193
21	Genome-wide association study identifies peanut allergy-specific loci and evidence of epigenetic mediation in US children. <i>Nature Communications</i> , 2015, 6, 6304.	5.8	192
22	Histone deacetylase inhibition rescues structural and functional brain deficits in a mouse model of Kabuki syndrome. <i>Science Translational Medicine</i> , 2014, 6, 256ra135.	5.8	142
23	Simultaneous profiling of chromatin accessibility and methylation on human cell lines with nanopore sequencing. <i>Nature Methods</i> , 2020, 17, 1191-1199.	9.0	133
24	Large-scale hypomethylated blocks associated with Epstein-Barr virus-induced B-cell immortalization. <i>Genome Research</i> , 2014, 24, 177-184.	2.4	130
25	Advanced Paternal Age and Risk of Fetal Death: A Cohort Study. <i>American Journal of Epidemiology</i> , 2004, 160, 1214-1222.	1.6	126
26	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. <i>Nature Neuroscience</i> , 2019, 22, 307-316.	7.1	120
27	Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. <i>Genome Biology</i> , 2015, 16, 80.	3.8	111
28	recount3: summaries and queries for large-scale RNA-seq expression and splicing. <i>Genome Biology</i> , 2021, 22, 323.	3.8	103
29	A ketogenic diet rescues hippocampal memory defects in a mouse model of Kabuki syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 125-130.	3.3	102
30	Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. <i>Genome Biology</i> , 2016, 17, 266.	3.8	94
31	A mammalian methylation array for profiling methylation levels at conserved sequences. <i>Nature Communications</i> , 2022, 13, 783.	5.8	93
32	Whole-genome analysis of the methylome and hydroxymethylome in normal and malignant lung and liver. <i>Genome Research</i> , 2016, 26, 1730-1741.	2.4	91
33	Genome-Wide Identification of Alternative Splice Forms Down-Regulated by Nonsense-Mediated mRNA Decay in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2009, 5, e1000525.	1.5	87
34	Software for the Integration of Multiomics Experiments in Bioconductor. <i>Cancer Research</i> , 2017, 77, e39-e42.	0.4	80
35	Common DNA sequence variation influences 3-dimensional conformation of the human genome. <i>Genome Biology</i> , 2019, 20, 255.	3.8	65
36	illuminaio: An open source IDAT parsing tool for Illumina microarrays. <i>F1000Research</i> , 2013, 2, 264.	0.8	65

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37	“Gap hunting” to characterize clustered probe signals in Illumina methylation array data. <i>Epigenetics and Chromatin</i> , 2016, 9, 56.	1.8	61
38	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. <i>Nature Methods</i> , 2017, 14, 216-217.	9.0	59
39	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. <i>Cell Genomics</i> , 2022, 2, 100085.	3.0	59
40	Differential expression analysis of RNA-seq data at single-base resolution. <i>Biostatistics</i> , 2014, 15, 413-426.	0.9	56
41	DNA methylation is stable during replication and cell cycle arrest. <i>Scientific Reports</i> , 2016, 5, 17911.	1.6	44
42	Metabolic effects of air pollution exposure and reversibility. <i>Journal of Clinical Investigation</i> , 2020, 130, 6034-6040.	3.9	43
43	Coexpression patterns define epigenetic regulators associated with neurological dysfunction. <i>Genome Research</i> , 2019, 29, 532-542.	2.4	42
44	Precocious neuronal differentiation and disrupted oxygen responses in Kabuki syndrome. <i>JCI Insight</i> , 2019, 4, .	2.3	41
45	Fertility pattern does not explain social gradient in breast cancer in denmark. <i>International Journal of Cancer</i> , 2004, 111, 451-456.	2.3	39
46	Novel Low Abundance and Transient RNAs in Yeast Revealed by Tiling Microarrays and Ultra High-Throughput Sequencing Are Not Conserved Across Closely Related Yeast Species. <i>PLoS Genetics</i> , 2008, 4, e1000299.	1.5	31
47	A screen of 1,049 schizophrenia and 30 Alzheimer’s-associated variants for regulatory potential. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 61-73.	1.1	31
48	Universal prediction of cell-cycle position using transfer learning. <i>Genome Biology</i> , 2022, 23, 41.	3.8	30
49	Precocious chondrocyte differentiation disrupts skeletal growth in Kabuki syndrome mice. <i>JCI Insight</i> , 2019, 4, .	2.3	29
50	Analyzing whole genome bisulfite sequencing data from highly divergent genotypes. <i>Nucleic Acids Research</i> , 2019, 47, e117-e117.	6.5	22
51	Human brain region-specific variably methylated regions are enriched for heritability of distinct neuropsychiatric traits. <i>Genome Biology</i> , 2021, 22, 116.	3.8	22
52	Laser captured hepatocytes show association of butyrylcholinesterase gene loss and fibrosis progression in hepatitis C-infected drug users. <i>Hepatology</i> , 2012, 56, 544-554.	3.6	15
53	Promoter CpG Density Predicts Downstream Gene Loss-of-Function Intolerance. <i>American Journal of Human Genetics</i> , 2020, 107, 487-498.	2.6	12
54	Human methylome variation across Infinium 450K data on the Gene Expression Omnibus. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab025.	1.5	12

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55	Addressing the mean-correlation relationship in co-expression analysis. PLoS Computational Biology, 2022, 18, e1009954.	1.5	11
56	Leveraging the Mendelian disorders of the epigenetic machinery to systematically map functional epigenetic variation. ELife, 2021, 10, .	2.8	10
57	Joint Bounding of Peaks Across Samples Improves Differential Analysis in Mass Spectrometry-Based Metabolomics. Analytical Chemistry, 2017, 89, 3517-3523.	3.2	7
58	The Bioconductor channel in F1000Research. F1000Research, 2015, 4, 217.	0.8	6
59	Rail-dbGaP: analyzing dbGaP-protected data in the cloud with Amazon Elastic MapReduce. Bioinformatics, 2016, 32, 2551-2553.	1.8	5
60	Use of census data for construction of fertility history for Danish women. Scandinavian Journal of Public Health, 2004, 32, 435-441.	1.2	2