Kasper D. Hansen

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

75	11,856	36	91
papers	citations	h-index	g-index
91	**15,715**	**13.5**	**6.33**
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
75	Orchestrating high-throughput genomic analysis with Bioconductor. *Nature Methods*, **2015**, 12, 115-21	21.6	1949
74	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. *Bioinformatics*, **2014**, 30, 1363-9	7.2	1941
73	Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments. *BMC Bioinformatics*, **2010**, 11, 94	3.6	1132
72	Identification of functional elements and regulatory circuits by Drosophila modENCODE. *Science*, **2010**, 330, 1787-97	33.3	892
71	Increased methylation variation in epigenetic domains across cancer types. *Nature Genetics*, **2011**, 43, 768-75	36.3	825
70	Biases in Illumina transcriptome sequencing caused by random hexamer priming. *Nucleic Acids Research*, **2010**, 38, e131	20.1	471
69	BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions. *Genome Biology*, **2012**, 13, R83	18.3	445
68	Functional normalization of 450k methylation array data improves replication in large cancer studies. *Genome Biology*, **2014**, 15, 503	18.3	435
67	Removing technical variability in RNA-seq data using conditional quantile normalization. *Biostatistics*, **2012**, 13, 204-16	3.7	378
66	Preprocessing, normalization and integration of the Illumina HumanMethylationEPIC array with minfi. *Bioinformatics*, **2017**, 33, 558-560	7.2	248
65	Reversible switching between epigenetic states in honeybee behavioral subcastes. *Nature Neuroscience*, **2012**, 15, 1371-3	25.5	237
64	Cloud-scale RNA-sequencing differential expression analysis with Myrna. *Genome Biology*, **2010**, 11, R83	18.3	227
63	Reproducible RNA-seq analysis using recount2. *Nature Biotechnology*, **2017**, 35, 319-321	44.5	211
62	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, 6490-5	11.5	208
61	Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. *Nature Methods*, **2015**, 12, 230-2, 1 p following 232	21.6	171
60	Conservation of an RNA regulatory map between Drosophila and mammals. *Genome Research*, **2011** , 21, 193-202	9.7	165
59	Genome-wide association study identifies peanut allergy-specific loci and evidence of epigenetic mediation in US children. *Nature Communications*, **2015**, 6, 6304	17.4	152

58	Sequencing technology does not eliminate biological variability. *Nature Biotechnology*, **2011**, 29, 572-3	44.5	143
57	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. *Genome Research*, **2015**, 25, 1801-11	9.7	138
56	Reconstructing A/B compartments as revealed by Hi-C using long-range correlations in epigenetic data. *Genome Biology*, **2015**, 16, 180	18.3	132
55	Histone deacetylase inhibition rescues structural and functional brain deficits in a mouse model of Kabuki syndrome. *Science Translational Medicine*, **2014**, 6, 256ra135	17.5	104
54	Advanced paternal age and risk of fetal death: a cohort study. *American Journal of Epidemiology*, **2004**, 160, 1214-22	3.8	104
53	Large-scale hypomethylated blocks associated with Epstein-Barr virus-induced B-cell immortalization. *Genome Research*, **2014**, 24, 177-84	9.7	99
52	Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. *Genome Biology*, **2015**, 16, 80	18.3	83
51	Genome-wide identification of alternative splice forms down-regulated by nonsense-mediated mRNA decay in Drosophila. *PLoS Genetics*, **2009**, 5, e1000525	6	68
50	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. *Nature Neuroscience*, **2019**, 22, 307-316	25.5	68
49	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	18.3	65
48	Linear models enable powerful differential activity analysis in massively parallel reporter assays. *BMC Genomics*, **2019**, 20, 209	4.5	63
47	Whole-genome analysis of the methylome and hydroxymethylome in normal and malignant lung and liver. *Genome Research*, **2016**, 26, 1730-1741	9.7	61
46	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	11.5	56
45	Software for the Integration of Multiomics Experiments in Bioconductor. *Cancer Research*, **2017**, 77, e39-e42	10.1	53
44	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. *Nature Methods*, **2017**, 14, 216-217	21.6	47
43	illuminaio: An open source IDAT parsing tool for Illumina microarrays. *F1000Research*, **2013**, 2, 264	3.6	47
42	Differential expression analysis of RNA-seq data at single-base resolution. *Biostatistics*, **2014**, 15, 413-26	3.7	42
41	Simultaneous profiling of chromatin accessibility and methylation on human cell lines with nanopore sequencing. *Nature Methods*, **2020**, 17, 1191-1199	21.6	40

40	Fertility pattern does not explain social gradient in breast cancer in denmark. *International Journal of Cancer*, **2004**, 111, 451-6	7.5	36
39	Common DNA sequence variation influences 3-dimensional conformation of the human genome. *Genome Biology*, **2019**, 20, 255	18.3	36
38	"Gap hunting" to characterize clustered probe signals in Illumina methylation array data. *Epigenetics and Chromatin*, **2016**, 9, 56	5.8	34
37	DNA methylation is stable during replication and cell cycle arrest. *Scientific Reports*, **2015**, 5, 17911	4.9	32
36	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. *PLoS Genetics*, **2008**, 4, e1000299	6	29
35	Coexpression patterns define epigenetic regulators associated with neurological dysfunction. *Genome Research*, **2019**, 29, 532-542	9.7	20
34	Precocious neuronal differentiation and disrupted oxygen responses in Kabuki syndrome. *JCI Insight*, **2019**, 4,	9.9	19
33	Metabolic effects of air pollution exposure and reversibility. *Journal of Clinical Investigation*, **2020**, 130, 6034-6040	15.9	16
32	A mammalian methylation array for profiling methylation levels at conserved sequences.. *Nature Communications*, **2022**, 13, 783	17.4	15
31	Laser captured hepatocytes show association of butyrylcholinesterase gene loss and fibrosis progression in hepatitis C-infected drug users. *Hepatology*, **2012**, 56, 544-54	11.2	14
30	Precocious chondrocyte differentiation disrupts skeletal growth in Kabuki syndrome mice. *JCI Insight*, **2019**, 4,	9.9	10
29	Analyzing whole genome bisulfite sequencing data from highly divergent genotypes. *Nucleic Acids Research*, **2019**, 47, e117	20.1	8
28	Preprocessing, normalization and integration of the Illumina HumanMethylationEPIC array		8
27	A screen of 1,049 schizophrenia and 30 Alzheimer's-associated variants for regulatory potential. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2020**, 183, 61-73	3.5	8
26	Joint Bounding of Peaks Across Samples Improves Differential Analysis in Mass Spectrometry-Based Metabolomics. *Analytical Chemistry*, **2017**, 89, 3517-3523	7.8	7
25	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space.. *Cell Genomics*, **2022**, 2, 100085-100085		6
24	Rail-dbGaP: analyzing dbGaP-protected data in the cloud with Amazon Elastic MapReduce. *Bioinformatics*, **2016**, 32, 2551-3	7.2	5
23	Functional normalization of 450k methylation array data improves replication in large cancer studies		5

22	Co-expression analysis is biased by a mean-correlation relationship		5
21	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space (AnVIL)		5
20	The Bioconductor channel in F1000Research. *F1000Research*, **2015**, 4, 217	3.6	4
19	Removing unwanted variation between samples in Hi-C experiments		4
18	Universal prediction of cell-cycle position using transfer learning.. *Genome Biology*, **2022**, 23, 41	18.3	3
17	recount3: summaries and queries for large-scale RNA-seq expression and splicing. *Genome Biology*, **2021**, 22, 323	18.3	3
16	Software for the integration of multi-omics experiments in Bioconductor		3
15	Human methylome variation across Infinium 450K data on the Gene Expression Omnibus. *NAR Genomics and Bioinformatics*, **2021**, 3, lqab025	3.7	3
14	Use of census data for construction of fertility history for Danish women. *Scandinavian Journal of Public Health*, **2004**, 32, 435-41	3	2
13	Purifying selection acts on germline methylation to modify the CpG mutation rate at promoters		2
12	Linear models enable powerful differential activity analysis in massively parallel reporter assays		2
11	A screen of 1,049 schizophrenia and 30 Alzheimer�-associated variants for regulatory potential		2
10	Promoter CpG Density Predicts Downstream Gene Loss-of-Function Intolerance. *American Journal of Human Genetics*, **2020**, 107, 487-498	11	2
9	Precocious neuronal differentiation and disrupted oxygen responses in Kabuki syndrome		1
8	Promoter CpG density predicts downstream gene loss-of-function intolerance		1
7	Human methylome variation across Infinium 450K data on the Gene Expression Omnibus		1
6	Analyzing whole genome bisulfite sequencing data from highly divergent genotypes		1
5	Universal prediction of cell cycle position using transfer learning		1

4	Human brain region-specific variably methylated regions are enriched for heritability of distinct neuropsychiatric traits. *Genome Biology*, **2021**, 22, 116	18.3	1
3	Compartmap enables inference of higher-order chromatin structure in individual cells from scRNA-seq and scATAC-seq		1
2	Addressing the mean-correlation relationship in co-expression analysis.. *PLoS Computational Biology*, **2022**, 18, e1009954	5	0
1	DNA Methylation **2019**, 933-948		