

Kasper D. Hansen

List of Publications by Year in Descending Order

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Version: 2024-04-25

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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
papers

11,856
citations

36
h-index

91
g-index

91
ext. papers

15,715
ext. citations

13.5
avg, IF

6.33
L-index

#	Paper	IF	Citations
75	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, 100085-100085		6
74	Universal prediction of cell-cycle position using transfer learning.. <i>Genome Biology</i> , 2022 , 23, 41	18.3	3
73	A mammalian methylation array for profiling methylation levels at conserved sequences.. <i>Nature Communications</i> , 2022 , 13, 783	17.4	15
72	Addressing the mean-correlation relationship in co-expression analysis.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009954	5	0
71	recount3: summaries and queries for large-scale RNA-seq expression and splicing. <i>Genome Biology</i> , 2021 , 22, 323	18.3	3
70	Human brain region-specific variably methylated regions are enriched for heritability of distinct neuropsychiatric traits. <i>Genome Biology</i> , 2021 , 22, 116	18.3	1
69	Human methylome variation across Infinium 450K data on the Gene Expression Omnibus. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab025	3.7	3
68	Metabolic effects of air pollution exposure and reversibility. <i>Journal of Clinical Investigation</i> , 2020 , 130, 6034-6040	15.9	16
67	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	3.5	8
66	Simultaneous profiling of chromatin accessibility and methylation on human cell lines with nanopore sequencing. <i>Nature Methods</i> , 2020 , 17, 1191-1199	21.6	40
65	Promoter CpG Density Predicts Downstream Gene Loss-of-Function Intolerance. <i>American Journal of Human Genetics</i> , 2020 , 107, 487-498	11	2
64	Coexpression patterns define epigenetic regulators associated with neurological dysfunction. <i>Genome Research</i> , 2019 , 29, 532-542	9.7	20
63	Analyzing whole genome bisulfite sequencing data from highly divergent genotypes. <i>Nucleic Acids Research</i> , 2019 , 47, e117	20.1	8
62	Linear models enable powerful differential activity analysis in massively parallel reporter assays. <i>BMC Genomics</i> , 2019 , 20, 209	4.5	63
61	Precocious neuronal differentiation and disrupted oxygen responses in Kabuki syndrome. <i>JCI Insight</i> , 2019 , 4,	9.9	19
60	Precocious chondrocyte differentiation disrupts skeletal growth in Kabuki syndrome mice. <i>JCI Insight</i> , 2019 , 4,	9.9	10
59	DNA Methylation 2019 , 933-948		

58	Common DNA sequence variation influences 3-dimensional conformation of the human genome. <i>Genome Biology</i> , 2019 , 20, 255	18.3	36
57	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. <i>Nature Neuroscience</i> , 2019 , 22, 307-316	25.5	68
56	Joint Bounding of Peaks Across Samples Improves Differential Analysis in Mass Spectrometry-Based Metabolomics. <i>Analytical Chemistry</i> , 2017 , 89, 3517-3523	7.8	7
55	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. <i>Nature Methods</i> , 2017 , 14, 216-217	21.6	47
54	Reproducible RNA-seq analysis using recount2. <i>Nature Biotechnology</i> , 2017 , 35, 319-321	44.5	211
53	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	11.5	56
52	Software for the Integration of Multiomics Experiments in Bioconductor. <i>Cancer Research</i> , 2017 , 77, e39142	14.2	53
51	Preprocessing, normalization and integration of the Illumina HumanMethylationEPIC array with minfi. <i>Bioinformatics</i> , 2017 , 33, 558-560	7.2	248
50	"Gap hunting" to characterize clustered probe signals in Illumina methylation array data. <i>Epigenetics and Chromatin</i> , 2016 , 9, 56	5.8	34
49	Rail-dbGaP: analyzing dbGaP-protected data in the cloud with Amazon Elastic MapReduce. <i>Bioinformatics</i> , 2016 , 32, 2551-3	7.2	5
48	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	18.3	65
47	Whole-genome analysis of the methylome and hydroxymethylome in normal and malignant lung and liver. <i>Genome Research</i> , 2016 , 26, 1730-1741	9.7	61
46	Genome-wide association study identifies peanut allergy-specific loci and evidence of epigenetic mediation in US children. <i>Nature Communications</i> , 2015 , 6, 6304	17.4	152
45	Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. <i>Genome Biology</i> , 2015 , 16, 80	18.3	83
44	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015 , 25, 1801-11	9.7	138
43	Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. <i>Nature Methods</i> , 2015 , 12, 230-2, 1 p following 232	21.6	171
42	DNA methylation is stable during replication and cell cycle arrest. <i>Scientific Reports</i> , 2015 , 5, 17911	4.9	32
41	Reconstructing A/B compartments as revealed by Hi-C using long-range correlations in epigenetic data. <i>Genome Biology</i> , 2015 , 16, 180	18.3	132

40	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015 , 12, 115-21	21.6	1949
39	The Bioconductor channel in F1000Research. <i>F1000Research</i> , 2015 , 4, 217	3.6	4
38	Differential expression analysis of RNA-seq data at single-base resolution. <i>Biostatistics</i> , 2014 , 15, 413-263.7	42	
37	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. <i>Bioinformatics</i> , 2014 , 30, 1363-9	7.2	1941
36	Functional normalization of 450k methylation array data improves replication in large cancer studies. <i>Genome Biology</i> , 2014 , 15, 503	18.3	435
35	Large-scale hypomethylated blocks associated with Epstein-Barr virus-induced B-cell immortalization. <i>Genome Research</i> , 2014 , 24, 177-84	9.7	99
34	Histone deacetylase inhibition rescues structural and functional brain deficits in a mouse model of Kabuki syndrome. <i>Science Translational Medicine</i> , 2014 , 6, 256ra135	17.5	104
33	illuminaio: An open source IDAT parsing tool for Illumina microarrays. <i>F1000Research</i> , 2013 , 2, 264	3.6	47
32	BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions. <i>Genome Biology</i> , 2012 , 13, R83	18.3	445
31	Reversible switching between epigenetic states in honeybee behavioral subcastes. <i>Nature Neuroscience</i> , 2012 , 15, 1371-3	25.5	237
30	Laser captured hepatocytes show association of butyrylcholinesterase gene loss and fibrosis progression in hepatitis C-infected drug users. <i>Hepatology</i> , 2012 , 56, 544-54	11.2	14
29	Removing technical variability in RNA-seq data using conditional quantile normalization. <i>Biostatistics</i> , 2012 , 13, 204-16	3.7	378
28	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, 6490-5	11.5	208
27	Sequencing technology does not eliminate biological variability. <i>Nature Biotechnology</i> , 2011 , 29, 572-3	44.5	143
26	Increased methylation variation in epigenetic domains across cancer types. <i>Nature Genetics</i> , 2011 , 43, 768-75	36.3	825
25	Conservation of an RNA regulatory map between Drosophila and mammals. <i>Genome Research</i> , 2011 , 21, 193-202	9.7	165
24	Identification of functional elements and regulatory circuits by Drosophila modENCODE. <i>Science</i> , 2010 , 330, 1787-97	33.3	892
23	Biases in Illumina transcriptome sequencing caused by random hexamer priming. <i>Nucleic Acids Research</i> , 2010 , 38, e131	20.1	471

22	Cloud-scale RNA-sequencing differential expression analysis with Myrna. <i>Genome Biology</i> , 2010 , 11, R83 18,3	227
21	Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments. <i>BMC Bioinformatics</i> , 2010 , 11, 94	3.6 1132
20	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	6 68
19	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	6 29
18	Advanced paternal age and risk of fetal death: a cohort study. <i>American Journal of Epidemiology</i> , 2004 , 160, 1214-22	3.8 104
17	Use of census data for construction of fertility history for Danish women. <i>Scandinavian Journal of Public Health</i> , 2004 , 32, 435-41	3 2
16	Fertility pattern does not explain social gradient in breast cancer in denmark. <i>International Journal of Cancer</i> , 2004 , 111, 451-6	7.5 36
15	Removing unwanted variation between samples in Hi-C experiments	4
14	Precocious neuronal differentiation and disrupted oxygen responses in Kabuki syndrome	1
13	Promoter CpG density predicts downstream gene loss-of-function intolerance	1
12	Purifying selection acts on germline methylation to modify the CpG mutation rate at promoters	2
11	Functional normalization of 450k methylation array data improves replication in large cancer studies	5
10	Preprocessing, normalization and integration of the Illumina HumanMethylationEPIC array	8
9	Software for the integration of multi-omics experiments in Bioconductor	3
8	Linear models enable powerful differential activity analysis in massively parallel reporter assays	2
7	Co-expression analysis is biased by a mean-correlation relationship	5
6	Human methylome variation across Infinium 450K data on the Gene Expression Omnibus	1
5	A screen of 1,049 schizophrenia and 30 Alzheimer's-associated variants for regulatory potential	2

4	Analyzing whole genome bisulfite sequencing data from highly divergent genotypes	1
3	Universal prediction of cell cycle position using transfer learning	1
2	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space (AnVIL)	5
1	Compartmap enables inference of higher-order chromatin structure in individual cells from scRNA-seq and scATAC-seq	1