

Kasper D Hansen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12003270/publications.pdf>

Version: 2024-02-01

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	Human methylome variation across Infinium 450K data on the Gene Expression Omnibus. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab025.	3.2	12
2	recount3: summaries and queries for large-scale RNA-seq expression and splicing. <i>Genome Biology</i> , 2021, 22, 323.	8.8	103
3	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. <i>Nature Neuroscience</i> , 2019, 22, 307-316.	14.8	120
4	Preprocessing, normalization and integration of the Illumina HumanMethylationEPIC array with minfi. <i>Bioinformatics</i> , 2017, 33, 558-560.	4.1	583
5	Reproducible RNA-seq analysis using recount2. <i>Nature Biotechnology</i> , 2017, 35, 319-321.	17.5	395
6	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.	7.1	102
7	Software for the Integration of Multiomics Experiments in Bioconductor. <i>Cancer Research</i> , 2017, 77, e39-e42.	0.9	80
8	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.	8.8	94
9	DNA methylation is stable during replication and cell cycle arrest. <i>Scientific Reports</i> , 2016, 5, 17911.	3.3	44
10	Rail-dbGaP: analyzing dbGaP-protected data in the cloud with Amazon Elastic MapReduce. <i>Bioinformatics</i> , 2016, 32, 2551-2553.	4.1	5
11	Public data and open source tools for multi-assay genomic investigation of disease. <i>Briefings in Bioinformatics</i> , 2016, 17, 603-615.	6.5	46
12	Reconstructing A/B compartments as revealed by Hi-C using long-range correlations in epigenetic data. <i>Genome Biology</i> , 2015, 16, 180.	8.8	232
13	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	19.0	3,070
14	Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. <i>Nature Methods</i> , 2015, 12, 230-232.	19.0	248
15	Large-scale hypomethylated blocks associated with Epstein-Barr virus-induced B-cell immortalization. <i>Genome Research</i> , 2014, 24, 177-184.	5.5	130
16	Differential expression analysis of RNA-seq data at single-base resolution. <i>Biostatistics</i> , 2014, 15, 413-426.	1.5	56
17	Removing technical variability in RNA-seq data using conditional quantile normalization. <i>Biostatistics</i> , 2012, 13, 204-216.	1.5	532
18	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.	7.1	257

#	ARTICLE	IF	CITATIONS
19	BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions. <i>Genome Biology</i> , 2012, 13, R83.	9.6	650
20	Sequencing technology does not eliminate biological variability. <i>Nature Biotechnology</i> , 2011, 29, 572-573.	17.5	193
21	Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments. <i>BMC Bioinformatics</i> , 2010, 11, 94.	2.6	1,421
22	Biases in Illumina transcriptome sequencing caused by random hexamer priming. <i>Nucleic Acids Research</i> , 2010, 38, e131-e131.	14.5	573
23	Cloud-scale RNA-sequencing differential expression analysis with Myrna. <i>Genome Biology</i> , 2010, 11, R83.	9.6	268