Jakob Skou Pedersen

List of Publications by Year
in descending order

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66 papers	21,834 citations	66250 44 h-index	124990 64 g-index
81 all docs	81 docs citations	81 times ranked	37974 citing authors

#	Article	IF	Citations
1	Error Characterization and Statistical Modeling Improves Circulating Tumor DNA Detection by Droplet Digital PCR. Clinical Chemistry, 2022, 68, 657-667.	1.5	9
2	The transcriptional landscape and biomarker potential of circular RNAs in prostate cancer. Genome Medicine, 2022, 14, 8.	3.6	19
3	miRNA activity inferred from single cell mRNA expression. Scientific Reports, 2021, 11, 9170.	1.6	16
4	The landscape and driver potential of site-specific hotspots across cancer genomes. Npj Genomic Medicine, 2021, 6, 33.	1.7	8
5	Transcriptome-wide profiles of circular RNA and RNA-binding protein interactions reveal effects on circular RNA biogenesis and cancer pathway expression. Genome Medicine, 2020, 12, 112.	3.6	106
6	Molecular correlates of cisplatin-based chemotherapy response in muscle invasive bladder cancer by integrated multi-omics analysis. Nature Communications, 2020, 11, 4858.	5.8	124
7	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	5.8	27
8	Epigenetic and transcriptomic consequences of excess Xâ€¢chromosome material in 47,<scp>XXX</scp> syndromeâ€”A comparison with Turner syndrome and 46,<scp>XX</scp> females. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2020, 184, 279-293.	0.7	21
9	Passenger Mutations in More Than 2,500 Cancer Genomes: Overall Molecular Functional Impact and Consequences. Cell, 2020, 180, 915-927.e16.	13.5	98
10	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	5.8	73
11	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
12	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. Communications Biology, 2020, 3, 56.	2.0	140
13	ncdDetect2: improved models of the site-specific mutation rate in cancer and driver detection with robust significance evaluation. Bioinformatics, 2019, 35, 189-199.	1.8	6
14	Deficiency of nucleotide excision repair is associated with mutational signature observed in cancer. Genome Research, 2019, 29, 1067-1077.	2.4	66
15	EBADIMEX: an empirical Bayes approach to detect joint differential expression and methylation and to classify samples. Statistical Applications in Genetics and Molecular Biology, 2019, 18, .	0.2	0
16	Pan-cancer screen for mutations in non-coding elements with conservation and cancer specificity reveals correlations with expression and survival. Npj Genomic Medicine, 2018, 3, 1.	1.7	79
17	Optimized targeted sequencing of cell-free plasma DNA from bladder cancer patients. Scientific Reports, 2018, 8, 1917.	1.6	50
18	A site specific model and analysis of the neutral somatic mutation rate in whole-genome cancer data. BMC Bioinformatics, 2018, 19, 147.	1.2	11

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19	Regmex: a statistical tool for exploring motifs in ranked sequence lists from genomics experiments. Algorithms for Molecular Biology, 2018, 13, 17.	0.3	5
20	DNA hypermethylation and differential gene expression associated with Klinefelter syndrome. Scientific Reports, 2018, 8, 13740.	1.6	75
21	APD-Containing Cyclolipodepsipeptides Target Mitochondrial Function in Hypoxic Cancer Cells. Cell Chemical Biology, 2018, 25, 1337-1349.e12.	2.5	27
22	epiG: statistical inference and profiling of DNA methylation from whole-genome bisulfite sequencing data. Genome Biology, 2017, 18, 38.	3.8	6
23	Circular RNA expression is abundant and correlated to aggressiveness in early-stage bladder cancer. Npj Genomic Medicine, 2017, 2, 36.	1.7	105
24	Significance evaluation in factor graphs. BMC Bioinformatics, 2017, 18, 199.	1.2	2
25	RHCG and TCAF1 promoter hypermethylation predicts biochemical recurrence in prostate cancer patients treated by radical prostatectomy. Oncotarget, 2017, 8, 5774-5788.	0.8	22
26	Non-coding cancer driver candidates identified with a sample- and position-specific model of the somatic mutation rate. ELife, 2017, 6, .	2.8	36
27	SNHG16 is regulated by the Wnt pathway in colorectal cancer and affects genes involved in lipid metabolism. Molecular Oncology, 2016, 10, 1266-1282.	2.1	151
28	SNHG5 promotes colorectal cancer cell survival by counteracting STAU1-mediated mRNA destabilization. Nature Communications, 2016, 7, 13875.	5.8	170
29	ProbFold: a probabilistic method for integration of probing data in RNA secondary structure prediction. Bioinformatics, 2016, 32, 2626-2635.	1.8	9
30	Paired Exome Analysis Reveals Clonal Evolution and Potential Therapeutic Targets in Urothelial Carcinoma. Cancer Research, 2016, 76, 5894-5906.	0.4	87
31	Fast, Accurate and Automatic Ancient Nucleosome and Methylation Maps with epiPALEOMIX. Molecular Biology and Evolution, 2016, 33, 3284-3298.	3.5	53
32	miR-625-3p regulates oxaliplatin resistance by targeting MAP2K6-p38 signalling in human colorectal adenocarcinoma cells. Nature Communications, 2016, 7, 12436.	5.8	82
33	Widespread DNA hypomethylation and differential gene expression in Turner syndrome. Scientific Reports, 2016, 6, 34220.	1.6	106
34	Comprehensive Transcriptional Analysis of Early-Stage Urothelial Carcinoma. Cancer Cell, 2016, 30, 27-42.	7.7	486
35	Analysis of circulating tumour DNA to monitor disease burden following colorectal cancer surgery. Gut, 2016, 65, 625-634.	6.1	381
36	PINCAGE: probabilistic integration of cancer genomics data for perturbed gene identification and sample classification. Bioinformatics, 2016, 32, 1353-1365.	1.8	12

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37	The lncRNA MIR31HG regulates p16INK4A expression to modulate senescence. Nature Communications, 2015, 6, 6967.	5.8	161
38	Next-Generation Sequencing of RNA and DNA Isolated from Paired Fresh-Frozen and Formalin-Fixed Paraffin-Embedded Samples of Human Cancer and Normal Tissue. PLoS ONE, 2014, 9, e98187.	1.1	284
39	SNPest: a probabilistic graphical model for estimating genotypes. BMC Research Notes, 2014, 7, 698.	0.6	6
40	Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. Genome Research, 2014, 24, 454-466.	2.4	161
41	Identification of expressed and conserved human noncoding RNAs. Rna, 2014, 20, 236-251.	1.6	47
42	Cellular Disposal of miR23b by RAB27-Dependent Exosome Release Is Linked to Acquisition of Metastatic Properties. Cancer Research, 2014, 74, 5758-5771.	0.4	237
43	A Dual Program for Translation Regulation in Cellular Proliferation and Differentiation. Cell, 2014, 158, 1281-1292.	13.5	414
44	Mutational Context and Diverse Clonal Development in Early and Late Bladder Cancer. Cell Reports, 2014, 7, 1649-1663.	2.9	128
45	Abstract 3153: Whole genome and transcriptome analysis reveals novel genomic alterations in bladder cancer.. , 2013, , .		0
46	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	13.7	1,016
47	Tumor-specific usage of alternative transcription start sites in colorectal cancer identified by genome-wide exon array analysis. BMC Genomics, 2011, 12, 505.	1.2	57
48	Locating protein-coding sequences under selection for additional, overlapping functions in 29 mammalian genomes. Genome Research, 2011, 21, 1916-1928.	2.4	83
49	New families of human regulatory RNA structures identified by comparative analysis of vertebrate genomes. Genome Research, 2011, 21, 1929-1943.	2.4	100
50	Ancient human genome sequence of an extinct Palaeo-Eskimo. Nature, 2010, 463, 757-762.	13.7	750
51	Posttranscriptional Crossregulation between Drosha and DGCR8. Cell, 2009, 136, 75-84.	13.5	380
52	The UCSC genome browser database: update 2007. Nucleic Acids Research, 2007, 35, D668-D673.	6.5	260
53	Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864.	2.4	150
54	The UCSC Genome Browser Database: 2008 update. Nucleic Acids Research, 2007, 36, D773-D779.	6.5	459

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55	Editing modifies the GABAA receptor subunit Â3. Rna, 2007, 13, 698-703.	1.6	184
56	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
57	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. Nature, 2007, 450, 219-232.	13.7	573
58	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	13.7	1,886
59	An RNA gene expressed during cortical development evolved rapidly in humans. Nature, 2006, 443, 167-172.	13.7	884
60	The UCSC Genome Browser Database: update 2006. Nucleic Acids Research, 2006, 34, D590-D598.	6.5	1,156
61	Identification and Classification of Conserved RNA Secondary Structures in the Human Genome. PLoS Computational Biology, 2006, 2, e33.	1.5	439
62	Forces Shaping the Fastest Evolving Regions in the Human Genome. PLoS Genetics, 2006, 2, e168.	1.5	399
63	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. Genome Research, 2005, 15, 1034-1050.	2.4	3,517
64	An Evolutionary Model for Protein-Coding Regions with Conserved RNA Structure. Molecular Biology and Evolution, 2004, 21, 1913-1922.	3.5	36
65	A comparative method for finding and folding RNA secondary structures within protein-coding regions. Nucleic Acids Research, 2004, 32, 4925-4936.	6.5	82
66	Gene finding with a hidden Markov model of genome structure and evolution. Bioinformatics, 2003, 19, 219-227.	1.8	96