

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.

90 papers	22,364 citations	47 h-index	98 g-index
98 ext. papers	27,318 ext. citations	21.9 avg, IF	6.49 L-index

#	Paper	IF	Citations
90	A comparative risk assessment of burden of disease and injury attributable to 67 risk factors and risk factor clusters in 21 regions, 1990-2010: a systematic analysis for the Global Burden of Disease Study 2010. <i>Lancet, The</i> , 2012 , 380, 2224-60	40	7625
89	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
88	GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. <i>Nature Biotechnology</i> , 2015 , 33, 187-197	44.5	1275
87	Engineered CRISPR-Cas9 nucleases with altered PAM specificities. <i>Nature</i> , 2015 , 523, 481-5	50.4	1061
86	Differential methylation of tissue- and cancer-specific CpG island shores distinguishes human induced pluripotent stem cells, embryonic stem cells and fibroblasts. <i>Nature Genetics</i> , 2009 , 41, 1350-3	36.3	936
85	Dimeric CRISPR RNA-guided FokI nucleases for highly specific genome editing. <i>Nature Biotechnology</i> , 2014 , 32, 569-76	44.5	738
84	Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis. <i>Nature Biotechnology</i> , 2013 , 31, 142-7	44.5	691
83	Comprehensive methylome map of lineage commitment from haematopoietic progenitors. <i>Nature</i> , 2010 , 467, 338-42	50.4	484
82	Donor cell type can influence the epigenome and differentiation potential of human induced pluripotent stem cells. <i>Nature Biotechnology</i> , 2011 , 29, 1117-9	44.5	443
81	Androgen-induced TOP2B-mediated double-strand breaks and prostate cancer gene rearrangements. <i>Nature Genetics</i> , 2010 , 42, 668-75	36.3	436
80	Global causes of diarrheal disease mortality in children . <i>PLoS ONE</i> , 2013 , 8, e72788	3.7	421
79	Genome-wide specificities of CRISPR-Cas Cpf1 nucleases in human cells. <i>Nature Biotechnology</i> , 2016 , 34, 869-74	44.5	415
78	CIRCLE-seq: a highly sensitive in vitro screen for genome-wide CRISPR-Cas9 nuclease off-targets. <i>Nature Methods</i> , 2017 , 14, 607-614	21.6	397
77	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. <i>Cell</i> , 2018 , 173, 1535-1548.e16	56.2	292
76	Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors. <i>Nature</i> , 2019 , 569, 433-437	50.4	270
75	A cell epigenotype specific model for the correction of brain cellular heterogeneity bias and its application to age, brain region and major depression. <i>Epigenetics</i> , 2013 , 8, 290-302	5.7	266
74	Personalized epigenomic signatures that are stable over time and covary with body mass index. <i>Science Translational Medicine</i> , 2010 , 2, 49ra67	17.5	254

73	Reversible switching between epigenetic states in honeybee behavioral subcastes. <i>Nature Neuroscience</i> , 2012 , 15, 1371-3	25.5	237
72	Engineered CRISPR-Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. <i>Nature Biotechnology</i> , 2019 , 37, 276-282	44.5	235
71	EWS-FLI1 utilizes divergent chromatin remodeling mechanisms to directly activate or repress enhancer elements in Ewing sarcoma. <i>Cancer Cell</i> , 2014 , 26, 668-681	24.3	223
70	Stromal Microenvironment Shapes the Intratumoral Architecture of Pancreatic Cancer. <i>Cell</i> , 2019 , 178, 160-175.e27	56.2	211
69	In vivo CRISPR editing with no detectable genome-wide off-target mutations. <i>Nature</i> , 2018 , 561, 416-419	30.4	202
68	A DNA hypermethylation module for the stem/progenitor cell signature of cancer. <i>Genome Research</i> , 2012 , 22, 837-49	9.7	196
67	DNA methylation alterations exhibit intraindividual stability and interindividual heterogeneity in prostate cancer metastases. <i>Science Translational Medicine</i> , 2013 , 5, 169ra10	17.5	190
66	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. <i>Cell</i> , 2019 , 176, 1325-1339.e22	56.2	174
65	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
64	Epigenome-wide association studies without the need for cell-type composition. <i>Nature Methods</i> , 2014 , 11, 309-11	21.6	171
63	Droplet-based combinatorial indexing for massive-scale single-cell chromatin accessibility. <i>Nature Biotechnology</i> , 2019 , 37, 916-924	44.5	152
62	CRISPR DNA base editors with reduced RNA off-target and self-editing activities. <i>Nature Biotechnology</i> , 2019 , 37, 1041-1048	44.5	146
61	Activities and specificities of CRISPR/Cas9 and Cas12a nucleases for targeted mutagenesis in maize. <i>Plant Biotechnology Journal</i> , 2019 , 17, 362-372	11.6	125
60	High levels of AAV vector integration into CRISPR-induced DNA breaks. <i>Nature Communications</i> , 2019 , 10, 4439	17.4	119
59	Genome-wide DNA methylation scan in major depressive disorder. <i>PLoS ONE</i> , 2012 , 7, e34451	3.7	113
58	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019 , 569, 576-580	50.4	104
57	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , 2019 , 10, 1903	17.4	97
56	Estimating diarrhea mortality among young children in low and middle income countries. <i>PLoS ONE</i> , 2012 , 7, e29151	3.7	92

55	Dissecting hematopoietic and renal cell heterogeneity in adult zebrafish at single-cell resolution using RNA sequencing. <i>Journal of Experimental Medicine</i> , 2017 , 214, 2875-2887	16.6	82
54	Alterations in nucleolar structure and gene expression programs in prostatic neoplasia are driven by the MYC oncogene. <i>American Journal of Pathology</i> , 2011 , 178, 1824-34	5.8	82
53	Interrogation of human hematopoiesis at single-cell and single-variant resolution. <i>Nature Genetics</i> , 2019 , 51, 683-693	36.3	77
52	GeMes, clusters of DNA methylation under genetic control, can inform genetic and epigenetic analysis of disease. <i>American Journal of Human Genetics</i> , 2014 , 94, 485-95	11	76
51	An improved empirical bayes approach to estimating differential gene expression in microarray time-course data: BETR (Bayesian Estimation of Temporal Regulation). <i>BMC Bioinformatics</i> , 2009 , 10, 409	3.6	75
50	A dual-deaminase CRISPR base editor enables concurrent adenine and cytosine editing. <i>Nature Biotechnology</i> , 2020 , 38, 861-864	44.5	72
49	hichipper: a preprocessing pipeline for calling DNA loops from HiChIP data. <i>Nature Methods</i> , 2018 , 15, 155-156	21.6	72
48	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. <i>Cell Reports</i> , 2019 , 27, 3228-3240.e7	10.6	70
47	MET Exon 14 Skipping in Non-Small Cell Lung Cancer. <i>Oncologist</i> , 2016 , 21, 481-6	5.7	67
46	Accurate genome-scale percentage DNA methylation estimates from microarray data. <i>Biostatistics</i> , 2011 , 12, 197-210	3.7	62
45	DNA methylation shows genome-wide association of NFIX, RAPGEF2 and MSRB3 with gestational age at birth. <i>International Journal of Epidemiology</i> , 2012 , 41, 188-99	7.8	60
44	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. <i>Nature Biotechnology</i> , 2021 , 39, 451-461	44.5	59
43	Defining CRISPR-Cas9 genome-wide nuclease activities with CIRCLE-seq. <i>Nature Protocols</i> , 2018 , 13, 2615-2642	18.8	46
42	Subset quantile normalization using negative control features. <i>Journal of Computational Biology</i> , 2010 , 17, 1385-95	1.7	44
41	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. <i>Cell</i> , 2020 , 182, 1474-1489.e23	56.2	41
40	Enhancer histone-QTLs are enriched on autoimmune risk haplotypes and influence gene expression within chromatin networks. <i>Nature Communications</i> , 2018 , 9, 2905	17.4	36
39	Open-source guideseq software for analysis of GUIDE-seq data. <i>Nature Biotechnology</i> , 2016 , 34, 483	44.5	34
38	OTX2 Activity at Distal Regulatory Elements Shapes the Chromatin Landscape of Group 3 Medulloblastoma. <i>Cancer Discovery</i> , 2017 , 7, 288-301	24.4	32

37	Lysine demethylase KDM4A associates with translation machinery and regulates protein synthesis. <i>Cancer Discovery</i> , 2015 , 5, 255-63	24.4	31
36	diffloop: a computational framework for identifying and analyzing differential DNA loops from sequencing data. <i>Bioinformatics</i> , 2018 , 34, 672-674	7.2	28
35	The early pregnancy placenta foreshadows DNA methylation alterations of solid tumors. <i>Epigenetics</i> , 2017 , 12, 793-803	5.7	27
34	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". <i>Nature Methods</i> , 2018 , 15, 238-239	2.6	25
33	Feature Selection and Dimension Reduction for Single Cell RNA-Seq based on a Multinomial Model		24
32	Inconsistency and features of single nucleotide variants detected in whole exome sequencing versus transcriptome sequencing: A case study in lung cancer. <i>Methods</i> , 2015 , 83, 118-27	4.6	22
31	Survival in Quiescence Requires the Euchromatic Deployment of Ctr4/SUV39H by Argonaute-Associated Small RNAs. <i>Molecular Cell</i> , 2016 , 64, 1088-1101	17.6	20
30	High-specificity bioinformatics framework for epigenomic profiling of discordant twins reveals specific and shared markers for ACPA and ACPA-positive rheumatoid arthritis. <i>Genome Medicine</i> , 2016 , 8, 124	14.4	20
29	Data-Driven Polymer Model for Mechanistic Exploration of Diploid Genome Organization. <i>Biophysical Journal</i> , 2020 , 119, 1905-1916	2.9	19
28	Detection and Analysis of Circulating Epithelial Cells in Liquid Biopsies From Patients With Liver Disease. <i>Gastroenterology</i> , 2018 , 155, 2016-2018.e11	13.3	19
27	Therapeutic implications of GIPC1 silencing in cancer. <i>PLoS ONE</i> , 2010 , 5, e15581	3.7	18
26	Adaptation of the CHARM DNA methylation platform for the rat genome reveals novel brain region-specific differences. <i>Epigenetics</i> , 2011 , 6, 1378-90	5.7	17
25	Magnetic Resonance Spectroscopy-based Metabolomic Biomarkers for Typing, Staging, and Survival Estimation of Early-Stage Human Lung Cancer. <i>Scientific Reports</i> , 2019 , 9, 10319	4.9	14
24	Diverse repetitive element RNA expression defines epigenetic and immunologic features of colon cancer. <i>JCI Insight</i> , 2017 , 2, e91078	9.9	13
23	Interrogation of human hematopoiesis at single-cell and single-variant resolution		7
22	STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. <i>Cancer Cell</i> , 2021 , 39, 827-844.e10	24.3	7
21	Smart-RRBS for single-cell methylome and transcriptome analysis. <i>Nature Protocols</i> , 2021 , 16, 4004-4030	18.8	7
20	Unexpected mutations after CRISPR-Cas9 editing in vivo are most likely pre-existing sequence variants and not nuclease-induced mutations		6

19	In vivo CRISPR-Cas gene editing with no detectable genome-wide off-target mutations		5
18	A (fire)cloud-based DNA methylation data preprocessing and quality control platform. <i>BMC Bioinformatics</i> , 2019 , 20, 160	3.6	4
17	Varying-Censoring Aware Matrix Factorization for Single Cell RNA-Sequencing		4
16	STREAM: Single-cell Trajectories Reconstruction, Exploration And Mapping of omics data		4
15	Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. <i>Nature Biotechnology</i> , 2021 , 39, 1086-1094	44.5	4
14	A novel method for detecting association between DNA methylation and diseases using spatial information. <i>Genetic Epidemiology</i> , 2014 , 38, 714-21	2.6	3
13	Screening human lung cancer with predictive models of serum magnetic resonance spectroscopy metabolomics.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
12	hichipper: A preprocessing pipeline for assessing library quality and DNA loops from HiChIP data		3
11	A Congenital Anemia Reveals Distinct Targeting Mechanisms for Master Transcription Factor GATA1.. <i>Blood</i> , 2022 ,	2.2	2
10	Genome-wide specificity profiles of CRISPR-Cas Cpf1 nucleases in human cells		2
9	Global-scale CRISPR gene editor specificity profiling by ONE-seq identifies population-specific, variant off-target effects		2
8	diffloop: a computational framework for identifying and analyzing differential DNA loops from sequencing data		1
7	Preprocessing and Computational Analysis of Single-Cell Epigenomic Datasets. <i>Methods in Molecular Biology</i> , 2019 , 1935, 187-202	1.4	1
6	Augmenting and directing long-range CRISPR-mediated activation in human cells. <i>Nature Methods</i> , 2021 , 18, 1075-1081	21.6	1
5	CRISPR-Cas9 treatment partially restores amyloid- β 42/40 in human fibroblasts with the Alzheimer's disease M146L mutation.. <i>Molecular Therapy - Nucleic Acids</i> , 2022 , 28, 450-461	10.7	1
4	Genome-wide DNA methylation patterns reveal clinically relevant predictive and prognostic subtypes in human osteosarcoma.. <i>Communications Biology</i> , 2022 , 5, 213	6.7	1
3	EWSR1-ATF1 dependent 3D connectivity regulates oncogenic and differentiation programs in Clear Cell Sarcoma.. <i>Nature Communications</i> , 2022 , 13, 2267	17.4	1
2	Defining genome-wide CRISPR-Cas genome-editing nuclease activity with GUIDE-seq. <i>Nature Protocols</i> , 2021 , 16, 5592-5615	18.8	0

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