

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.

120 papers	15,823 citations	55 h-index	125 g-index
132 ext. papers	19,362 ext. citations	18.4 avg, IF	6.3 L-index

#	Paper	IF	Citations
120	Accurate multiplex polony sequencing of an evolved bacterial genome. <i>Science</i> , 2005 , 309, 1728-32	33.3	1011
119	Somatic coding mutations in human induced pluripotent stem cells. <i>Nature</i> , 2011 , 471, 63-7	50.4	998
118	Increased methylation variation in epigenetic domains across cancer types. <i>Nature Genetics</i> , 2011 , 43, 768-75	36.3	825
117	Interrogating a high-density SNP map for signatures of natural selection. <i>Genome Research</i> , 2002 , 12, 1805-14	9.7	678
116	In vivo genome editing via CRISPR/Cas9 mediated homology-independent targeted integration. <i>Nature</i> , 2016 , 540, 144-149	50.4	645
115	Neuronal subtypes and diversity revealed by single-nucleus RNA sequencing of the human brain. <i>Science</i> , 2016 , 352, 1586-90	33.3	531
114	Genome-wide regulation of 5hmC, 5mC, and gene expression by Tet1 hydroxylase in mouse embryonic stem cells. <i>Molecular Cell</i> , 2011 , 42, 451-64	17.6	493
113	Integrative single-cell analysis of transcriptional and epigenetic states in the human adult brain. <i>Nature Biotechnology</i> , 2018 , 36, 70-80	44.5	433
112	Recapitulation of premature ageing with iPSCs from Hutchinson-Gilford progeria syndrome. <i>Nature</i> , 2011 , 472, 221-5	50.4	428
111	Genome-wide identification of human RNA editing sites by parallel DNA capturing and sequencing. <i>Science</i> , 2009 , 324, 1210-3	33.3	415
110	Targeted bisulfite sequencing reveals changes in DNA methylation associated with nuclear reprogramming. <i>Nature Biotechnology</i> , 2009 , 27, 353-60	44.5	409
109	Whole-genome sequencing in autism identifies hot spots for de novo germline mutation. <i>Cell</i> , 2012 , 151, 1431-42	56.2	392
108	Genome-wide analysis reveals TET- and TDG-dependent 5-methylcytosine oxidation dynamics. <i>Cell</i> , 2013 , 153, 692-706	56.2	390
107	The metabolome of induced pluripotent stem cells reveals metabolic changes occurring in somatic cell reprogramming. <i>Cell Research</i> , 2012 , 22, 168-77	24.7	388
106	Multiplex amplification of large sets of human exons. <i>Nature Methods</i> , 2007 , 4, 931-6	21.6	357
105	Sequencing genomes from single cells by polymerase cloning. <i>Nature Biotechnology</i> , 2006 , 24, 680-6	44.5	353
104	Distribution of recombination crossovers and the origin of haplotype blocks: the interplay of population history, recombination, and mutation. <i>American Journal of Human Genetics</i> , 2002 , 71, 1227-34 ¹	41	351

103	Fluorescent in situ sequencing (FISSEQ) of RNA for gene expression profiling in intact cells and tissues. <i>Nature Protocols</i> , 2015 , 10, 442-58	18.8	280
102	Allele-specific methylation is prevalent and is contributed by CpG-SNPs in the human genome. <i>Genome Research</i> , 2010 , 20, 883-9	9.7	273
101	Characterizing transcriptional heterogeneity through pathway and gene set overdispersion analysis. <i>Nature Methods</i> , 2016 , 13, 241-4	21.6	257
100	Identification of methylation haplotype blocks aids in deconvolution of heterogeneous tissue samples and tumor tissue-of-origin mapping from plasma DNA. <i>Nature Genetics</i> , 2017 , 49, 635-642	36.3	237
99	High-throughput sequencing of the transcriptome and chromatin accessibility in the same cell. <i>Nature Biotechnology</i> , 2019 , 37, 1452-1457	44.5	227
98	Evolutionary history and adaptation from high-coverage whole-genome sequences of diverse African hunter-gatherers. <i>Cell</i> , 2012 , 150, 457-69	56.2	226
97	Tet1 controls meiosis by regulating meiotic gene expression. <i>Nature</i> , 2012 , 492, 443-7	50.4	207
96	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016 , 34, 726-37	44.5	204
95	Massively parallel polymerase cloning and genome sequencing of single cells using nanoliter microwells. <i>Nature Biotechnology</i> , 2013 , 31, 1126-32	44.5	188
94	Targeted gene correction of laminopathy-associated LMNA mutations in patient-specific iPSCs. <i>Cell Stem Cell</i> , 2011 , 8, 688-94	18	188
93	Advances in the profiling of DNA modifications: cytosine methylation and beyond. <i>Nature Reviews Genetics</i> , 2014 , 15, 647-61	30.1	183
92	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. <i>Nature Neuroscience</i> , 2018 , 21, 432-439	25.5	172
91	Human oocytes reprogram somatic cells to a pluripotent state. <i>Nature</i> , 2011 , 478, 70-5	50.4	169
90	Humanized Mice Reveal Differential Immunogenicity of Cells Derived from Autologous Induced Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2015 , 17, 353-9	18	167
89	A public resource facilitating clinical use of genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 11920-7	11.5	154
88	Optimal timing of inner cell mass isolation increases the efficiency of human embryonic stem cell derivation and allows generation of sibling cell lines. <i>Cell Stem Cell</i> , 2009 , 4, 103-6	18	148
87	Digital RNA allelotyping reveals tissue-specific and allele-specific gene expression in human. <i>Nature Methods</i> , 2009 , 6, 613-8	21.6	136
86	Genetic correction and analysis of induced pluripotent stem cells from a patient with gyrate atrophy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 6537-42	11.5	136

85	Non-invasive early detection of cancer four years before conventional diagnosis using a blood test. <i>Nature Communications</i> , 2020 , 11, 3475	17.4	135
84	The presenilin-1 E9 mutation results in reduced β -secretase activity, but not total loss of PS1 function, in isogenic human stem cells. <i>Cell Reports</i> , 2013 , 5, 974-85	10.6	133
83	Identification of a specific reprogramming-associated epigenetic signature in human induced pluripotent stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 16196-201	11.5	129
82	The regulation of integrin function by divalent cations. <i>Cell Adhesion and Migration</i> , 2012 , 6, 20-9	3.2	126
81	Dynamics of 5-methylcytosine and 5-hydroxymethylcytosine during germ cell reprogramming. <i>Cell Research</i> , 2013 , 23, 329-39	24.7	125
80	A comparative strategy for single-nucleus and single-cell transcriptomes confirms accuracy in predicted cell-type expression from nuclear RNA. <i>Scientific Reports</i> , 2017 , 7, 6031	4.9	115
79	HaploBlockFinder: haplotype block analyses. <i>Bioinformatics</i> , 2003 , 19, 1300-1	7.2	108
78	The lncRNA DEANR1 facilitates human endoderm differentiation by activating FOXA2 expression. <i>Cell Reports</i> , 2015 , 11, 137-48	10.6	102
77	Performance evaluation of pathogenicity-computation methods for missense variants. <i>Nucleic Acids Research</i> , 2018 , 46, 7793-7804	20.1	100
76	A single-nucleus RNA-sequencing pipeline to decipher the molecular anatomy and pathophysiology of human kidneys. <i>Nature Communications</i> , 2019 , 10, 2832	17.4	100
75	The effect that genotyping errors have on the robustness of common linkage-disequilibrium measures. <i>American Journal of Human Genetics</i> , 2001 , 68, 1447-56	11	97
74	Comparable frequencies of coding mutations and loss of imprinting in human pluripotent cells derived by nuclear transfer and defined factors. <i>Cell Stem Cell</i> , 2014 , 15, 634-42	18	93
73	VarCards: an integrated genetic and clinical database for coding variants in the human genome. <i>Nucleic Acids Research</i> , 2018 , 46, D1039-D1048	20.1	86
72	Modelling Fanconi anemia pathogenesis and therapeutics using integration-free patient-derived iPSCs. <i>Nature Communications</i> , 2014 , 5, 4330	17.4	84
71	Library-free methylation sequencing with bisulfite padlock probes. <i>Nature Methods</i> , 2012 , 9, 270-2	21.6	84
70	Long-range polony haplotyping of individual human chromosome molecules. <i>Nature Genetics</i> , 2006 , 38, 382-7	36.3	80
69	The Action of Discoidin Domain Receptor 2 in Basal Tumor Cells and Stromal Cancer-Associated Fibroblasts Is Critical for Breast Cancer Metastasis. <i>Cell Reports</i> , 2016 , 15, 2510-23	10.6	64
68	Finding the needles in the metagenome haystack. <i>Microbial Ecology</i> , 2007 , 53, 475-85	4.4	60

67	Multiplex padlock targeted sequencing reveals human hypermutable CpG variations. <i>Genome Research</i> , 2009 , 19, 1606-15	9.7	59
66	The effect of single nucleotide polymorphism identification strategies on estimates of linkage disequilibrium. <i>Molecular Biology and Evolution</i> , 2003 , 20, 232-42	8.3	59
65	Chromatin signature of widespread monoallelic expression. <i>ELife</i> , 2013 , 2, e01256	8.9	55
64	Targeted bisulfite sequencing by solution hybrid selection and massively parallel sequencing. <i>Nucleic Acids Research</i> , 2011 , 39, e127	20.1	54
63	Targeted sequencing and functional analysis reveal brain-size-related genes and their networks in autism spectrum disorders. <i>Molecular Psychiatry</i> , 2017 , 22, 1282-1290	15.1	53
62	Analysis of protein-coding mutations in hiPSCs and their possible role during somatic cell reprogramming. <i>Nature Communications</i> , 2013 , 4, 1382	17.4	51
61	A robust approach to identifying tissue-specific gene expression regulatory variants using personalized human induced pluripotent stem cells. <i>PLoS Genetics</i> , 2009 , 5, e1000718	6	46
60	Distinct chemokine signaling regulates integrin ligand specificity to dictate tissue-specific lymphocyte homing. <i>Developmental Cell</i> , 2014 , 30, 61-70	10.2	45
59	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021 , 598, 86-102	50.4	44
58	Specific sorting of single bacterial cells with microfabricated fluorescence-activated cell sorting and tyramide signal amplification fluorescence in situ hybridization. <i>Analytical Chemistry</i> , 2011 , 83, 7269-75	7.8	42
57	Transcriptomic signature associated with carcinogenesis and aggressiveness of papillary thyroid carcinoma. <i>Theranostics</i> , 2018 , 8, 4345-4358	12.1	41
56	Mechanical signals regulate and activate SNAIL1 protein to control the fibrogenic response of cancer-associated fibroblasts. <i>Journal of Cell Science</i> , 2016 , 129, 1989-2002	5.3	41
55	Characterization of chromatin accessibility with a transposome hypersensitive sites sequencing (THS-seq) assay. <i>Genome Biology</i> , 2016 , 17, 20	18.3	40
54	AJUBA LIM Proteins Limit Hippo Activity in Proliferating Cells by Sequestering the Hippo Core Kinase Complex in the Cytosol. <i>Molecular and Cellular Biology</i> , 2016 , 36, 2526-42	4.8	39
53	Randomly distributed crossovers may generate block-like patterns of linkage disequilibrium: an act of genetic drift. <i>Human Genetics</i> , 2003 , 113, 51-9	6.3	38
52	Fever Promotes T Lymphocyte Trafficking via a Thermal Sensory Pathway Involving Heat Shock Protein 90 and β Integrins. <i>Immunity</i> , 2019 , 50, 137-151.e6	32.3	38
51	PAK2 Haploinsufficiency Results in Synaptic Cytoskeleton Impairment and Autism-Related Behavior. <i>Cell Reports</i> , 2018 , 24, 2029-2041	10.6	37
50	Targeted methylation sequencing reveals dysregulated Wnt signaling in Parkinson disease. <i>Journal of Genetics and Genomics</i> , 2016 , 43, 587-592	4	35

49	Evolution of cellular diversity in primary motor cortex of human, marmoset monkey, and mouse		33
48	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021 , 598, 111-119.	50.4	31
47	Genetic evidence of gender difference in autism spectrum disorder supports the female-protective effect. <i>Translational Psychiatry</i> , 2020 , 10, 4	8.6	30
46	Visualizing and Interpreting Single-Cell Gene Expression Datasets with Similarity Weighted Nonnegative Embedding. <i>Cell Systems</i> , 2018 , 7, 656-666.e4	10.6	30
45	Tools for the analysis of high-dimensional single-cell RNA sequencing data. <i>Nature Reviews Nephrology</i> , 2020 , 16, 408-421	14.9	29
44	Ultraaccurate genome sequencing and haplotyping of single human cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 12512-12517	11.5	27
43	Precise in vivo genome editing via single homology arm donor mediated intron-targeting gene integration for genetic disease correction. <i>Cell Research</i> , 2019 , 29, 804-819	24.7	26
42	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. <i>Protein and Cell</i> , 2014 , 5, 59-68	7.2	21
41	Rapid identification of heterozygous mutations in <i>Drosophila melanogaster</i> using genomic capture sequencing. <i>Genome Research</i> , 2010 , 20, 981-8	9.7	21
40	DNA methylation identifies genetically and prognostically distinct subtypes of myelodysplastic syndromes. <i>Blood Advances</i> , 2019 , 3, 2845-2858	7.8	21
39	A multimodal and integrated approach to interrogate human kidney biopsies with rigor and reproducibility: guidelines from the Kidney Precision Medicine Project. <i>Physiological Genomics</i> , 2021 , 53, 1-11	3.6	21
38	A comparative study of the genetic components of three subcategories of autism spectrum disorder. <i>Molecular Psychiatry</i> , 2019 , 24, 1720-1731	15.1	18
37	Mouse SCNT ESCs have lower somatic mutation load than syngeneic iPSCs. <i>Stem Cell Reports</i> , 2014 , 2, 399-405	8	17
36	On the design of clone-based haplotyping. <i>Genome Biology</i> , 2013 , 14, R100	18.3	17
35	Vitamin D-related genes are subjected to significant de novo mutation burdens in autism spectrum disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017 , 174, 568-577	3.5	15
34	Mapping Cellular Reprogramming via Pooled Overexpression Screens with Paired Fitness and Single-Cell RNA-Sequencing Readout. <i>Cell Systems</i> , 2018 , 7, 548-555.e8	10.6	15
33	Defining the Teratoma as a Model for Multi-lineage Human Development. <i>Cell</i> , 2020 , 183, 1402-1419.e18	18.2	12
32	A multimodal cell census and atlas of the mammalian primary motor cortex		12

31	Development and bias assessment of a method for targeted metagenomic sequencing of marine cyanobacteria. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 1116-25	4.8	11
30	Microfluidic devices with permeable polymer barriers for capture and transport of biomolecules and cells. <i>Lab on A Chip</i> , 2013 , 13, 3389-97	7.2	11
29	An atlas of healthy and injured cell states and niches in the human kidney		10
28	Characterization of genome-methylome interactions in 22 nuclear pedigrees. <i>PLoS ONE</i> , 2014 , 9, e99313	3.7	9
27	The role of the NMD factor UPF3B in olfactory sensory neurons. <i>ELife</i> , 2020 , 9,	8.9	9
26	RETrace: simultaneous retrospective lineage tracing and methylation profiling of single cells. <i>Genome Research</i> , 2020 , 30, 602-610	9.7	8
25	Mediators and dynamics of DNA methylation. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011 , 3, 281-98	6.6	7
24	High-resolution RNA allelotyping along the inactive X chromosome: evidence of RNA polymerase III in regulating chromatin configuration. <i>Scientific Reports</i> , 2017 , 7, 45460	4.9	6
23	Cellular Recruitment by Podocyte-Derived Pro-migratory Factors in Assembly of the Human Renal Filter. <i>IScience</i> , 2019 , 20, 402-414	6.1	6
22	The unique disulfide bond-stabilized W1 α - β loop in the β propeller domain regulates integrin α β affinity and signaling. <i>Journal of Biological Chemistry</i> , 2013 , 288, 14228-14237	5.4	6
21	Disruption of disulfide restriction at integrin knees induces activation and ligand-independent signaling of α Journal of Cell Science, 2013 , 126, 5030-41	5.3	6
20	Integrative single-cell analysis by transcriptional and epigenetic states in human adult brain		5
19	Linking transcriptome and chromatin accessibility in nanoliter droplets for single-cell sequencing		3
18	Epigenetically Silenced Candidate Tumor Suppressor Genes in Prostate Cancer: Identified by Modeling Methylation Stratification and Applied to Progression Prediction. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 198-207	4	3
17	Gel-seq: whole-genome and transcriptome sequencing by simultaneous low-input DNA and RNA library preparation using semi-permeable hydrogel barriers. <i>Lab on A Chip</i> , 2017 , 17, 2619-2630	7.2	2
16	Scalable dual-omics profiling with single-nucleus chromatin accessibility and mRNA expression sequencing 2 (SNARE-seq2). <i>Nature Protocols</i> , 2021 , 16, 4992-5029	18.8	2
15	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. <i>Protein and Cell</i> , 2013 , 5, 59	7.2	2
14	Single nucleus analysis of the chromatin landscape in mouse forebrain development		2

13	A reference tissue atlas for the human kidney		2
12	TET1s deficiency exacerbates oscillatory shear flow-induced atherosclerosis.. <i>International Journal of Biological Sciences</i> , 2022 , 18, 2163-2180	11.2	2
11	Gel-seq: A Method for Simultaneous Sequencing Library Preparation of DNA and RNA Using Hydrogel Matrices. <i>Journal of Visualized Experiments</i> , 2018 ,	1.6	1
10	Temporal analyses of postnatal liver development and maturation by single-cell transcriptomics.. <i>Developmental Cell</i> , 2022 , 57, 398-414.e5	10.2	1
9	Discovery of genomic loci of the human cerebral cortex using genetically informed brain atlases.. <i>Science</i> , 2022 , 375, 522-528	33.3	1
8	Visualizing and interpreting single-cell gene expression datasets with Similarity Weighted Nonnegative Embedding		1
7	A Multimodal and Integrated Approach to Interrogate Human Kidney Biopsies with Rigor and Reproducibility: The Kidney Precision Medicine Project		1
6	5-Azacytidine Transiently Restores Dysregulated Erythroid Differentiation Gene Expression in TET2-Deficient Erythroleukemia Cells. <i>Molecular Cancer Research</i> , 2021 , 19, 451-464	6.6	1
5	Large-Scale Targeted DNA Methylation Analysis Using Bisulfite Padlock Probes. <i>Methods in Molecular Biology</i> , 2018 , 1708, 365-382	1.4	1
4	Reply to DNA methylation haplotypes as cancer markersT <i>Nature Genetics</i> , 2018 , 50, 1063-1066	36.3	0
3	Charting oncogenicity of genes and variants across lineages via multiplexed screens in teratomas. <i>IScience</i> , 2021 , 24, 103149	6.1	0
2	Genome-wide mapping of the sixth base. <i>Genome Biology</i> , 2011 , 12, 116	18.3	
1	DNA Methylation Identifies Genetically and Prognostically Distinct Subtypes of MDS. <i>Blood</i> , 2018 , 132, 106-106	2.2	