

Hongcang Gu

List of Publications by Year in Descending Order

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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.

63

papers

13,505

citations

38

h-index

68

g-index

68

ext. papers

15,702

ext. citations

21.1

avg, IF

5.77

L-index

#	Paper	IF	Citations
63	Preneoplastic Alterations Define CLL DNA Methylome and Persist through Disease Progression and Therapy. <i>Blood Cancer Discovery</i> , 2021 , 2, 54-69	7	6
62	Smart-RRBS for single-cell methylome and transcriptome analysis. <i>Nature Protocols</i> , 2021 , 16, 4004-4030	18.8	7
61	A Male Case of Kagami-Ogata Syndrome Caused by Paternal Unipaternal Disomy 14 as a Result of a Robertsonian Translocation. <i>Frontiers in Pediatrics</i> , 2020 , 8, 88	3.4	4
60	Differential DNA methylation of vocal and facial anatomy genes in modern humans. <i>Nature Communications</i> , 2020 , 11, 1189	17.4	27
59	Disorders Associated With Diverse, Recurrent Deletions and Duplications at 1q21.1. <i>Frontiers in Genetics</i> , 2020 , 11, 577	4.5	4
58	Fusion Gene in Acute Leukemia and Myeloid Neoplasms: Report of Three Cases and a Literature Review. <i>OncoTargets and Therapy</i> , 2020 , 13, 7665-7681	4.4	2
57	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. <i>Cell Stem Cell</i> , 2019 , 25, 622-638.e13	18	35
56	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019 , 569, 576-580	50.4	104
55	Corrupted coordination of epigenetic modifications leads to diverging chromatin states and transcriptional heterogeneity in CLL. <i>Nature Communications</i> , 2019 , 10, 1874	17.4	38
54	Myeloid/Lymphoid Neoplasm With FGFR1 Rearrangement Accompanying and Gene Mutations. <i>Frontiers in Oncology</i> , 2019 , 9, 1304	5.3	
53	Genome-wide tracking of dCas9-methyltransferase footprints. <i>Nature Communications</i> , 2018 , 9, 597	17.4	85
52	Genetic determinants and epigenetic effects of pioneer-factor occupancy. <i>Nature Genetics</i> , 2018 , 50, 250-258	36.3	85
51	Dissecting the Functional Consequences of De Novo DNA Methylation Dynamics in Human Motor Neuron Differentiation and Physiology. <i>Cell Stem Cell</i> , 2018 , 22, 559-574.e9	18	36
50	Global delay in nascent strand DNA methylation. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 327-332	32.6	32
49	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. <i>Cell Stem Cell</i> , 2018 , 23, 289-305.e5	18	34
48	Reduced MEK inhibition preserves genomic stability in naive human embryonic stem cells. <i>Nature Methods</i> , 2018 , 15, 732-740	21.6	44
47	Targets and genomic constraints of ectopic Dnmt3b expression. <i>ELife</i> , 2018 , 7,	8.9	16

46	Multimodal Single-Cell Profiling Defines the Epigenetic Determinants of Chronic Lymphocytic Leukemia Evolution. <i>Blood</i> , 2018 , 132, 1312-1312	2.2	
45	Comparative genomic analysis of embryonic, lineage-converted and stem cell-derived motor neurons. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	8
44	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017 , 20, 706-719.e7	18	43
43	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. <i>Nature</i> , 2017 , 548, 219-223	50.4	135
42	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. <i>Nature</i> , 2017 , 549, 543-547	50.4	86
41	Epigenetic Memory Underlies Cell-Autonomous Heterogeneous Behavior of Hematopoietic Stem Cells. <i>Cell</i> , 2016 , 167, 1310-1322.e17	56.2	124
40	LKB1 loss links serine metabolism to DNA methylation and tumorigenesis. <i>Nature</i> , 2016 , 539, 390-395	50.4	173
39	Single Cell Bisulfite Sequencing Defines Epigenetic Diversification in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2016 , 128, 1047-1047	2.2	1
38	Targeted bisulfite sequencing of the dynamic DNA methylome. <i>Epigenetics and Chromatin</i> , 2016 , 9, 55	5.8	17
37	Qualitative and Semiquantitative Analysis of Fecal Bifidobacterium Species in Centenarians Living in Bama, Guangxi, China. <i>Current Microbiology</i> , 2015 , 71, 143-9	2.4	20
36	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. <i>Nature Genetics</i> , 2015 , 47, 469-78	36.3	288
35	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , 2015 , 518, 355-359	50.4	140
34	Genetic and Epigenetic Variation, but Not Diet, Shape the Sperm Methylome. <i>Developmental Cell</i> , 2015 , 35, 750-8	10.2	102
33	Transcription factor binding dynamics during human ES cell differentiation. <i>Nature</i> , 2015 , 518, 344-9	50.4	232
32	Epigenomic profiling of young and aged HSCs reveals concerted changes during aging that reinforce self-renewal. <i>Cell Stem Cell</i> , 2014 , 14, 673-88	18	399
31	DNA methylation signatures link prenatal famine exposure to growth and metabolism. <i>Nature Communications</i> , 2014 , 5, 5592	17.4	368
30	Locally disordered methylation forms the basis of intratumor methylome variation in chronic lymphocytic leukemia. <i>Cancer Cell</i> , 2014 , 26, 813-825	24.3	216
29	Charting a dynamic DNA methylation landscape of the human genome. <i>Nature</i> , 2013 , 500, 477-81	50.4	932

28	Genome-wide map of quantified epigenetic changes during in vitro chondrogenic differentiation of primary human mesenchymal stem cells. <i>BMC Genomics</i> , 2013 , 14, 105	4.5	61
27	Cellular source and mechanisms of high transcriptome complexity in the mammalian testis. <i>Cell Reports</i> , 2013 , 3, 2179-90	10.6	334
26	Proliferation-dependent alterations of the DNA methylation landscape underlie hematopoietic stem cell aging. <i>Cell Stem Cell</i> , 2013 , 12, 413-25	18	322
25	Transcriptional and epigenetic dynamics during specification of human embryonic stem cells. <i>Cell</i> , 2013 , 153, 1149-63	56.2	332
24	Gel-free multiplexed reduced representation bisulfite sequencing for large-scale DNA methylation profiling. <i>Genome Biology</i> , 2012 , 13, R92	18.3	183
23	DNA methylation dynamics during in vivo differentiation of blood and skin stem cells. <i>Molecular Cell</i> , 2012 , 47, 633-47	17.6	271
22	The polyoma virus large T binding protein p150 is a transcriptional repressor of c-MYC. <i>PLoS ONE</i> , 2012 , 7, e46486	3.7	15
21	A unique regulatory phase of DNA methylation in the early mammalian embryo. <i>Nature</i> , 2012 , 484, 339-44	46.4	723
20	Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. <i>Genome Research</i> , 2012 , 22, 1128-38	9.7	277
19	Highly efficient derivation of ventricular cardiomyocytes from induced pluripotent stem cells with a distinct epigenetic signature. <i>Cell Research</i> , 2012 , 22, 142-54	24.7	70
18	Dnmt3a is essential for hematopoietic stem cell differentiation. <i>Nature Genetics</i> , 2011 , 44, 23-31	36.3	737
17	Reference Maps of human ES and iPS cell variation enable high-throughput characterization of pluripotent cell lines. <i>Cell</i> , 2011 , 144, 439-52	56.2	756
16	DNA-binding and regulatory properties of the transcription factor and putative tumor suppressor p150(Sal2). <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2011 , 1809, 276-83	6	18
15	Reprogramming factor expression initiates widespread targeted chromatin remodeling. <i>Cell Stem Cell</i> , 2011 , 8, 96-105	18	295
14	Preparation of reduced representation bisulfite sequencing libraries for genome-scale DNA methylation profiling. <i>Nature Protocols</i> , 2011 , 6, 468-81	18.8	505
13	Genomic distribution and inter-sample variation of non-CpG methylation across human cell types. <i>PLoS Genetics</i> , 2011 , 7, e1002389	6	295
12	Genome Wide DNA Methylation and Transcriptome Analysis in HSC Aging. <i>Blood</i> , 2011 , 118, 2367-2367	2.2	
11	Quantitative comparison of genome-wide DNA methylation mapping technologies. <i>Nature Biotechnology</i> , 2010 , 28, 1106-14	44.5	486

10	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010 , 28, 1097-105	44.5	570
9	Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. <i>Nature Methods</i> , 2010 , 7, 133-6	21.6	258
8	Paternally induced transgenerational environmental reprogramming of metabolic gene expression in mammals. <i>Cell</i> , 2010 , 143, 1084-96	56.2	831
7	High-throughput bisulfite sequencing in mammalian genomes. <i>Methods</i> , 2009 , 48, 226-32	4.6	161
6	Genome-scale DNA methylation maps of pluripotent and differentiated cells. <i>Nature</i> , 2008 , 454, 766-70	50.4	1999
5	Novel Naturally Occurring Bean pod mottle virus Reassortants with Mixed Heterologous RNA1 Genomes. <i>Phytopathology</i> , 2007 , 97, 79-86	3.8	11
4	Molecular Characterization of Naturally Occurring RNA1 Recombinants of the Comovirus Bean pod mottle virus. <i>Phytopathology</i> , 2007 , 97, 1255-62	3.8	14
3	The Bean pod mottle virus proteinase cofactor and putative helicase are symptom severity determinants. <i>Virology</i> , 2005 , 333, 271-83	3.6	38
2	Diversity Among Isolates of Bean pod mottle virus. <i>Phytopathology</i> , 2002 , 92, 446-52	3.8	36
1	Genes Affecting Vocal and Facial Anatomy Went Through Extensive Regulatory Divergence in Modern Humans		7