

# Hongcang Gu

## List of Publications by Year in descending order

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Version: 2024-02-01

63  
papers

17,103  
citations

61857

43  
h-index

110170

64  
g-index

68  
all docs

68  
docs citations

68  
times ranked

24552  
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA methylation and expression profiles of placenta and umbilical cord blood reveal the characteristics of gestational diabetes mellitus patients and offspring. <i>Clinical Epigenetics</i> , 2022, 14, .	1.8	13
2	Preneoplastic Alterations Define CLL DNA Methylome and Persist through Disease Progression and Therapy. <i>Blood Cancer Discovery</i> , 2021, 2, 54-69.	2.6	16
3	Smart-RRBS for single-cell methylome and transcriptome analysis. <i>Nature Protocols</i> , 2021, 16, 4004-4030.	5.5	34
4	<p><em>SET-CAN</em> Fusion Gene in Acute Leukemia and Myeloid Neoplasms: Report of Three Cases and a Literature Review</p>. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 7665-7681.	1.0	6
5	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.	0.9	7
6	Differential DNA methylation of vocal and facial anatomy genes in modern humans. <i>Nature Communications</i> , 2020, 11, 1189.	5.8	69
7	Disorders Associated With Diverse, Recurrent Deletions and Duplications at 1q21.1. <i>Frontiers in Genetics</i> , 2020, 11, 577.	1.1	17
8	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. <i>Cell Stem Cell</i> , 2019, 25, 622-638.e13.	5.2	82
9	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019, 569, 576-580.	13.7	195
10	Corrupted coordination of epigenetic modifications leads to diverging chromatin states and transcriptional heterogeneity in CLL. <i>Nature Communications</i> , 2019, 10, 1874.	5.8	63
11	Myeloid/Lymphoid Neoplasm With FGFR1 Rearrangement Accompanying RUNX1 and NOTCH1 Gene Mutations. <i>Frontiers in Oncology</i> , 2019, 9, 1304.	1.3	1
12	Genome-wide tracking of dCas9-methyltransferase footprints. <i>Nature Communications</i> , 2018, 9, 597.	5.8	114
13	Genetic determinants and epigenetic effects of pioneer-factor occupancy. <i>Nature Genetics</i> , 2018, 50, 250-258.	9.4	139
14	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.	5.2	53
15	Global delay in nascent strand DNA methylation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 327-332.	3.6	56
16	Comparative genomic analysis of embryonic, lineage-converted, and stem cell-derived motor neurons. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	10
17	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. <i>Cell Stem Cell</i> , 2018, 23, 289-305.e5.	5.2	60
18	Reduced MEK inhibition preserves genomic stability in naive human embryonic stem cells. <i>Nature Methods</i> , 2018, 15, 732-740.	9.0	74

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19	Targets and genomic constraints of ectopic Dnmt3b expression. <i>ELife</i> , 2018, 7, .	2.8	26
20	Multimodal Single-Cell Profiling Defines the Epigenetic Determinants of Chronic Lymphocytic Leukemia Evolution. <i>Blood</i> , 2018, 132, 1312-1312.	0.6	0
21	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 706-719.e7.	5.2	63
22	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. <i>Nature</i> , 2017, 549, 543-547.	13.7	146
23	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. <i>Nature</i> , 2017, 548, 219-223.	13.7	211
24	Targeted bisulfite sequencing of the dynamic DNA methylome. <i>Epigenetics and Chromatin</i> , 2016, 9, 55.	1.8	18
25	Epigenetic Memory Underlies Cell-Autonomous Heterogeneous Behavior of Hematopoietic Stem Cells. <i>Cell</i> , 2016, 167, 1310-1322.e17.	13.5	153
26	LKB1 loss links serine metabolism to DNA methylation and tumorigenesis. <i>Nature</i> , 2016, 539, 390-395.	13.7	248
27	Single Cell Bisulfite Sequencing Defines Epigenetic Diversification in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2016, 128, 1047-1047.	0.6	1
28	Genetic and Epigenetic Variation, but Not Diet, Shape the Sperm Methylome. <i>Developmental Cell</i> , 2015, 35, 750-758.	3.1	130
29	Transcription factor binding dynamics during human ES cell differentiation. <i>Nature</i> , 2015, 518, 344-349.	13.7	318
30	Qualitative and Semiquantitative Analysis of Fecal Bifidobacterium Species in Centenarians Living in Bama, Guangxi, China. <i>Current Microbiology</i> , 2015, 71, 143-149.	1.0	29
31	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. <i>Nature Genetics</i> , 2015, 47, 469-478.	9.4	409
32	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , 2015, 518, 355-359.	13.7	172
33	DNA methylation signatures link prenatal famine exposure to growth and metabolism. <i>Nature Communications</i> , 2014, 5, 5592.	5.8	494
34	Locally Disordered Methylation Forms the Basis of Intratumor Methylome Variation in Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2014, 26, 813-825.	7.7	323
35	Epigenomic Profiling of Young and Aged HSCs Reveals Concerted Changes during Aging that Reinforce Self-Renewal. <i>Cell Stem Cell</i> , 2014, 14, 673-688.	5.2	524
36	Charting a dynamic DNA methylation landscape of the human genome. <i>Nature</i> , 2013, 500, 477-481.	13.7	1,168

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37	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.	1.2	69
38	Cellular Source and Mechanisms of High Transcriptome Complexity in the Mammalian Testis. <i>Cell Reports</i> , 2013, 3, 2179-2190.	2.9	497
39	Proliferation-Dependent Alterations of the DNA Methylation Landscape Underlie Hematopoietic Stem Cell Aging. <i>Cell Stem Cell</i> , 2013, 12, 413-425.	5.2	401
40	Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1149-1163.	13.5	419
41	Highly efficient derivation of ventricular cardiomyocytes from induced pluripotent stem cells with a distinct epigenetic signature. <i>Cell Research</i> , 2012, 22, 142-154.	5.7	77
42	Gel-free multiplexed reduced representation bisulfite sequencing for large-scale DNA methylation profiling. <i>Genome Biology</i> , 2012, 13, R92.	13.9	244
43	DNA Methylation Dynamics during In Vivo Differentiation of Blood and Skin Stem Cells. <i>Molecular Cell</i> , 2012, 47, 633-647.	4.5	338
44	The Polyoma Virus Large T Binding Protein p150 Is a Transcriptional Repressor of c-MYC. <i>PLoS ONE</i> , 2012, 7, e46486.	1.1	19
45	A unique regulatory phase of DNA methylation in the early mammalian embryo. <i>Nature</i> , 2012, 484, 339-344.	13.7	860
46	Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. <i>Genome Research</i> , 2012, 22, 1128-1138.	2.4	344
47	Dnmt3a is essential for hematopoietic stem cell differentiation. <i>Nature Genetics</i> , 2012, 44, 23-31.	9.4	916
48	Reference Maps of Human ES and iPS Cell Variation Enable High-Throughput Characterization of Pluripotent Cell Lines. <i>Cell</i> , 2011, 144, 439-452.	13.5	899
49	DNA-binding and regulatory properties of the transcription factor and putative tumor suppressor p150Sal2. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2011, 1809, 276-283.	0.9	23
50	Reprogramming Factor Expression Initiates Widespread Targeted Chromatin Remodeling. <i>Cell Stem Cell</i> , 2011, 8, 96-105.	5.2	345
51	Preparation of reduced representation bisulfite sequencing libraries for genome-scale DNA methylation profiling. <i>Nature Protocols</i> , 2011, 6, 468-481.	5.5	667
52	Genomic Distribution and Inter-Sample Variation of Non-CpG Methylation across Human Cell Types. <i>PLoS Genetics</i> , 2011, 7, e1002389.	1.5	345
53	Genome Wide DNA Methylation and Transcriptome Analysis in HSC Aging. <i>Blood</i> , 2011, 118, 2367-2367.	0.6	0
54	Quantitative comparison of genome-wide DNA methylation mapping technologies. <i>Nature Biotechnology</i> , 2010, 28, 1106-1114.	9.4	534

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55	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010, 28, 1097-1105.	9.4	647
56	Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. <i>Nature Methods</i> , 2010, 7, 133-136.	9.0	302
57	Paternally Induced Transgenerational Environmental Reprogramming of Metabolic Gene Expression in Mammals. <i>Cell</i> , 2010, 143, 1084-1096.	13.5	990
58	High-throughput bisulfite sequencing in mammalian genomes. <i>Methods</i> , 2009, 48, 226-232.	1.9	191
59	Genome-scale DNA methylation maps of pluripotent and differentiated cells. <i>Nature</i> , 2008, 454, 766-770.	13.7	2,267
60	Novel Naturally Occurring Bean pod mottle virus Reassortants with Mixed Heterologous RNA1 Genomes. <i>Phytopathology</i> , 2007, 97, 79-86.	1.1	16
61	Molecular Characterization of Naturally Occurring RNA1 Recombinants of the Comovirus <i>Bean pod mottle virus</i>. <i>Phytopathology</i> , 2007, 97, 1255-1262.	1.1	16
62	The Bean pod mottle virus proteinase cofactor and putative helicase are symptom severity determinants. <i>Virology</i> , 2005, 333, 271-283.	1.1	42
63	Diversity Among Isolates of Bean pod mottle virus. <i>Phytopathology</i> , 2002, 92, 446-452.	1.1	42