Hongcang Gu

List of Publications by Year
in descending order

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63 papers	17,103 citations	71004 43 h-index	124990 64 g-index
68 all docs	68 docs citations	68 times ranked	27228 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. Clinical Epigenetics, 2022, 14, .	1.8	13
2	Preneoplastic Alterations Define CLL DNA Methylome and Persist through Disease Progression and Therapy. Blood Cancer Discovery, 2021, 2, 54-69.	2.6	16
3	Smart-RRBS for single-cell methylome and transcriptome analysis. Nature Protocols, 2021, 16, 4004-4030.	5.5	34
4	SET-CAN Fusion Gene in Acute Leukemia and Myeloid Neoplasms: Report of Three Cases and a Literature Review . OncoTargets and Therapy, 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. Frontiers in Pediatrics, 2020, 8, 88.	0.9	7
6	Differential DNA methylation of vocal and facial anatomy genes in modern humans. Nature Communications, 2020, 11, 1189.	5.8	69
7	Disorders Associated With Diverse, Recurrent Deletions and Duplications at 1q21.1. Frontiers in Genetics, 2020, 11, 577.	1.1	17
8	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. Cell Stem Cell, 2019, 25, 622-638.e13.	5.2	82
9	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. Nature, 2019, 569, 576-580.	13.7	195
10	Corrupted coordination of epigenetic modifications leads to diverging chromatin states and transcriptional heterogeneity in CLL. Nature Communications, 2019, 10, 1874.	5.8	63
11	Myeloid/Lymphoid Neoplasm With FGFR1 Rearrangement Accompanying RUNX1 and NOTCH1 Gene Mutations. Frontiers in Oncology, 2019, 9, 1304.	1.3	1
12	Genome-wide tracking of dCas9-methyltransferase footprints. Nature Communications, 2018, 9, 597.	5.8	114
13	Genetic determinants and epigenetic effects of pioneer-factor occupancy. Nature Genetics, 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. Cell Stem Cell, 2018, 22, 559-574.e9.	5.2	53
15	Global delay in nascent strand DNA methylation. Nature Structural and Molecular Biology, 2018, 25, 327-332.	3.6	56
16	Comparative genomic analysis of embryonic, lineage-converted, and stem cell-derived motor neurons. Development (Cambridge), 2018, 145, .	1.2	10
17	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. Cell Stem Cell, 2018, 23, 289-305.e5.	5.2	60
18	Reduced MEK inhibition preserves genomic stability in naive human embryonic stem cells. Nature Methods, 2018, 15, 732-740.	9.0	74

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19	Targets and genomic constraints of ectopic Dnmt3b expression. ELife, 2018, 7, .	2.8	26
20	Multimodal Single-Cell Profiling Defines the Epigenetic Determinants of Chronic Lymphocytic Leukemia Evolution. Blood, 2018, 132, 1312-1312.	0.6	0
21	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. Cell Stem Cell, 2017, 20, 706-719.e7.	5.2	63
22	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. Nature, 2017, 549, 543-547.	13.7	146
23	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. Nature, 2017, 548, 219-223.	13.7	211
24	Targeted bisulfite sequencing of the dynamic DNA methylome. Epigenetics and Chromatin, 2016, 9, 55.	1.8	18
25	Epigenetic Memory Underlies Cell-Autonomous Heterogeneous Behavior of Hematopoietic Stem Cells. Cell, 2016, 167, 1310-1322.e17.	13.5	153
26	LKB1 loss links serine metabolism to DNA methylation and tumorigenesis. Nature, 2016, 539, 390-395.	13.7	248
27	Single Cell Bisulfite Sequencing Defines Epigenetic Diversification in Chronic Lymphocytic Leukemia. Blood, 2016, 128, 1047-1047.	0.6	1
28	Genetic and Epigenetic Variation, but Not Diet, Shape the Sperm Methylome. Developmental Cell, 2015, 35, 750-758.	3.1	130
29	Transcription factor binding dynamics during human ES cell differentiation. Nature, 2015, 518, 344-349.	13.7	318
30	Qualitative and Semiquantitative Analysis of Fecal Bifidobacterium Species in Centenarians Living in Bama, Guangxi, China. Current Microbiology, 2015, 71, 143-149.	1.0	29
31	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. Nature Genetics, 2015, 47, 469-478.	9.4	409
32	Dissecting neural differentiation regulatory networks through epigenetic footprinting. Nature, 2015, 518, 355-359.	13.7	172
33	DNA methylation signatures link prenatal famine exposure to growth and metabolism. Nature Communications, 2014, 5, 5592.	5.8	494
34	Locally Disordered Methylation Forms the Basis of Intratumor Methylome Variation in Chronic Lymphocytic Leukemia. Cancer Cell, 2014, 26, 813-825.	7.7	323
35	Epigenomic Profiling of Young and Aged HSCs Reveals Concerted Changes during Aging that Reinforce Self-Renewal. Cell Stem Cell, 2014, 14, 673-688.	5.2	524
36	Charting a dynamic DNA methylation landscape of the human genome. Nature, 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. BMC Genomics, 2013, 14, 105.	1.2	69
38	Cellular Source and Mechanisms of High Transcriptome Complexity in the Mammalian Testis. Cell Reports, 2013, 3, 2179-2190.	2.9	497
39	Proliferation-Dependent Alterations of the DNA Methylation Landscape Underlie Hematopoietic Stem Cell Aging. Cell Stem Cell, 2013, 12, 413-425.	5.2	401
40	Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. Cell, 2013, 153, 1149-1163.	13.5	419
41	Highly efficient derivation of ventricular cardiomyocytes from induced pluripotent stem cells with a distinct epigenetic signature. Cell Research, 2012, 22, 142-154.	5.7	77
42	Gel-free multiplexed reduced representation bisulfite sequencing for large-scale DNA methylation profiling. Genome Biology, 2012, 13, R92.	13.9	244
43	DNA Methylation Dynamics during InÂVivo Differentiation of Blood and Skin Stem Cells. Molecular Cell, 2012, 47, 633-647.	4.5	338
44	The Polyoma Virus Large T Binding Protein p150 Is a Transcriptional Repressor of c-MYC. PLoS ONE, 2012, 7, e46486.	1.1	19
45	A unique regulatory phase of DNA methylation in the early mammalian embryo. Nature, 2012, 484, 339-344.	13.7	860
46	Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. Genome Research, 2012, 22, 1128-1138.	2.4	344
47	Dnmt3a is essential for hematopoietic stem cell differentiation. Nature Genetics, 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. Cell, 2011, 144, 439-452.	13.5	899
49	DNA-binding and regulatory properties of the transcription factor and putative tumor suppressor p150Sal2. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2011, 1809, 276-283.	0.9	23
50	Reprogramming Factor Expression Initiates Widespread Targeted Chromatin Remodeling. Cell Stem Cell, 2011, 8, 96-105.	5.2	345
51	Preparation of reduced representation bisulfite sequencing libraries for genome-scale DNA methylation profiling. Nature Protocols, 2011, 6, 468-481.	5.5	667
52	Genomic Distribution and Inter-Sample Variation of Non-CpG Methylation across Human Cell Types. PLoS Genetics, 2011, 7, e1002389.	1.5	345
53	Genome Wide DNA Methylation and Transcriptome Analysis in HSC Aging. Blood, 2011, 118, 2367-2367.	0.6	0
54	Quantitative comparison of genome-wide DNA methylation mapping technologies. Nature Biotechnology, 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. Nature Biotechnology, 2010, 28, 1097-1105.	9.4	647
56	Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. Nature Methods, 2010, 7, 133-136.	9.0	302
57	Paternally Induced Transgenerational Environmental Reprogramming of Metabolic Gene Expression in Mammals. Cell, 2010, 143, 1084-1096.	13.5	990
58	High-throughput bisulfite sequencing in mammalian genomes. Methods, 2009, 48, 226-232.	1.9	191
59	Genome-scale DNA methylation maps of pluripotent and differentiated cells. Nature, 2008, 454, 766-770.	13.7	2,267
60	Novel Naturally Occurring Bean pod mottle virus Reassortants with Mixed Heterologous RNA1 Genomes. Phytopathology, 2007, 97, 79-86.	1.1	16
61	Molecular Characterization of Naturally Occurring RNA1 Recombinants of the Comovirus Bean pod mottle virus. Phytopathology, 2007, 97, 1255-1262.	1.1	16
62	The Bean pod mottle virus proteinase cofactor and putative helicase are symptom severity determinants. Virology, 2005, 333, 271-283.	1.1	42
63	Diversity Among Isolates of Bean pod mottle virus. Phytopathology, 2002, 92, 446-452.	1.1	42