Martin Hirst

List of Publications by Year in descending order

96 papers	30,541 citations	41344 49 h-index	39675 94 g-index
102 all docs	102 docs citations	102 times ranked	50927 citing authors

#	Article	IF	Citations
1	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	27.8	5,653
2	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
3	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	27.8	1,778
4	The NIH Roadmap Epigenomics Mapping Consortium. Nature Biotechnology, 2010, 28, 1045-1048.	17.5	1,705
5	Conserved role of intragenic DNA methylation in regulating alternative promoters. Nature, 2010, 466, 253-257.	27.8	1,568
6	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. Nature Genetics, 2010, 42, 181-185.	21.4	1,504
7	ARID1AMutations in Endometriosis-Associated Ovarian Carcinomas. New England Journal of Medicine, 2010, 363, 1532-1543.	27.0	1,460
8	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	27.8	1,428
9	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. Nature Methods, 2007, 4, 651-657.	19.0	1,254
10	Vitaminâ€‰C induces Tet-dependent DNA demethylation and a blastocyst-like state in ES cells. Nature, 2013, 500, 222-226.	27.8	715
11	Mutation ofFOXL2in Granulosa-Cell Tumors of the Ovary. New England Journal of Medicine, 2009, 360, 2719-2729.	27.0	706
12	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. Nature Biotechnology, 2010, 28, 1097-1105.	17.5	647
13	Identification of miR-145 and miR-146a as mediators of the 5qâ€“ syndrome phenotype. Nature Medicine, 2010, 16, 49-58.	30.7	588
14	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. Nature, 2014, 506, 445-450.	27.8	521
15	deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data. PLoS Computational Biology, 2011, 7, e1001138.	3.2	477
16	Applications of New Sequencing Technologies for Transcriptome Analysis. Annual Review of Genomics and Human Genetics, 2009, 10, 135-151.	6.2	457
17	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
18	De novo transcriptome assembly with ABySS. Bioinformatics, 2009, 25, 2872-2877.	4.1	371

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19	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. BioTechniques, 2008, 45, 81-94.	1.8	355
20	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. Nature, 2017, 549, 227-232.	27.8	321
21	The Human Epigenome Browser at Washington University. Nature Methods, 2011, 8, 989-990.	19.0	302
22	Concurrent CIC mutations, IDH mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. Journal of Pathology, 2012, 226, 7-16.	4.5	272
23	Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. Genome Research, 2012, 22, 1995-2007.	5.5	237
24	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. Nature Genetics, 2013, 45, 836-841.	21.4	207
25	Massively parallel sequencing of the polyadenylated transcriptome of C. elegans. Genome Research, 2009, 19, 657-666.	5.5	169
26	Identification and characterization of Hoxa9 binding sites in hematopoietic cells. Blood, 2012, 119, 388-398.	1.4	165
27	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. Genome Research, 2008, 18, 1906-1917.	5.5	163
28	In-depth characterization of the microRNA transcriptome in a leukemia progression model. Genome Research, 2008, 18, 1787-1797.	5.5	162
29	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. Genome Research, 2013, 23, 1522-1540.	5.5	162
30	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. Genome Biology, 2010, 11, R82.	9.6	159
31	Estimating absolute methylation levels at single-CpG resolution from methylation enrichment and restriction enzyme sequencing methods. Genome Research, 2013, 23, 1541-1553.	5.5	138
32	Autophagy Regulation of Metabolism Is Required for CD8+ T Cell Anti-tumor Immunity. Cell Reports, 2019, 27, 502-513.e5.	6.4	134
33	Feature-based classifiers for somatic mutation detection in tumourâ€“normal paired sequencing data. Bioinformatics, 2012, 28, 167-175.	4.1	130
34	Genome-wide identification of human microRNAs located in leukemia-associated genomic alterations. Blood, 2011, 117, 595-607.	1.4	105
35	Genome-Wide Profiles of Extra-cranial Malignant Rhabdoid Tumors Reveal Heterogeneity and Dysregulated Developmental Pathways. Cancer Cell, 2016, 29, 394-406.	16.8	105
36	Barcoding reveals complex clonal dynamics of de novo transformed human mammary cells. Nature, 2015, 528, 267-271.	27.8	101

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37	Epigenetics and human disease. International Journal of Biochemistry and Cell Biology, 2009, 41, 136-146.	2.8	99
38	Intermediate DNA methylation is a conserved signature of genome regulation. Nature Communications, 2015, 6, 6363.	12.8	91
39	Analysis of the clonal growth and differentiation dynamics of primitive barcoded human cord blood cells in NSG mice. Blood, 2013, 122, 3129-3137.	1.4	90
40	Analysis of Normal Human Mammary Epigenomes Reveals Cell-Specific Active Enhancer States and Associated Transcription Factor Networks. Cell Reports, 2016, 17, 2060-2074.	6.4	90
41	DNA barcoding reveals diverse growth kinetics of human breast tumour subclones in serially passaged xenografts. Nature Communications, 2014, 5, 5871.	12.8	86
42	High-Resolution Single-Cell DNA Methylation Measurements Reveal Epigenetically Distinct Hematopoietic Stem Cell Subpopulations. Stem Cell Reports, 2018, 11, 578-592.	4.8	79
43	A transgenic mouse model demonstrating the oncogenic role of mutations in the polycomb-group gene EZH2 in lymphomagenesis. Blood, 2014, 123, 3914-3924.	1.4	69
44	Next generation sequencing based approaches to epigenomics. Briefings in Functional Genomics, 2010, 9, 455-465.	2.7	60
45	Clonal Analysis via Barcoding Reveals Diverse Growth and Differentiation of Transplanted Mouse and Human Mammary Stem Cells. Cell Stem Cell, 2014, 14, 253-263.	11.1	57
46	Vitamin C-induced epigenomic remodelling in IDH1 mutant acute myeloid leukaemia. Leukemia, 2018, 32, 11-20.	7.2	57
47	Epigenetic and transcriptional determinants of the human breast. Nature Communications, 2015, 6, 6351.	12.8	56
48	The genomic and transcriptomic landscape of anaplastic thyroid cancer: implications for therapy. BMC Cancer, 2015, 15, 984.	2.6	55
49	Hepatocyte Nuclear Factor 4â€Alpha Is Essential for the Active Epigenetic State at Enhancers in Mouse Liver. Hepatology, 2019, 70, 1360-1376.	7.3	52
50	MEF2B mutations in non-Hodgkin lymphoma dysregulate cell migration by decreasing MEF2B target gene activation. Nature Communications, 2015, 6, 7953.	12.8	50
51	Nucleosome Density ChIP-Seq Identifies Distinct Chromatin Modification Signatures Associated with MNase Accessibility. Cell Reports, 2016, 17, 2112-2124.	6.4	46
52	Robust high-performance nanoliter-volume single-cell multiple displacement amplification on planar substrates. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8484-8489.	7.1	45
53	Epigenetic therapy restores normal hematopoiesis in a zebrafish model of NUP98â€“HOXA9-induced myeloid disease. Leukemia, 2015, 29, 2086-2097.	7.2	38
54	Single-cell analysis identifies a CD33+ subset of human cord blood cells with high regenerative potential. Nature Cell Biology, 2018, 20, 710-720.	10.3	36

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55	Altered microRNA expression links IL6 and TNF-induced inflammaging with myeloid malignancy in humans and mice. Blood, 2020, 135, 2235-2251.	1.4	35
56	Epigenome data release: a participant-centered approach to privacy protection. Genome Biology, 2015, 16, 142.	8.8	34
57	Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. Developmental Cell, 2021, 56, 1238-1252.e5.	7.0	29
58	Draft Genome Sequence of the Pelagic Photoferrotroph Chlorobium phaeoferrooxidans. Genome Announcements, 2017, 5, .	0.8	28
59	Prenatal Alcohol Exposure: Profiling Developmental DNA Methylation Patterns in Central and Peripheral Tissues. Frontiers in Genetics, 2018, 9, 610.	2.3	27
60	Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. Nature Communications, 2014, 5, 5442.	12.8	25
61	Genome-wide detection of imprinted differentially methylated regions using nanopore sequencing. ELife, 0, 11, .	6.0	21
62	The prolyl isomerase FKBP25 regulates microtubule polymerization impacting cell cycle progression and genomic stability. Nucleic Acids Research, 2018, 46, 2459-2478.	14.5	19
63	Epigenetic Restoration of Fetal-like IGF1 Signaling Inhibits Leukemia Stem Cell Activity. Cell Stem Cell, 2018, 23, 714-726.e7.	11.1	19
64	The Pathognomonic FOXL2 C134W Mutation Alters DNA-Binding Specificity. Cancer Research, 2020, 80, 3480-3491.	0.9	19
65	Initiation of human mammary cell tumorigenesis by mutant KRAS requires YAP inactivation. Oncogene, 2020, 39, 1957-1968.	5.9	18
66	Epiclomal: Probabilistic clustering of sparse single-cell DNA methylation data. PLoS Computational Biology, 2020, 16, e1008270.	3.2	18
67	Clinical response to nivolumab in an INI1-deficient pediatric chordoma correlates with immunogenic recognition of brachyury. Npj Precision Oncology, 2021, 5, 103.	5.4	18
68	Whole-genome analysis reveals unexpected dynamics of mutant subclone development in a patient with JAK2-V617F-positive chronic myeloid leukemia. Experimental Hematology, 2017, 53, 48-58.	0.4	15
69	Dynamics of the cell-free DNA methylome of metastatic prostate cancer during androgen-targeting treatment. Epigenomics, 2020, 12, 1317-1332.	2.1	15
70	MYC-induced human acute myeloid leukemia requires a continuing IL-3/GM-CSF costimulus. Blood, 2020, 136, 2764-2773.	1.4	15
71	Atrophin controls developmental signaling pathways via interactions with Trithorax-like. ELife, 2017, 6, .	6.0	15
72	MicroRNA-708 is a novel regulator of the Hoxa9 program in myeloid cells. Leukemia, 2020, 34, 1253-1265.	7.2	12

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73	Complete Bordetella avium, Bordetella hinzii and Bordetella trematum lipid A structures and genomic sequence analyses of the loci involved in their modifications. Innate Immunity, 2014, 20, 659-672.	2.4	10
74	Prenatal Adversity Alters the Epigenetic Profile of the Prefrontal Cortex: Sexually Dimorphic Effects of Prenatal Alcohol Exposure and Food-Related Stress. Genes, 2021, 12, 1773.	2.4	10
75	Epigenomic programming in early fetal brain development. Epigenomics, 2020, 12, 1053-1070.	2.1	9
76	Characterization of the human thyroid epigenome. Journal of Endocrinology, 2017, 235, 153-165.	2.6	8
77	RUNX1 promotes cell growth in human T-cell acute lymphoblastic leukemia by transcriptional regulation of key target genes. Experimental Hematology, 2018, 64, 84-96.	0.4	8
78	Synthetic modeling reveals HOXB genes are critical for the initiation and maintenance of human leukemia. Nature Communications, 2019, 10, 2913.	12.8	8
79	Distinct DNA methylation patterns associated with treatment resistance in metastatic castration resistant prostate cancer. Scientific Reports, 2021, 11, 6630.	3.3	8
80	Micro-ribonucleic acid-155 is a direct target of Meis1, but not a driver in acute myeloid leukemia. Haematologica, 2018, 103, 246-255.	3.5	7
81	Delineating MEIS1 cis-regulatory elements active in hematopoietic cells. Leukemia, 2014, 28, 433-436.	7.2	6
82	Regulatory variation: an emerging vantage point for cancer biology. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2014, 6, 37-59.	6.6	6
83	Elucidating the importance and regulation of key enhancers for human MEIS1 expression. Leukemia, 2022, 36, 1980-1989.	7.2	6
84	Generation of Native Chromatin Immunoprecipitation Sequencing Libraries for Nucleosome Density Analysis. Journal of Visualized Experiments, 2017, , .	0.3	5
85	Polycomb contraction differentially regulates terminal human hematopoietic differentiation programs. BMC Biology, 2022, 20, 104.	3.8	5
86	Histone Chaperone Paralogs Have Redundant, Cooperative, and Divergent Functions in Yeast. Genetics, 2019, 213, 1301-1316.	2.9	4
87	CRIS: complete reconstruction of immunoglobulin V-D-J sequences from RNA-seq data. Bioinformatics Advances, 2021, 1, vbab021.	2.4	4
88	Optimization of magnetic bead-based nucleic acid extraction for SARS-CoV-2 testing using readily available reagents. Journal of Virological Methods, 2022, 299, 114339.	2.1	4
89	Epigenomics: Sequencing the Methylome. Methods in Molecular Biology, 2013, 973, 39-54.	0.9	3
90	Stress hematopoiesis induces a proliferative advantage in TET2 deficiency. Leukemia, 2022, 36, 809-820.	7.2	3

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91	A novel methylated cell-free DNA marker panel to monitor treatment response in metastatic prostate cancer. Epigenomics, 2022, 14, 811-822.	2.1	3
92	SnapShot: Epigenomic Assays. Cell, 2016, 167, 1430-1430.e1.	28.9	2
93	Epigenetic and functional changes imposed by NUP98-HOXA9 in a genetically engineered model of chronic myeloid leukemia progression. Haematologica, 2021, 106, 881-885.	3.5	1
94	NOTCH1 Induces Differential Epigenomic Patterning and Genomic Organization in Fetal Liver- and Adult Bone Marrow-Derived Hematopoietic Progentiors. Blood, 2015, 126, 3637-3637.	1.4	1
95	ISDN2014_0378: Prenatal alcohol exposure alters the developmental methylation profile of the rat hypothalamus. International Journal of Developmental Neuroscience, 2015, 47, 109-109.	1.6	0
96	Clonal Analysis of Mouse Mammary Luminal Epithelial Cell Transplants. Stem Cells and Development, 2019, 28, 353-355.	2.1	0