

Alexander Meissner

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109
papers

23,890
citations

48
h-index

122
g-index

122
ext. papers

28,803
ext. citations

22.5
avg, IF

6.74
L-index

#	Paper	IF	Citations
109	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015 , 518, 317-30	50.4	3849
108	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. <i>Nature</i> , 2007 , 448, 553-60	50.4	3296
107	Genome-scale DNA methylation maps of pluripotent and differentiated cells. <i>Nature</i> , 2008 , 454, 766-70	50.4	1999
106	DNA methylation: roles in mammalian development. <i>Nature Reviews Genetics</i> , 2013 , 14, 204-20	30.1	1935
105	Dissecting direct reprogramming through integrative genomic analysis. <i>Nature</i> , 2008 , 454, 49-55	50.4	1205
104	Charting a dynamic DNA methylation landscape of the human genome. <i>Nature</i> , 2013 , 500, 477-81	50.4	932
103	Reduced representation bisulfite sequencing for comparative high-resolution DNA methylation analysis. <i>Nucleic Acids Research</i> , 2005 , 33, 5868-77	20.1	823
102	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
101	Dnmt3a is essential for hematopoietic stem cell differentiation. <i>Nature Genetics</i> , 2011 , 44, 23-31	36.3	737
100	A unique regulatory phase of DNA methylation in the early mammalian embryo. <i>Nature</i> , 2012 , 484, 339-44	50.4	723
99	Preparation of reduced representation bisulfite sequencing libraries for genome-scale DNA methylation profiling. <i>Nature Protocols</i> , 2011 , 6, 468-81	18.8	505
98	DNA methylation dynamics of the human preimplantation embryo. <i>Nature</i> , 2014 , 511, 611-5	50.4	390
97	DNA methylation signatures link prenatal famine exposure to growth and metabolism. <i>Nature Communications</i> , 2014 , 5, 5592	17.4	368
96	Transcriptional and epigenetic dynamics during specification of human embryonic stem cells. <i>Cell</i> , 2013 , 153, 1149-63	56.2	332
95	Epigenetic modifications in pluripotent and differentiated cells. <i>Nature Biotechnology</i> , 2010 , 28, 1079-88	44.5	302
94	Reprogramming factor expression initiates widespread targeted chromatin remodeling. <i>Cell Stem Cell</i> , 2011 , 8, 96-105	18	295
93	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. <i>Nature Genetics</i> , 2015 , 47, 469-78	36.3	288

92	In vivo control of CpG and non-CpG DNA methylation by DNA methyltransferases. <i>PLoS Genetics</i> , 2012 , 8, e1002750	6	279
91	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
90	DNA methylation dynamics during in vivo differentiation of blood and skin stem cells. <i>Molecular Cell</i> , 2012 , 47, 633-47	17.6	271
89	Transcription factor binding dynamics during human ES cell differentiation. <i>Nature</i> , 2015 , 518, 344-9	50.4	232
88	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
87	Gel-free multiplexed reduced representation bisulfite sequencing for large-scale DNA methylation profiling. <i>Genome Biology</i> , 2012 , 13, R92	18.3	183
86	Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. <i>Nature Methods</i> , 2015 , 12, 230-2, 1 p following 232	21.6	171
85	Integrative Analyses of Human Reprogramming Reveal Dynamic Nature of Induced Pluripotency. <i>Cell</i> , 2015 , 162, 412-424	56.2	148
84	Proto-oncogenic role of mutant IDH2 in leukemia initiation and maintenance. <i>Cell Stem Cell</i> , 2014 , 14, 329-41	18	141
83	Molecular recording of mammalian embryogenesis. <i>Nature</i> , 2019 , 570, 77-82	50.4	140
82	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , 2015 , 518, 355-359	50.4	140
81	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. <i>Nature</i> , 2017 , 548, 219-223	50.4	135
80	Epigenetic Memory Underlies Cell-Autonomous Heterogeneous Behavior of Hematopoietic Stem Cells. <i>Cell</i> , 2016 , 167, 1310-1322.e17	56.2	124
79	Molecular features of cellular reprogramming and development. <i>Nature Reviews Molecular Cell Biology</i> , 2016 , 17, 139-54	48.7	109
78	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019 , 569, 576-580	50.4	104
77	Genetic and Epigenetic Variation, but Not Diet, Shape the Sperm Methylome. <i>Developmental Cell</i> , 2015 , 35, 750-8	10.2	102
76	Epigenome-wide study uncovers large-scale changes in histone acetylation driven by tau pathology in aging and Alzheimer's human brains. <i>Nature Neuroscience</i> , 2019 , 22, 37-46	25.5	99
75	A qPCR ScoreCard quantifies the differentiation potential of human pluripotent stem cells. <i>Nature Biotechnology</i> , 2015 , 33, 1182-92	44.5	97

74	KDM5 Histone Demethylase Activity Links Cellular Transcriptomic Heterogeneity to Therapeutic Resistance. <i>Cancer Cell</i> , 2018 , 34, 939-953.e9	24.3	93
73	Induced Pluripotent Stem Cell Differentiation Enables Functional Validation of GWAS Variants in Metabolic Disease. <i>Cell Stem Cell</i> , 2017 , 20, 547-557.e7	18	86
72	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. <i>Nature</i> , 2017 , 549, 543-547	50.4	86
71	Genome-wide tracking of dCas9-methyltransferase footprints. <i>Nature Communications</i> , 2018 , 9, 597	17.4	85
70	Genetic determinants and epigenetic effects of pioneer-factor occupancy. <i>Nature Genetics</i> , 2018 , 50, 250-258	36.3	85
69	Ground State Conditions Induce Rapid Reorganization of Core Pluripotency Factor Binding before Global Epigenetic Reprogramming. <i>Cell Stem Cell</i> , 2015 , 17, 462-70	18	78
68	X chromosome reactivation dynamics reveal stages of reprogramming to pluripotency. <i>Cell</i> , 2014 , 159, 1681-97	56.2	77
67	Cancer-Germline Antigen Expression Discriminates Clinical Outcome to CTLA-4 Blockade. <i>Cell</i> , 2018 , 173, 624-633.e8	56.2	71
66	Long-term persistence and development of induced pancreatic beta cells generated by lineage conversion of acinar cells. <i>Nature Biotechnology</i> , 2014 , 32, 1223-30	44.5	71
65	Mouse embryonic stem cells self-organize into trunk-like structures with neural tube and somites. <i>Science</i> , 2020 , 370,	33.3	61
64	Circadian Entrainment Triggers Maturation of Human In Vitro Islets. <i>Cell Stem Cell</i> , 2020 , 26, 108-122.e108		57
63	Analysis of short tandem repeat expansions and their methylation state with nanopore sequencing. <i>Nature Biotechnology</i> , 2019 , 37, 1478-1481	44.5	57
62	Analysing human neural stem cell ontogeny by consecutive isolation of Notch active neural progenitors. <i>Nature Communications</i> , 2015 , 6, 6500	17.4	51
61	Notch inhibition allows oncogene-independent generation of iPS cells. <i>Nature Chemical Biology</i> , 2014 , 10, 632-639	11.7	48
60	PRC2 Is Required to Maintain Expression of the Maternal Gtl2-Rian-Mirg Locus by Preventing De Novo DNA Methylation in Mouse Embryonic Stem Cells. <i>Cell Reports</i> , 2015 , 12, 1456-70	10.6	46
59	The use of small molecules in somatic-cell reprogramming. <i>Trends in Cell Biology</i> , 2014 , 24, 179-87	18.3	46
58	Cross-Regulation between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. <i>Molecular Cell</i> , 2019 , 74, 951-965.e13	17.6	45
57	Reduced MEK inhibition preserves genomic stability in naive human embryonic stem cells. <i>Nature Methods</i> , 2018 , 15, 732-740	21.6	44

56	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017 , 20, 706-719.e7	18	43
55	The road ahead in genetics and genomics. <i>Nature Reviews Genetics</i> , 2020 , 21, 581-596	30.1	43
54	Aligning Single-Cell Developmental and Reprogramming Trajectories Identifies Molecular Determinants of Myogenic Reprogramming Outcome. <i>Cell Systems</i> , 2018 , 7, 258-268.e3	10.6	40
53	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
52	Unblending of Transcriptional Condensates in Human Repeat Expansion Disease. <i>Cell</i> , 2020 , 181, 1062-1072.e38	17.2	38
51	Zika Virus Alters DNA Methylation of Neural Genes in an Organoid Model of the Developing Human Brain. <i>MSystems</i> , 2018 , 3,	7.6	37
50	TETs compete with DNMT3 activity in pluripotent cells at thousands of methylated somatic enhancers. <i>Nature Genetics</i> , 2020 , 52, 819-827	36.3	36
49	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
48	Activation of neuronal genes via LINE-1 elements upon global DNA demethylation in human neural progenitors. <i>Nature Communications</i> , 2019 , 10, 3182	17.4	36
47	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. <i>Cell Stem Cell</i> , 2019 , 25, 622-638.e13	18	35
46	Age- and pregnancy-associated DNA methylation changes in mammary epithelial cells. <i>Stem Cell Reports</i> , 2015 , 4, 297-311	8	35
45	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. <i>Cell Stem Cell</i> , 2018 , 23, 289-305.e5	18	34
44	Global delay in nascent strand DNA methylation. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 327-332	17.6	32
43	An Intermediate Pluripotent State Controlled by MicroRNAs Is Required for the Naive-to-Primed Stem Cell Transition. <i>Cell Stem Cell</i> , 2018 , 22, 851-864.e5	18	31
42	Epigenetic regulator function through mouse gastrulation. <i>Nature</i> , 2020 , 584, 102-108	50.4	30
41	Enabling consistency in pluripotent stem cell-derived products for research and development and clinical applications through material standards. <i>Stem Cells Translational Medicine</i> , 2015 , 4, 217-23	6.9	29
40	Association of DNA methylation in the brain with age in older persons is confounded by common neuropathologies. <i>International Journal of Biochemistry and Cell Biology</i> , 2015 , 67, 58-64	5.6	27
39	Differential DNA methylation of vocal and facial anatomy genes in modern humans. <i>Nature Communications</i> , 2020 , 11, 1189	17.4	27

38	Transcriptional and Chromatin Dynamics of Muscle Regeneration after Severe Trauma. <i>Stem Cell Reports</i> , 2016 , 7, 983-997	8	26
37	A CLK3-HMGA2 Alternative Splicing Axis Impacts Human Hematopoietic Stem Cell Molecular Identity throughout Development. <i>Cell Stem Cell</i> , 2018 , 22, 575-588.e7	18	24
36	X Chromosome Dosage Influences DNA Methylation Dynamics during Reprogramming to Mouse iPSCs. <i>Stem Cell Reports</i> , 2018 , 10, 1537-1550	8	24
35	Derivation and manipulation of murine embryonic stem cells. <i>Methods in Molecular Biology</i> , 2009 , 482, 3-19	1.4	22
34	Inducible histone K-to-M mutations are dynamic tools to probe the physiological role of site-specific histone methylation in vitro and in vivo. <i>Nature Cell Biology</i> , 2019 , 21, 1449-1461	23.4	21
33	Dnmt1 has de novo activity targeted to transposable elements. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 594-603	17.6	21
32	Identification of distinct loci for de novo DNA methylation by DNMT3A and DNMT3B during mammalian development. <i>Nature Communications</i> , 2020 , 11, 3199	17.4	19
31	Chromatin-dependent allosteric regulation of DNMT3A activity by MeCP2. <i>Nucleic Acids Research</i> , 2018 , 46, 9044-9056	20.1	19
30	The simplest explanation: passive DNA demethylation in PGCs. <i>EMBO Journal</i> , 2013 , 32, 318-21	13	17
29	Targeted bisulfite sequencing of the dynamic DNA methylome. <i>Epigenetics and Chromatin</i> , 2016 , 9, 55	5.8	17
28	Epigenetic predisposition to reprogramming fates in somatic cells. <i>EMBO Reports</i> , 2015 , 16, 370-8	6.5	16
27	Targets and genomic constraints of ectopic Dnmt3b expression. <i>ELife</i> , 2018 , 7,	8.9	16
26	Netrin-1 promotes naive pluripotency through Neo1 and Unc5b co-regulation of Wnt and MAPK signalling. <i>Nature Cell Biology</i> , 2020 , 22, 389-400	23.4	13
25	In vivo Monitoring of Transcriptional Dynamics After Lower-Limb Muscle Injury Enables Quantitative Classification of Healing. <i>Scientific Reports</i> , 2015 , 5, 13885	4.9	13
24	In Vivo and in Vitro dynamics of undifferentiated embryonic cell transcription factor 1. <i>Stem Cell Reports</i> , 2014 , 2, 245-52	8	9
23	In vivo and deletion elucidates roles for autosomal gene regulation. <i>ELife</i> , 2019 , 8,	8.9	9
22	Mouse embryonic stem cells self-organize into trunk-like structures with neural tube and somites		8
21	Cell-specific transcriptional control of mitochondrial metabolism by TIF1 drives erythropoiesis. <i>Science</i> , 2021 , 372, 716-721	33.3	8

20	Comparative genomic analysis of embryonic, lineage-converted and stem cell-derived motor neurons. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	8
19	Guiding DNA methylation. <i>Cell Stem Cell</i> , 2011 , 9, 388-90	18	7
18	Smart-RRBS for single-cell methylome and transcriptome analysis. <i>Nature Protocols</i> , 2021 , 16, 4004-4030	8.8	7
17	Preneoplastic Alterations Define CLL DNA Methylome and Persist through Disease Progression and Therapy. <i>Blood Cancer Discovery</i> , 2021 , 2, 54-69	7	6
16	Loss of DNA methyltransferase activity in primed human ES cells triggers increased cell-cell variability and transcriptional repression. <i>Development (Cambridge)</i> , 2019 , 146,	6.6	5
15	Diverse epigenetic mechanisms maintain parental imprints within the embryonic and extraembryonic lineages. <i>Developmental Cell</i> , 2021 , 56, 2995-3005.e4	10.2	4
14	Chromatin-state barriers enforce an irreversible mammalian cell fate decision. <i>Cell Reports</i> , 2021 , 37, 109967	10.6	4
13	Systematic profiling of DNMT3A variants reveals protein instability mediated by the DCAF8 E3 ubiquitin ligase adaptor. <i>Cancer Discovery</i> , 2021 ,	24.4	4
12	Differential regulation of OCT4 targets facilitates reacquisition of pluripotency. <i>Nature Communications</i> , 2019 , 10, 4444	17.4	2
11	Nanotype: a modular and scalable nanopore data processing pipeline. <i>Bioinformatics</i> , 2019 , 35, 4770-4772	7.2	2
10	The CLL-1100 Project: Towards Complete Genomic Characterization and Improved Prognostics for CLL. <i>Blood</i> , 2020 , 136, 3-4	2.2	2
9	Integration of Hi-C and Nanopore Sequencing for Structural Variant Analysis in AML with a Complex Karyotype: (Chromothripsis) <i>Blood</i> , 2020 , 136, 28-28	2.2	2
8	Topological isolation of developmental regulators in mammalian genomes. <i>Nature Communications</i> , 2021 , 12, 4897	17.4	2
7	Emergence and patterning dynamics of mouse-definitive endoderm.. <i>IScience</i> , 2022 , 25, 103556	6.1	1
6	Activation of Notch and Myc signaling via B cell-restricted depletion of Dnmt3a generates a consistent murine model of chronic lymphocytic leukemia. <i>Cancer Research</i> , 2021 ,	10.1	1
5	Hypoxia induces a transcriptional early primitive streak signature in pluripotent cells enhancing spontaneous elongation and lineage representation in gastruloids		1
4	Generation of Mouse Pluripotent Stem Cell-derived Trunk-like Structures: An Model of Post-implantation Embryogenesis. <i>Bio-protocol</i> , 2021 , 11, e4042	0.9	1
3	Robust Discovery of Candidate DNA Methylation Cancer Drivers. <i>Blood</i> , 2020 , 136, 33-34	2.2	

- 2 B Cell-Restricted Depletion of Dnmt3a Activates Notch Signaling and Causes Chronic Lymphocytic Leukemia. *Blood*, **2021**, 138, 249-249 2.2
- 1 Deciphering the Role of Locally Disordered DNA Methylation on CLL Development In Vivo. *Blood*, **2019**, 134, 1737-1737 2.2