

Alexander Meissner

List of Publications by Year in descending order

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112
papers

31,838
citations

23567

58
h-index

24258

110
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123
all docs

123
docs citations

123
times ranked

44496
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic Profiling of <i>DNMT3A</i> Variants Reveals Protein Instability Mediated by the DCAF8 E3 Ubiquitin Ligase Adaptor. <i>Cancer Discovery</i> , 2022, 12, 220-235.	9.4	38
2	Emergence and patterning dynamics of mouse-definitive endoderm. <i>IScience</i> , 2022, 25, 103556.	4.1	9
3	DNA methylation: a historical perspective. <i>Trends in Genetics</i> , 2022, 38, 676-707.	6.7	176
4	Acute lymphoblastic leukemia displays a distinct highly methylated genome. <i>Nature Cancer</i> , 2022, 3, 768-782.	13.2	15
5	Single-cell technologies: a new lens into epigenetic regulation in development. <i>Current Opinion in Genetics and Development</i> , 2022, 76, 101947.	3.3	1
6	Preneoplastic Alterations Define CLL DNA Methylome and Persist through Disease Progression and Therapy. <i>Blood Cancer Discovery</i> , 2021, 2, 54-69.	5.0	16
7	Generation of Mouse Pluripotent Stem Cell-derived Trunk-like Structures: An in vitro Model of Post-implantation Embryogenesis. <i>Bio-protocol</i> , 2021, 11, e4042.	0.4	3
8	RLM: fast and simplified extraction of read-level methylation metrics from bisulfite sequencing data. <i>Bioinformatics</i> , 2021, 37, 3934-3935.	4.1	5
9	Cell-specific transcriptional control of mitochondrial metabolism by TIF1 ³ drives erythropoiesis. <i>Science</i> , 2021, 372, 716-721.	12.6	25
10	Dnmt1 has de novo activity targeted to transposable elements. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 594-603.	8.2	83
11	Smart-RRBS for single-cell methylome and transcriptome analysis. <i>Nature Protocols</i> , 2021, 16, 4004-4030.	12.0	34
12	Topological isolation of developmental regulators in mammalian genomes. <i>Nature Communications</i> , 2021, 12, 4897.	12.8	12
13	Activation of <i>Notch</i> and <i>Myc</i> Signaling via B-cell-Restricted Depletion of <i>Dnmt3a</i> Generates a Consistent Murine Model of Chronic Lymphocytic Leukemia. <i>Cancer Research</i> , 2021, 81, 6117-6130.	0.9	10
14	Diverse epigenetic mechanisms maintain parental imprints within the embryonic and extraembryonic lineages. <i>Developmental Cell</i> , 2021, 56, 2995-3005.e4.	7.0	33
15	Chromatin-state barriers enforce an irreversible mammalian cell fate decision. <i>Cell Reports</i> , 2021, 37, 109967.	6.4	28
16	B Cell-Restricted Depletion of Dnmt3a Activates Notch Signaling and Causes Chronic Lymphocytic Leukemia. <i>Blood</i> , 2021, 138, 249-249.	1.4	0
17	Circadian Entrainment Triggers Maturation of Human In Vitro Islets. <i>Cell Stem Cell</i> , 2020, 26, 108-122.e10.	11.1	127
18	Epigenetic regulator function through mouse gastrulation. <i>Nature</i> , 2020, 584, 102-108.	27.8	89

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19	The road ahead in genetics and genomics. <i>Nature Reviews Genetics</i> , 2020, 21, 581-596.	16.3	118
20	Mouse embryonic stem cells self-organize into trunk-like structures with neural tube and somites. <i>Science</i> , 2020, 370, .	12.6	193
21	Unblending of Transcriptional Condensates in Human Repeat Expansion Disease. <i>Cell</i> , 2020, 181, 1062-1079.e30.	28.9	115
22	TETs compete with DNMT3 activity in pluripotent cells at thousands of methylated somatic enhancers. <i>Nature Genetics</i> , 2020, 52, 819-827.	21.4	83
23	Netrin-1 promotes naive pluripotency through <i>Neo1</i> and <i>Unc5b</i> co-regulation of <i>Wnt</i> and <i>MAPK</i> signalling. <i>Nature Cell Biology</i> , 2020, 22, 389-400.	10.3	24
24	Differential DNA methylation of vocal and facial anatomy genes in modern humans. <i>Nature Communications</i> , 2020, 11, 1189.	12.8	69
25	Identification of distinct loci for de novo DNA methylation by DNMT3A and DNMT3B during mammalian development. <i>Nature Communications</i> , 2020, 11, 3199.	12.8	48
26	Integration of Hi-C and Nanopore Sequencing for Structural Variant Analysis in AML with a Complex Karyotype: (Chromothripsis) ^{A2} . <i>Blood</i> , 2020, 136, 28-28.	1.4	3
27	Robust Discovery of Candidate DNA Methylation Cancer Drivers. <i>Blood</i> , 2020, 136, 33-34.	1.4	0
28	The CLL-1100 Project: Towards Complete Genomic Characterization and Improved Prognostics for CLL. <i>Blood</i> , 2020, 136, 3-4.	1.4	2
29	Activation of neuronal genes via LINE-1 elements upon global DNA demethylation in human neural progenitors. <i>Nature Communications</i> , 2019, 10, 3182.	12.8	76
30	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.	10.3	40
31	Differential regulation of OCT4 targets facilitates reacquisition of pluripotency. <i>Nature Communications</i> , 2019, 10, 4444.	12.8	2
32	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. <i>Cell Stem Cell</i> , 2019, 25, 622-638.e13.	11.1	82
33	Nanopype: a modular and scalable nanopore data processing pipeline. <i>Bioinformatics</i> , 2019, 35, 4770-4772.	4.1	8
34	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019, 569, 576-580.	27.8	195
35	Molecular recording of mammalian embryogenesis. <i>Nature</i> , 2019, 570, 77-82.	27.8	257
36	Corrupted coordination of epigenetic modifications leads to diverging chromatin states and transcriptional heterogeneity in CLL. <i>Nature Communications</i> , 2019, 10, 1874.	12.8	63

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37	Cross-Regulation between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. <i>Molecular Cell</i> , 2019, 74, 951-965.e13.	9.7	85
38	Loss of DNA methyltransferase activity in primed human ES cells triggers increased cell-cell variability and transcriptional repression. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	9
39	Analysis of short tandem repeat expansions and their methylation state with nanopore sequencing. <i>Nature Biotechnology</i> , 2019, 37, 1478-1481.	17.5	117
40	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.	14.8	188
41	In vivo Firre and Dxz4 deletion elucidates roles for autosomal gene regulation. <i>ELife</i> , 2019, 8, .	6.0	18
42	Deciphering the Role of Locally Disordered DNA Methylation on CLL Development In Vivo. <i>Blood</i> , 2019, 134, 1737-1737.	1.4	0
43	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.	11.1	40
44	Cancer-Germline Antigen Expression Discriminates Clinical Outcome to CTLA-4 Blockade. <i>Cell</i> , 2018, 173, 624-633.e8.	28.9	113
45	Zika Virus Alters DNA Methylation of Neural Genes in an Organoid Model of the Developing Human Brain. <i>MSystems</i> , 2018, 3, .	3.8	53
46	Genome-wide tracking of dCas9-methyltransferase footprints. <i>Nature Communications</i> , 2018, 9, 597.	12.8	114
47	Genetic determinants and epigenetic effects of pioneer-factor occupancy. <i>Nature Genetics</i> , 2018, 50, 250-258.	21.4	139
48	X Chromosome Dosage Influences DNA Methylation Dynamics during Reprogramming to Mouse iPSCs. <i>Stem Cell Reports</i> , 2018, 10, 1537-1550.	4.8	39
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.	11.1	53
50	Global delay in nascent strand DNA methylation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 327-332.	8.2	56
51	KDM5 Histone Demethylase Activity Links Cellular Transcriptomic Heterogeneity to Therapeutic Resistance. <i>Cancer Cell</i> , 2018, 34, 939-953.e9.	16.8	170
52	Comparative genomic analysis of embryonic, lineage-converted, and stem cell-derived motor neurons. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	10
53	Aligning Single-Cell Developmental and Reprogramming Trajectories Identifies Molecular Determinants of Myogenic Reprogramming Outcome. <i>Cell Systems</i> , 2018, 7, 258-268.e3.	6.2	65
54	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.	11.1	47

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55	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. <i>Cell Stem Cell</i> , 2018, 23, 289-305.e5.	11.1	60
56	Reduced MEK inhibition preserves genomic stability in naive human embryonic stem cells. <i>Nature Methods</i> , 2018, 15, 732-740.	19.0	74
57	Chromatin-dependent allosteric regulation of DNMT3A activity by MeCP2. <i>Nucleic Acids Research</i> , 2018, 46, 9044-9056.	14.5	34
58	Targets and genomic constraints of ectopic Dnmt3b expression. <i>ELife</i> , 2018, 7, .	6.0	26
59	Induced Pluripotent Stem Cell Differentiation Enables Functional Validation of GWAS Variants in Metabolic Disease. <i>Cell Stem Cell</i> , 2017, 20, 547-557.e7.	11.1	129
60	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 706-719.e7.	11.1	63
61	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. <i>Nature</i> , 2017, 549, 543-547.	27.8	146
62	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. <i>Nature</i> , 2017, 548, 219-223.	27.8	211
63	Targeted bisulfite sequencing of the dynamic DNA methylome. <i>Epigenetics and Chromatin</i> , 2016, 9, 55.	3.9	18
64	Epigenetic Memory Underlies Cell-Autonomous Heterogeneous Behavior of Hematopoietic Stem Cells. <i>Cell</i> , 2016, 167, 1310-1322.e17.	28.9	153
65	Transcriptional and Chromatin Dynamics of Muscle Regeneration after Severe Trauma. <i>Stem Cell Reports</i> , 2016, 7, 983-997.	4.8	41
66	Molecular features of cellular reprogramming and development. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 139-154.	37.0	136
67	In vivo Monitoring of Transcriptional Dynamics After Lower-Limb Muscle Injury Enables Quantitative Classification of Healing. <i>Scientific Reports</i> , 2015, 5, 13885.	3.3	21
68	Genetic and Epigenetic Variation, but Not Diet, Shape the Sperm Methylome. <i>Developmental Cell</i> , 2015, 35, 750-758.	7.0	130
69	Age- and Pregnancy-Associated DNA Methylation Changes in Mammary Epithelial Cells. <i>Stem Cell Reports</i> , 2015, 4, 297-311.	4.8	45
70	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, 217-223.	3.3	30
71	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
72	Transcription factor binding dynamics during human ES cell differentiation. <i>Nature</i> , 2015, 518, 344-349.	27.8	318

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73	(Epi)Genomics approaches and their applications. <i>Methods</i> , 2015, 72, 1-2.	3.8	2
74	Epigenetic predisposition to reprogramming fates in somatic cells. <i>EMBO Reports</i> , 2015, 16, 370-378.	4.5	21
75	Ground State Conditions Induce Rapid Reorganization of Core Pluripotency Factor Binding before Global Epigenetic Reprogramming. <i>Cell Stem Cell</i> , 2015, 17, 462-470.	11.1	104
76	Integrative Analyses of Human Reprogramming Reveal Dynamic Nature of Induced Pluripotency. <i>Cell</i> , 2015, 162, 412-424.	28.9	206
77	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. <i>Nature Genetics</i> , 2015, 47, 469-478.	21.4	409
78	Analysing human neural stem cell ontogeny by consecutive isolation of Notch active neural progenitors. <i>Nature Communications</i> , 2015, 6, 6500.	12.8	73
79	A qPCR ScoreCard quantifies the differentiation potential of human pluripotent stem cells. <i>Nature Biotechnology</i> , 2015, 33, 1182-1192.	17.5	138
80	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, 1456-1470.	6.4	64
81	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.	2.8	34
82	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , 2015, 518, 355-359.	27.8	172
83	Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. <i>Nature Methods</i> , 2015, 12, 230-232.	19.0	248
84	DNA methylation signatures link prenatal famine exposure to growth and metabolism. <i>Nature Communications</i> , 2014, 5, 5592.	12.8	494
85	X Chromosome Reactivation Dynamics Reveal Stages of Reprogramming to Pluripotency. <i>Cell</i> , 2014, 159, 1681-1697.	28.9	97
86	Locally Disordered Methylation Forms the Basis of Intratumor Methylome Variation in Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2014, 26, 813-825.	16.8	323
87	The use of small molecules in somatic-cell reprogramming. <i>Trends in Cell Biology</i> , 2014, 24, 179-187.	7.9	60
88	Long-term persistence and development of induced pancreatic beta cells generated by lineage conversion of acinar cells. <i>Nature Biotechnology</i> , 2014, 32, 1223-1230.	17.5	89
89	DNA methylation dynamics of the human preimplantation embryo. <i>Nature</i> , 2014, 511, 611-615.	27.8	488
90	InÂVivo and InÂVitro Dynamics of Undifferentiated Embryonic Cell Transcription Factor 1. <i>Stem Cell Reports</i> , 2014, 2, 245-252.	4.8	13

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91	Proto-Oncogenic Role of Mutant IDH2 in Leukemia Initiation and Maintenance. <i>Cell Stem Cell</i> , 2014, 14, 329-341.	11.1	172
92	Notch inhibition allows oncogene-independent generation of iPS cells. <i>Nature Chemical Biology</i> , 2014, 10, 632-639.	8.0	64
93	Charting a dynamic DNA methylation landscape of the human genome. <i>Nature</i> , 2013, 500, 477-481.	27.8	1,168
94	DNA methylation: roles in mammalian development. <i>Nature Reviews Genetics</i> , 2013, 14, 204-220.	16.3	2,541
95	Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1149-1163.	28.9	419
96	The simplest explanation: passive DNA demethylation in PGCs. <i>EMBO Journal</i> , 2013, 32, 318-321.	7.8	18
97	In Vivo Control of CpG and Non-CpG DNA Methylation by DNA Methyltransferases. <i>PLoS Genetics</i> , 2012, 8, e1002750.	3.5	337
98	Gel-free multiplexed reduced representation bisulfite sequencing for large-scale DNA methylation profiling. <i>Genome Biology</i> , 2012, 13, R92.	9.6	244
99	DNA Methylation Dynamics during In Vivo Differentiation of Blood and Skin Stem Cells. <i>Molecular Cell</i> , 2012, 47, 633-647.	9.7	338
100	A unique regulatory phase of DNA methylation in the early mammalian embryo. <i>Nature</i> , 2012, 484, 339-344.	27.8	860
101	Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. <i>Genome Research</i> , 2012, 22, 1128-1138.	5.5	344
102	Dnmt3a is essential for hematopoietic stem cell differentiation. <i>Nature Genetics</i> , 2012, 44, 23-31.	21.4	916
103	Reference Maps of Human ES and iPS Cell Variation Enable High-Throughput Characterization of Pluripotent Cell Lines. <i>Cell</i> , 2011, 144, 439-452.	28.9	899
104	Reprogramming Factor Expression Initiates Widespread Targeted Chromatin Remodeling. <i>Cell Stem Cell</i> , 2011, 8, 96-105.	11.1	345
105	Guiding DNA Methylation. <i>Cell Stem Cell</i> , 2011, 9, 388-390.	11.1	8
106	Preparation of reduced representation bisulfite sequencing libraries for genome-scale DNA methylation profiling. <i>Nature Protocols</i> , 2011, 6, 468-481.	12.0	667
107	Epigenetic modifications in pluripotent and differentiated cells. <i>Nature Biotechnology</i> , 2010, 28, 1079-1088.	17.5	331
108	Derivation and Manipulation of Murine Embryonic Stem Cells. <i>Methods in Molecular Biology</i> , 2009, 482, 3-19.	0.9	26

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109	Dissecting direct reprogramming through integrative genomic analysis. Nature, 2008, 454, 49-55.	27.8	1,344
110	Genome-scale DNA methylation maps of pluripotent and differentiated cells. Nature, 2008, 454, 766-770.	27.8	2,267
111	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. Nature, 2007, 448, 553-560.	27.8	3,733
112	Reduced representation bisulfite sequencing for comparative high-resolution DNA methylation analysis. Nucleic Acids Research, 2005, 33, 5868-5877.	14.5	1,050