

# Alexander Meissner

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/1747404/alexander-meissner-publications-by-year.pdf>

**Version:** 2024-04-19

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Emergence and patterning dynamics of mouse-definitive endoderm.. <i>IScience</i> , <b>2022</b> , 25, 103556	6.1	1
108	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> , <b>2021</b> ,	10.1	1
107	Diverse epigenetic mechanisms maintain parental imprints within the embryonic and extraembryonic lineages. <i>Developmental Cell</i> , <b>2021</b> , 56, 2995-3005.e4	10.2	4
106	Chromatin-state barriers enforce an irreversible mammalian cell fate decision. <i>Cell Reports</i> , <b>2021</b> , 37, 109967	10.6	4
105	B Cell-Restricted Depletion of Dnmt3a Activates Notch Signaling and Causes Chronic Lymphocytic Leukemia. <i>Blood</i> , <b>2021</b> , 138, 249-249	2.2	
104	Cell-specific transcriptional control of mitochondrial metabolism by TIF1 $\beta$ drives erythropoiesis. <i>Science</i> , <b>2021</b> , 372, 716-721	33.3	8
103	Dnmt1 has de novo activity targeted to transposable elements. <i>Nature Structural and Molecular Biology</i> , <b>2021</b> , 28, 594-603	17.6	21
102	Preneoplastic Alterations Define CLL DNA Methylome and Persist through Disease Progression and Therapy. <i>Blood Cancer Discovery</i> , <b>2021</b> , 2, 54-69	7	6
101	Generation of Mouse Pluripotent Stem Cell-derived Trunk-like Structures: An Model of Post-implantation Embryogenesis. <i>Bio-protocol</i> , <b>2021</b> , 11, e4042	0.9	1
100	Smart-RRBS for single-cell methylome and transcriptome analysis. <i>Nature Protocols</i> , <b>2021</b> , 16, 4004-4030	18.8	7
99	Topological isolation of developmental regulators in mammalian genomes. <i>Nature Communications</i> , <b>2021</b> , 12, 4897	17.4	2
98	Systematic profiling of DNMT3A variants reveals protein instability mediated by the DCAF8 E3 ubiquitin ligase adaptor. <i>Cancer Discovery</i> , <b>2021</b> ,	24.4	4
97	Mouse embryonic stem cells self-organize into trunk-like structures with neural tube and somites. <i>Science</i> , <b>2020</b> , 370,	33.3	61
96	Unblending of Transcriptional Condensates in Human Repeat Expansion Disease. <i>Cell</i> , <b>2020</b> , 181, 1062-1072.e308	36.2	38
95	TETs compete with DNMT3 activity in pluripotent cells at thousands of methylated somatic enhancers. <i>Nature Genetics</i> , <b>2020</b> , 52, 819-827	36.3	36
94	Netrin-1 promotes naive pluripotency through Neo1 and Unc5b co-regulation of Wnt and MAPK signalling. <i>Nature Cell Biology</i> , <b>2020</b> , 22, 389-400	23.4	13
93	Differential DNA methylation of vocal and facial anatomy genes in modern humans. <i>Nature Communications</i> , <b>2020</b> , 11, 1189	17.4	27

92	Identification of distinct loci for de novo DNA methylation by DNMT3A and DNMT3B during mammalian development. <i>Nature Communications</i> , <b>2020</b> , 11, 3199	17.4	19
91	Robust Discovery of Candidate DNA Methylation Cancer Drivers. <i>Blood</i> , <b>2020</b> , 136, 33-34	2.2	
90	The CLL-1100 Project: Towards Complete Genomic Characterization and Improved Prognostics for CLL. <i>Blood</i> , <b>2020</b> , 136, 3-4	2.2	2
89	Integration of Hi-C and Nanopore Sequencing for Structural Variant Analysis in AML with a Complex Karyotype: (Chromothripsis) <i>Blood</i> , <b>2020</b> , 136, 28-28	2.2	2
88	Circadian Entrainment Triggers Maturation of Human In Vitro Islets. <i>Cell Stem Cell</i> , <b>2020</b> , 26, 108-122.e108	10.8	57
87	Epigenetic regulator function through mouse gastrulation. <i>Nature</i> , <b>2020</b> , 584, 102-108	50.4	30
86	The road ahead in genetics and genomics. <i>Nature Reviews Genetics</i> , <b>2020</b> , 21, 581-596	30.1	43
85	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> , <b>2019</b> , 21, 1449-1461	23.4	21
84	Differential regulation of OCT4 targets facilitates reacquisition of pluripotency. <i>Nature Communications</i> , <b>2019</b> , 10, 4444	17.4	2
83	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. <i>Cell Stem Cell</i> , <b>2019</b> , 25, 622-638.e13	18	35
82	Nanotype: a modular and scalable nanopore data processing pipeline. <i>Bioinformatics</i> , <b>2019</b> , 35, 4770-4772	2	
81	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , <b>2019</b> , 569, 576-580	50.4	104
80	Molecular recording of mammalian embryogenesis. <i>Nature</i> , <b>2019</b> , 570, 77-82	50.4	140
79	Corrupted coordination of epigenetic modifications leads to diverging chromatin states and transcriptional heterogeneity in CLL. <i>Nature Communications</i> , <b>2019</b> , 10, 1874	17.4	38
78	Cross-Regulation between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. <i>Molecular Cell</i> , <b>2019</b> , 74, 951-965.e13	17.6	45
77	Activation of neuronal genes via LINE-1 elements upon global DNA demethylation in human neural progenitors. <i>Nature Communications</i> , <b>2019</b> , 10, 3182	17.4	36
76	In vivo and deletion elucidates roles for autosomal gene regulation. <i>ELife</i> , <b>2019</b> , 8,	8.9	9
75	Deciphering the Role of Locally Disordered DNA Methylation on CLL Development In Vivo. <i>Blood</i> , <b>2019</b> , 134, 1737-1737	2.2	

74	Loss of DNA methyltransferase activity in primed human ES cells triggers increased cell-cell variability and transcriptional repression. <i>Development (Cambridge)</i> , <b>2019</b> , 146,	6.6	5
73	Analysis of short tandem repeat expansions and their methylation state with nanopore sequencing. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 1478-1481	44.5	57
72	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> , <b>2019</b> , 22, 37-46	25.5	99
71	A CLK3-HMGA2 Alternative Splicing Axis Impacts Human Hematopoietic Stem Cell Molecular Identity throughout Development. <i>Cell Stem Cell</i> , <b>2018</b> , 22, 575-588.e7	18	24
70	Cancer-Germline Antigen Expression Discriminates Clinical Outcome to CTLA-4 Blockade. <i>Cell</i> , <b>2018</b> , 173, 624-633.e8	56.2	71
69	Zika Virus Alters DNA Methylation of Neural Genes in an Organoid Model of the Developing Human Brain. <i>MSystems</i> , <b>2018</b> , 3,	7.6	37
68	Genome-wide tracking of dCas9-methyltransferase footprints. <i>Nature Communications</i> , <b>2018</b> , 9, 597	17.4	85
67	Genetic determinants and epigenetic effects of pioneer-factor occupancy. <i>Nature Genetics</i> , <b>2018</b> , 50, 250-258	36.3	85
66	X Chromosome Dosage Influences DNA Methylation Dynamics during Reprogramming to Mouse iPSCs. <i>Stem Cell Reports</i> , <b>2018</b> , 10, 1537-1550	8	24
65	Dissecting the Functional Consequences of De Novo DNA Methylation Dynamics in Human Motor Neuron Differentiation and Physiology. <i>Cell Stem Cell</i> , <b>2018</b> , 22, 559-574.e9	18	36
64	Global delay in nascent strand DNA methylation. <i>Nature Structural and Molecular Biology</i> , <b>2018</b> , 25, 327-332	32.6	32
63	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. <i>Cell Stem Cell</i> , <b>2018</b> , 23, 289-305.e5	18	34
62	Reduced MEK inhibition preserves genomic stability in naive human embryonic stem cells. <i>Nature Methods</i> , <b>2018</b> , 15, 732-740	21.6	44
61	Chromatin-dependent allosteric regulation of DNMT3A activity by MeCP2. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 9044-9056	20.1	19
60	Targets and genomic constraints of ectopic Dnmt3b expression. <i>ELife</i> , <b>2018</b> , 7,	8.9	16
59	KDM5 Histone Demethylase Activity Links Cellular Transcriptomic Heterogeneity to Therapeutic Resistance. <i>Cancer Cell</i> , <b>2018</b> , 34, 939-953.e9	24.3	93
58	Comparative genomic analysis of embryonic, lineage-converted and stem cell-derived motor neurons. <i>Development (Cambridge)</i> , <b>2018</b> , 145,	6.6	8
57	Aligning Single-Cell Developmental and Reprogramming Trajectories Identifies Molecular Determinants of Myogenic Reprogramming Outcome. <i>Cell Systems</i> , <b>2018</b> , 7, 258-268.e3	10.6	40

56	An Intermediate Pluripotent State Controlled by MicroRNAs Is Required for the Naive-to-Primed Stem Cell Transition. <i>Cell Stem Cell</i> , <b>2018</b> , 22, 851-864.e5	18	31
55	Induced Pluripotent Stem Cell Differentiation Enables Functional Validation of GWAS Variants in Metabolic Disease. <i>Cell Stem Cell</i> , <b>2017</b> , 20, 547-557.e7	18	86
54	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. <i>Cell Stem Cell</i> , <b>2017</b> , 20, 706-719.e7	18	43
53	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. <i>Nature</i> , <b>2017</b> , 548, 219-223	50.4	135
52	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. <i>Nature</i> , <b>2017</b> , 549, 543-547	50.4	86
51	Epigenetic Memory Underlies Cell-Autonomous Heterogeneous Behavior of Hematopoietic Stem Cells. <i>Cell</i> , <b>2016</b> , 167, 1310-1322.e17	56.2	124
50	Transcriptional and Chromatin Dynamics of Muscle Regeneration after Severe Trauma. <i>Stem Cell Reports</i> , <b>2016</b> , 7, 983-997	8	26
49	Molecular features of cellular reprogramming and development. <i>Nature Reviews Molecular Cell Biology</i> , <b>2016</b> , 17, 139-54	48.7	109
48	Targeted bisulfite sequencing of the dynamic DNA methylome. <i>Epigenetics and Chromatin</i> , <b>2016</b> , 9, 55	5.8	17
47	Ground State Conditions Induce Rapid Reorganization of Core Pluripotency Factor Binding before Global Epigenetic Reprogramming. <i>Cell Stem Cell</i> , <b>2015</b> , 17, 462-70	18	78
46	Integrative Analyses of Human Reprogramming Reveal Dynamic Nature of Induced Pluripotency. <i>Cell</i> , <b>2015</b> , 162, 412-424	56.2	148
45	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. <i>Nature Genetics</i> , <b>2015</b> , 47, 469-78	36.3	288
44	Analysing human neural stem cell ontogeny by consecutive isolation of Notch active neural progenitors. <i>Nature Communications</i> , <b>2015</b> , 6, 6500	17.4	51
43	A qPCR ScoreCard quantifies the differentiation potential of human pluripotent stem cells. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 1182-92	44.5	97
42	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> , <b>2015</b> , 12, 1456-70	10.6	46
41	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> , <b>2015</b> , 67, 58-64	5.6	27
40	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , <b>2015</b> , 518, 355-359	50.4	140
39	Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. <i>Nature Methods</i> , <b>2015</b> , 12, 230-2, 1 p following 232	21.6	171

38	In vivo Monitoring of Transcriptional Dynamics After Lower-Limb Muscle Injury Enables Quantitative Classification of Healing. <i>Scientific Reports</i> , <b>2015</b> , 5, 13885	4.9	13
37	Genetic and Epigenetic Variation, but Not Diet, Shape the Sperm Methylome. <i>Developmental Cell</i> , <b>2015</b> , 35, 750-8	10.2	102
36	Age- and pregnancy-associated DNA methylation changes in mammary epithelial cells. <i>Stem Cell Reports</i> , <b>2015</b> , 4, 297-311	8	35
35	Enabling consistency in pluripotent stem cell-derived products for research and development and clinical applications through material standards. <i>Stem Cells Translational Medicine</i> , <b>2015</b> , 4, 217-23	6.9	29
34	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , <b>2015</b> , 518, 317-30	50.4	3849
33	Transcription factor binding dynamics during human ES cell differentiation. <i>Nature</i> , <b>2015</b> , 518, 344-9	50.4	232
32	Epigenetic predisposition to reprogramming fates in somatic cells. <i>EMBO Reports</i> , <b>2015</b> , 16, 370-8	6.5	16
31	The use of small molecules in somatic-cell reprogramming. <i>Trends in Cell Biology</i> , <b>2014</b> , 24, 179-87	18.3	46
30	Long-term persistence and development of induced pancreatic beta cells generated by lineage conversion of acinar cells. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 1223-30	44.5	71
29	DNA methylation dynamics of the human preimplantation embryo. <i>Nature</i> , <b>2014</b> , 511, 611-5	50.4	390
28	In Vivo and In Vitro dynamics of undifferentiated embryonic cell transcription factor 1. <i>Stem Cell Reports</i> , <b>2014</b> , 2, 245-52	8	9
27	Proto-oncogenic role of mutant IDH2 in leukemia initiation and maintenance. <i>Cell Stem Cell</i> , <b>2014</b> , 14, 329-41	18	141
26	Notch inhibition allows oncogene-independent generation of iPS cells. <i>Nature Chemical Biology</i> , <b>2014</b> , 10, 632-639	11.7	48
25	DNA methylation signatures link prenatal famine exposure to growth and metabolism. <i>Nature Communications</i> , <b>2014</b> , 5, 5592	17.4	368
24	X chromosome reactivation dynamics reveal stages of reprogramming to pluripotency. <i>Cell</i> , <b>2014</b> , 159, 1681-97	56.2	77
23	Locally disordered methylation forms the basis of intratumor methylome variation in chronic lymphocytic leukemia. <i>Cancer Cell</i> , <b>2014</b> , 26, 813-825	24.3	216
22	Charting a dynamic DNA methylation landscape of the human genome. <i>Nature</i> , <b>2013</b> , 500, 477-81	50.4	932
21	DNA methylation: roles in mammalian development. <i>Nature Reviews Genetics</i> , <b>2013</b> , 14, 204-20	30.1	1935

20	Transcriptional and epigenetic dynamics during specification of human embryonic stem cells. <i>Cell</i> , <b>2013</b> , 153, 1149-63	56.2	332
19	The simplest explanation: passive DNA demethylation in PGCs. <i>EMBO Journal</i> , <b>2013</b> , 32, 318-21	13	17
18	Gel-free multiplexed reduced representation bisulfite sequencing for large-scale DNA methylation profiling. <i>Genome Biology</i> , <b>2012</b> , 13, R92	18.3	183
17	DNA methylation dynamics during in vivo differentiation of blood and skin stem cells. <i>Molecular Cell</i> , <b>2012</b> , 47, 633-47	17.6	271
16	A unique regulatory phase of DNA methylation in the early mammalian embryo. <i>Nature</i> , <b>2012</b> , 484, 339-44	50.4	723
15	Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. <i>Genome Research</i> , <b>2012</b> , 22, 1128-38	9.7	277
14	In vivo control of CpG and non-CpG DNA methylation by DNA methyltransferases. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002750	6	279
13	Dnmt3a is essential for hematopoietic stem cell differentiation. <i>Nature Genetics</i> , <b>2011</b> , 44, 23-31	36.3	737
12	Reference Maps of human ES and iPS cell variation enable high-throughput characterization of pluripotent cell lines. <i>Cell</i> , <b>2011</b> , 144, 439-52	56.2	756
11	Reprogramming factor expression initiates widespread targeted chromatin remodeling. <i>Cell Stem Cell</i> , <b>2011</b> , 8, 96-105	18	295
10	Guiding DNA methylation. <i>Cell Stem Cell</i> , <b>2011</b> , 9, 388-90	18	7
9	Preparation of reduced representation bisulfite sequencing libraries for genome-scale DNA methylation profiling. <i>Nature Protocols</i> , <b>2011</b> , 6, 468-81	18.8	505
8	Epigenetic modifications in pluripotent and differentiated cells. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 1079-88	44.5	302
7	Derivation and manipulation of murine embryonic stem cells. <i>Methods in Molecular Biology</i> , <b>2009</b> , 482, 3-19	1.4	22
6	Dissecting direct reprogramming through integrative genomic analysis. <i>Nature</i> , <b>2008</b> , 454, 49-55	50.4	1205
5	Genome-scale DNA methylation maps of pluripotent and differentiated cells. <i>Nature</i> , <b>2008</b> , 454, 766-70	50.4	1999
4	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. <i>Nature</i> , <b>2007</b> , 448, 553-60	50.4	3296
3	Reduced representation bisulfite sequencing for comparative high-resolution DNA methylation analysis. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 5868-77	20.1	823

- 2 Mouse embryonic stem cells self-organize into trunk-like structures with neural tube and somites 8
- 1 Hypoxia induces a transcriptional early primitive streak signature in pluripotent cells enhancing spontaneous elongation and lineage representation in gastruloids 1