

Matthew C Lorincz

List of Publications by Year in descending order

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62
papers

6,888
citations

87888

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h-index

110387

64
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71
all docs

71
docs citations

71
times ranked

9061
citing authors

#	ARTICLE	IF	CITATIONS
1	Vitamin C induces Tet-dependent DNA demethylation and a blastocyst-like state in ES cells. <i>Nature</i> , 2013, 500, 222-226.	27.8	715
2	Proviral silencing in embryonic stem cells requires the histone methyltransferase ESET. <i>Nature</i> , 2010, 464, 927-931.	27.8	681
3	Intragenic DNA methylation alters chromatin structure and elongation efficiency in mammalian cells. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 1068-1075.	8.2	443
4	DNA Methylation and SETDB1/H3K9me3 Regulate Predominantly Distinct Sets of Genes, Retroelements, and Chimeric Transcripts in mESCs. <i>Cell Stem Cell</i> , 2011, 8, 676-687.	11.1	427
5	Primate-specific endogenous retrovirus-driven transcription defines naive-like stem cells. <i>Nature</i> , 2014, 516, 405-409.	27.8	372
6	An ultra-low-input native ChIP-seq protocol for genome-wide profiling of rare cell populations. <i>Nature Communications</i> , 2015, 6, 6033.	12.8	322
7	<i>Setdb1</i> is required for germline development and silencing of H3K9me3-marked endogenous retroviruses in primordial germ cells. <i>Genes and Development</i> , 2014, 28, 2041-2055.	5.9	228
8	Long Terminal Repeats: From Parasitic Elements to Building Blocks of the Transcriptional Regulatory Repertoire. <i>Molecular Cell</i> , 2016, 62, 766-776.	9.7	219
9	DNA methylation in ES cells requires the lysine methyltransferase G9a but not its catalytic activity. <i>EMBO Journal</i> , 2008, 27, 2691-2701.	7.8	207
10	SETD2 regulates the maternal epigenome, genomic imprinting and embryonic development. <i>Nature Genetics</i> , 2019, 51, 844-856.	21.4	207
11	Systematic Identification of Factors for Provirus Silencing in Embryonic Stem Cells. <i>Cell</i> , 2015, 163, 230-245.	28.9	162
12	Distinct roles of KAP1, HP1 and G9a/GLP in silencing of the two-cell-specific retrotransposon MERVL in mouse ES cells. <i>Epigenetics and Chromatin</i> , 2013, 6, 15.	3.9	153
13	Genomic Targeting of Methylated DNA: Influence of Methylation on Transcription, Replication, Chromatin Structure, and Histone Acetylation. <i>Molecular and Cellular Biology</i> , 2000, 20, 9103-9112.	2.3	147
14	Retrotransposon-Induced Heterochromatin Spreading in the Mouse Revealed by Insertional Polymorphisms. <i>PLoS Genetics</i> , 2011, 7, e1002301.	3.5	129
15	Dynamic Analysis of Proviral Induction and De Novo Methylation: Implications for a Histone Deacetylase-Independent, Methylation Density-Dependent Mechanism of Transcriptional Repression. <i>Molecular and Cellular Biology</i> , 2000, 20, 842-850.	2.3	124
16	DNA Methylation Density Influences the Stability of an Epigenetic Imprint and Dnmt3a/b-Independent De Novo Methylation. <i>Molecular and Cellular Biology</i> , 2002, 22, 7572-7580.	2.3	120
17	Dynamic and flexible H3K9me3 bridging via HP1 ¹² dimerization establishes a plastic state of condensed chromatin. <i>Nature Communications</i> , 2016, 7, 11310.	12.8	115
18	Silencing of endogenous retroviruses: when and why do histone marks predominate?. <i>Trends in Biochemical Sciences</i> , 2012, 37, 127-133.	7.5	112

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19	Simultaneous fluorescence-activated cell sorter analysis of two distinct transcriptional elements within a single cell using engineered green fluorescent proteins.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 8508-8511.	7.1	105
20	Lysine methyltransferase G9a is required for de novo DNA methylation and the establishment, but not the maintenance, of proviral silencing. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5718-5723.	7.1	105
21	Methylation-Mediated Proviral Silencing Is Associated with MeCP2 Recruitment and Localized Histone H3 Deacetylation. Molecular and Cellular Biology, 2001, 21, 7913-7922.	2.3	97
22	NSD1-deposited H3K36me2 directs de novo methylation in the mouse male germline and counteracts Polycomb-associated silencing. Nature Genetics, 2020, 52, 1088-1098.	21.4	96
23	Regulation of DNA methylation turnover at LTR retrotransposons and imprinted loci by the histone methyltransferase Setdb1. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6690-6695.	7.1	89
24	Transcription shapes genome-wide histone acetylation patterns. Nature Communications, 2021, 12, 210.	12.8	84
25	Vertebrate diapause preserves organisms long term through Polycomb complex members. Science, 2020, 367, 870-874.	12.6	79
26	Activation of Endogenous Retroviruses in Dnmt1 $\alpha^{\prime}/\alpha^{\prime\prime}$ ESCs Involves Disruption of SETDB1-Mediated Repression by NP95 Binding to Hemimethylated DNA. Cell Stem Cell, 2016, 19, 81-94.	11.1	77
27	Targeting of EZH2 to a defined genomic site is sufficient for recruitment of Dnmt3a but not de novo DNA methylation. Epigenetics, 2009, 4, 404-414.	2.7	74
28	Position Effects Are Influenced by the Orientation of a Transgene with Respect to Flanking Chromatin. Molecular and Cellular Biology, 2001, 21, 298-309.	2.3	73
29	Dynamics, stability and inheritance of somatic DNA methylation imprints. Journal of Theoretical Biology, 2006, 242, 890-899.	1.7	73
30	Histone H3 lysine 4 trimethylation in sperm is transmitted to the embryo and associated with diet-induced phenotypes in the offspring. Developmental Cell, 2021, 56, 671-686.e6.	7.0	70
31	VisRseq: R-based visual framework for analysis of sequencing data. BMC Bioinformatics, 2015, 16, S2.	2.6	66
32	LTR retrotransposons transcribed in oocytes drive species-specific and heritable changes in DNA methylation. Nature Communications, 2018, 9, 3331.	12.8	65
33	Interplay between chromatin marks in development and disease. Nature Reviews Genetics, 2022, 23, 137-153.	16.3	65
34	hnRNP K Coordinates Transcriptional Silencing by SETDB1 in Embryonic Stem Cells. PLoS Genetics, 2015, 11, e1004933.	3.5	64
35	Histone H3K9 Methyltransferase G9a in Oocytes Is Essential for Preimplantation Development but Dispensable for CG Methylation Protection. Cell Reports, 2019, 27, 282-293.e4.	6.4	62
36	An Unmethylated $3\text{a}\epsilon^2$ Promoter-Proximal Region Is Required for Efficient Transcription Initiation. PLoS Genetics, 2007, 3, e27.	3.5	59

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37	Histone H3K4 demethylation is negatively regulated by histone H3 acetylation in <i>Saccharomyces cerevisiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18505-18510.	7.1	52
38	H3K9me3-binding proteins are dispensable for SETDB1/H3K9me3-dependent retroviral silencing. Epigenetics and Chromatin, 2011, 4, 12.	3.9	43
39	H3S10ph broadly marks early-replicating domains in interphase ESCs and shows reciprocal antagonism with H3K9me2. Genome Research, 2018, 28, 37-51.	5.5	43
40	ZFP57 regulation of transposable elements and gene expression within and beyond imprinted domains. Epigenetics and Chromatin, 2019, 12, 49.	3.9	42
41	Detection and Isolation of Gene-Corrected Cells in Gaucher Disease Via a Fluorescence-Activated Cell Sorter Assay for Lysosomal Glucocerebrosidase Activity. Blood, 1997, 89, 3412-3420.	1.4	40
42	Evolution of imprinting via lineage-specific insertion of retroviral promoters. Nature Communications, 2019, 10, 5674.	12.8	39
43	Development and application of an integrated allele-specific pipeline for methylomic and epigenomic analysis (MEA). BMC Genomics, 2018, 19, 463.	2.8	38
44	CmC(a/t)GG methylation: A new epigenetic mark in mammalian DNA?. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 10034-10036.	7.1	37
45	ChAsE: chromatin analysis and exploration tool. Bioinformatics, 2016, 32, 3324-3326.	4.1	32
46	Evidence for Converging DNA Methylation Pathways in Placenta and Cancer. Developmental Cell, 2017, 43, 257-258.	7.0	26
47	Repression of germline genes by PRC1.6 and SETDB1 in the early embryo precedes DNA methylation-mediated silencing. Nature Communications, 2021, 12, 7020.	12.8	26
48	Kinetics and Epigenetics of Retroviral Silencing in Mouse Embryonic Stem Cells Defined by Deletion of the D4Z4 Element. Molecular Therapy, 2013, 21, 1536-1550.	8.2	21
49	Enzyme-generated intracellular fluorescence for single-cell reporter gene analysis utilizing <i>Escherichia coli</i> β -glucuronidase. Cytometry, 1996, 24, 321-329.	1.8	20
50	On the role of H3.3 in retroviral silencing. Nature, 2017, 548, E1-E3.	27.8	19
51	ALEA: a toolbox for allele-specific epigenomics analysis. Bioinformatics, 2014, 30, 1172-1174.	4.1	18
52	H2A.Z and DNA methylation: irreconcilable differences. Trends in Biochemical Sciences, 2009, 34, 158-161.	7.5	16
53	Single Cell Analysis and Selection of Living Retrovirus Vector-corrected Mucopolysaccharidosis VII Cells Using a Fluorescence-activated Cell Sorting-based Assay for Mammalian β -Glucuronidase Enzymatic Activity. Journal of Biological Chemistry, 1999, 274, 657-665.	3.4	15
54	Paternal MTHFR deficiency leads to hypomethylation of young retrotransposons and reproductive decline across two successive generations. Development (Cambridge), 2021, 148, .	2.5	15

#	ARTICLE	IF	CITATIONS
55	RNA Polymerase II: Just Stopping By. <i>Cell</i> , 2007, 130, 16-18.	28.9	12
56	Maternal DNMT3A-dependent de novo methylation of the paternal genome inhibits gene expression in the early embryo. <i>Nature Communications</i> , 2020, 11, 5417.	12.8	12
57	An Interactive Analysis and Exploration Tool for Epigenomic Data. <i>Computer Graphics Forum</i> , 2013, 32, 91-100.	3.0	9
58	Inter-Strain Epigenomic Profiling Reveals a Candidate IAP Master Copy in C3H Mice. <i>Viruses</i> , 2020, 12, 783.	3.3	9
59	Epigenetic modifier drugs trigger widespread transcription of endogenous retroviruses. <i>Nature Genetics</i> , 2017, 49, 974-975.	21.4	7
60	Genome-wide mapping of chromatin marks from 1,000 cells to study epigenetic reprogramming in primordial germ cells. <i>Epigenetics and Chromatin</i> , 2013, 6, .	3.9	1
61	HP1 proteins safeguard embryonic stem cells. <i>Nature</i> , 2018, 557, 640-641.	27.8	1
62	Setting the chromatin stage in oocytes. <i>Nature Cell Biology</i> , 2020, 22, 355-357.	10.3	1