

Matthew C Lorincz

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7604930/publications.pdf>

Version: 2024-02-01

62
papers

6,888
citations

87888

38
h-index

110387

64
g-index

71
all docs

71
docs citations

71
times ranked

9061
citing authors

#	ARTICLE	IF	CITATIONS
1	Interplay between chromatin marks in development and disease. <i>Nature Reviews Genetics</i> , 2022, 23, 137-153.	16.3	65
2	Histone H3 lysine 4 trimethylation in sperm is transmitted to the embryo and associated with diet-induced phenotypes in the offspring. <i>Developmental Cell</i> , 2021, 56, 671-686.e6.	7.0	70
3	Paternal MTHFR deficiency leads to hypomethylation of young retrotransposons and reproductive decline across two successive generations. <i>Development (Cambridge)</i> , 2021, 148, .	2.5	15
4	Transcription shapes genome-wide histone acetylation patterns. <i>Nature Communications</i> , 2021, 12, 210.	12.8	84
5	Repression of germline genes by PRC1.6 and SETDB1 in the early embryo precedes DNA methylation-mediated silencing. <i>Nature Communications</i> , 2021, 12, 7020.	12.8	26
6	Inter-Strain Epigenomic Profiling Reveals a Candidate IAP Master Copy in C3H Mice. <i>Viruses</i> , 2020, 12, 783.	3.3	9
7	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
8	NSD1-deposited H3K36me2 directs de novo methylation in the mouse male germline and counteracts Polycomb-associated silencing. <i>Nature Genetics</i> , 2020, 52, 1088-1098.	21.4	96
9	Vertebrate diapause preserves organisms long term through Polycomb complex members. <i>Science</i> , 2020, 367, 870-874.	12.6	79
10	Setting the chromatin stage in oocytes. <i>Nature Cell Biology</i> , 2020, 22, 355-357.	10.3	1
11	ZFP57 regulation of transposable elements and gene expression within and beyond imprinted domains. <i>Epigenetics and Chromatin</i> , 2019, 12, 49.	3.9	42
12	SETD2 regulates the maternal epigenome, genomic imprinting and embryonic development. <i>Nature Genetics</i> , 2019, 51, 844-856.	21.4	207
13	Histone H3K9 Methyltransferase G9a in Oocytes Is Essential for Preimplantation Development but Dispensable for CG Methylation Protection. <i>Cell Reports</i> , 2019, 27, 282-293.e4.	6.4	62
14	Evolution of imprinting via lineage-specific insertion of retroviral promoters. <i>Nature Communications</i> , 2019, 10, 5674.	12.8	39
15	H3S10ph broadly marks early-replicating domains in interphase ESCs and shows reciprocal antagonism with H3K9me2. <i>Genome Research</i> , 2018, 28, 37-51.	5.5	43
16	Development and application of an integrated allele-specific pipeline for methylomic and epigenomic analysis (MEA). <i>BMC Genomics</i> , 2018, 19, 463.	2.8	38
17	LTR retrotransposons transcribed in oocytes drive species-specific and heritable changes in DNA methylation. <i>Nature Communications</i> , 2018, 9, 3331.	12.8	65
18	HP1 proteins safeguard embryonic stem cells. <i>Nature</i> , 2018, 557, 640-641.	27.8	1

#	ARTICLE	IF	CITATIONS
19	On the role of H3.3 in retroviral silencing. <i>Nature</i> , 2017, 548, E1-E3.	27.8	19
20	Evidence for Converging DNA Methylation Pathways in Placenta and Cancer. <i>Developmental Cell</i> , 2017, 43, 257-258.	7.0	26
21	Epigenetic modifier drugs trigger widespread transcription of endogenous retroviruses. <i>Nature Genetics</i> , 2017, 49, 974-975.	21.4	7
22	ChAsE: chromatin analysis and exploration tool. <i>Bioinformatics</i> , 2016, 32, 3324-3326.	4.1	32
23	Dynamic and flexible H3K9me3 bridging via HP1 ² dimerization establishes a plastic state of condensed chromatin. <i>Nature Communications</i> , 2016, 7, 11310.	12.8	115
24	Activation of Endogenous Retroviruses in Dnmt1 ^{-/-} ESCs Involves Disruption of SETDB1-Mediated Repression by NP95 Binding to Hemimethylated DNA. <i>Cell Stem Cell</i> , 2016, 19, 81-94.	11.1	77
25	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
26	VisRseq: R-based visual framework for analysis of sequencing data. <i>BMC Bioinformatics</i> , 2015, 16, S2.	2.6	66
27	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
28	hnRNP K Coordinates Transcriptional Silencing by SETDB1 in Embryonic Stem Cells. <i>PLoS Genetics</i> , 2015, 11, e1004933.	3.5	64
29	Systematic Identification of Factors for Provirus Silencing in Embryonic Stem Cells. <i>Cell</i> , 2015, 163, 230-245.	28.9	162
30	ALEA: a toolbox for allele-specific epigenomics analysis. <i>Bioinformatics</i> , 2014, 30, 1172-1174.	4.1	18
31	Regulation of DNA methylation turnover at LTR retrotransposons and imprinted loci by the histone methyltransferase Setdb1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6690-6695.	7.1	89
32	Setdb1 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
33	Primate-specific endogenous retrovirus-driven transcription defines naive-like stem cells. <i>Nature</i> , 2014, 516, 405-409.	27.8	372
34	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
35	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
36	Kinetics and Epigenetics of Retroviral Silencing in Mouse Embryonic Stem Cells Defined by Deletion of the D4Z4 Element. <i>Molecular Therapy</i> , 2013, 21, 1536-1550.	8.2	21

#	ARTICLE	IF	CITATIONS
37	An Interactive Analysis and Exploration Tool for Epigenomic Data. <i>Computer Graphics Forum</i> , 2013, 32, 91-100.	3.0	9
38	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
39	Histone H3K4 demethylation is negatively regulated by histone H3 acetylation in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18505-18510.	7.1	52
40	Silencing of endogenous retroviruses: when and why do histone marks predominate?. <i>Trends in Biochemical Sciences</i> , 2012, 37, 127-133.	7.5	112
41	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
42	H3K9me3-binding proteins are dispensable for SETDB1/H3K9me3-dependent retroviral silencing. <i>Epigenetics and Chromatin</i> , 2011, 4, 12.	3.9	43
43	Lysine methyltransferase G9a is required for de novo DNA methylation and the establishment, but not the maintenance, of proviral silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5718-5723.	7.1	105
44	Retrotransposon-Induced Heterochromatin Spreading in the Mouse Revealed by Insertional Polymorphisms. <i>PLoS Genetics</i> , 2011, 7, e1002301.	3.5	129
45	Proviral silencing in embryonic stem cells requires the histone methyltransferase ESET. <i>Nature</i> , 2010, 464, 927-931.	27.8	681
46	Targeting of EZH2 to a defined genomic site is sufficient for recruitment of Dnmt3a but not de novo DNA methylation. <i>Epigenetics</i> , 2009, 4, 404-414.	2.7	74
47	H2A.Z and DNA methylation: irreconcilable differences. <i>Trends in Biochemical Sciences</i> , 2009, 34, 158-161.	7.5	16
48	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
49	An Unmethylated 3' Promoter-Proximal Region Is Required for Efficient Transcription Initiation. <i>PLoS Genetics</i> , 2007, 3, e27.	3.5	59
50	RNA Polymerase II: Just Stopping By. <i>Cell</i> , 2007, 130, 16-18.	28.9	12
51	Dynamics, stability and inheritance of somatic DNA methylation imprints. <i>Journal of Theoretical Biology</i> , 2006, 242, 890-899.	1.7	73
52	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
53	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
54	Position Effects Are Influenced by the Orientation of a Transgene with Respect to Flanking Chromatin. <i>Molecular and Cellular Biology</i> , 2001, 21, 298-309.	2.3	73

#	ARTICLE	IF	CITATIONS
55	Methylation-Mediated Proviral Silencing Is Associated with MeCP2 Recruitment and Localized Histone H3 Deacetylation. <i>Molecular and Cellular Biology</i> , 2001, 21, 7913-7922.	2.3	97
56	5mC(a/t)GG methylation: A new epigenetic mark in mammalian DNA?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 10034-10036.	7.1	37
57	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
58	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
59	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. <i>Journal of Biological Chemistry</i> , 1999, 274, 657-665.	3.4	15
60	Detection and Isolation of Gene-Corrected Cells in Gaucher Disease Via a Fluorescence-Activated Cell Sorter Assay for Lysosomal Glucocerebrosidase Activity. <i>Blood</i> , 1997, 89, 3412-3420.	1.4	40
61	Simultaneous fluorescence-activated cell sorter analysis of two distinct transcriptional elements within a single cell using engineered green fluorescent proteins.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 8508-8511.	7.1	105
62	Enzyme-generated intracellular fluorescence for single-cell reporter gene analysis utilizing <i>Escherichia coli</i> β -glucuronidase. <i>Cytometry</i> , 1996, 24, 321-329.	1.8	20