

Richard Meehan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/704099/publications.pdf>

Version: 2024-02-01

102
papers

9,222
citations

36203

51
h-index

40881

93
g-index

107
all docs

107
docs citations

107
times ranked

14185
citing authors

#	ARTICLE	IF	CITATIONS
1	Purification, sequence, and cellular localization of a novel chromosomal protein that binds to Methylated DNA. <i>Cell</i> , 1992, 69, 905-914.	13.5	1,253
2	Ageing of blood can be tracked by DNA methylation changes at just three CpG sites. <i>Genome Biology</i> , 2014, 15, R24.	13.9	709
3	Cholangiocytes act as facultative liver stem cells during impaired hepatocyte regeneration. <i>Nature</i> , 2017, 547, 350-354.	13.7	405
4	Tissue type is a major modifier of the 5-hydroxymethylcytosine content of human genes. <i>Genome Research</i> , 2012, 22, 467-477.	2.4	348
5	Senescent cells harbour features of the cancer epigenome. <i>Nature Cell Biology</i> , 2013, 15, 1495-1506.	4.6	300
6	A component of the transcriptional repressor MeCP1 shares a motif with DNA methyltransferase and HRX proteins. <i>Nature Genetics</i> , 1997, 16, 256-259.	9.4	222
7	Effect of Limited DNA Methylation Reprogramming in the Normal Sheep Embryo on Somatic Cell Nuclear Transfer1. <i>Biology of Reproduction</i> , 2004, 71, 185-193.	1.2	210
8	Non-conservation of mammalian preimplantation methylation dynamics. <i>Current Biology</i> , 2004, 14, R266-R267.	1.8	207
9	Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. <i>Genome Biology</i> , 2013, 14, R25.	13.9	200
10	Enzymatic approaches and bisulfite sequencing cannot distinguish between 5-methylcytosine and 5-hydroxymethylcytosine in DNA. <i>BioTechniques</i> , 2010, 48, 317-319.	0.8	193
11	Human pluripotent stem cell-derived acinar/ductal organoids generate human pancreas upon orthotopic transplantation and allow disease modelling. <i>Gut</i> , 2017, 66, 473-486.	6.1	174
12	Modules, networks and systems medicine for understanding disease and aiding diagnosis. <i>Genome Medicine</i> , 2014, 6, 82.	3.6	169
13	Diverse interventions that extend mouse lifespan suppress shared age-associated epigenetic changes at critical gene regulatory regions. <i>Genome Biology</i> , 2017, 18, 58.	3.8	147
14	Transcriptionally repressed genes become aberrantly methylated and distinguish tumors of different lineages in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4364-4369.	3.3	144
15	Tissue of origin determines cancer-associated CpG island promoter hypermethylation patterns. <i>Genome Biology</i> , 2012, 13, R84.	13.9	140
16	Rapid reprogramming of epigenetic and transcriptional profiles in mammalian culture systems. <i>Genome Biology</i> , 2015, 16, 11.	3.8	137
17	SMCHD1 mutations associated with a rare muscular dystrophy can also cause isolated arhinia and Bosma arhinia microphthalmia syndrome. <i>Nature Genetics</i> , 2017, 49, 238-248.	9.4	131
18	Promoter DNA methylation couples genome-defence mechanisms to epigenetic reprogramming in the mouse germline. <i>Development (Cambridge)</i> , 2012, 139, 3623-3632.	1.2	130

#	ARTICLE	IF	CITATIONS
19	HP1 binding to native chromatin in vitro is determined by the hinge region and not by the chromodomain. <i>EMBO Journal</i> , 2003, 22, 3164-3174.	3.5	126
20	An unbalanced maternal diet in pregnancy associates with offspring epigenetic changes in genes controlling glucocorticoid action and foetal growth. <i>Clinical Endocrinology</i> , 2012, 77, 808-815.	1.2	115
21	The effect of interspecific oocytes on demethylation of sperm DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7636-7640.	3.3	112
22	Pluripotent stem cells escape from senescence-associated DNA methylation changes. <i>Genome Research</i> , 2013, 23, 248-259.	2.4	107
23	Genomic insights into cancer-associated aberrant CpG island hypermethylation. <i>Briefings in Functional Genomics</i> , 2013, 12, 174-190.	1.3	105
24	Kaiso is a genome-wide repressor of transcription that is essential for amphibian development. <i>Development (Cambridge)</i> , 2004, 131, 6185-6194.	1.2	102
25	Applying 'omics technologies in chemicals risk assessment: Report of an ECETOC workshop. <i>Regulatory Toxicology and Pharmacology</i> , 2017, 91, S3-S13.	1.3	102
26	Defending the genome from the enemy within: mechanisms of retrotransposon suppression in the mouse germline. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 1581-1605.	2.4	99
27	Epigenetic Aging Signatures Are Coherently Modified in Cancer. <i>PLoS Genetics</i> , 2015, 11, e1005334.	1.5	99
28	DNA Methylation at Promoter Regions Regulates the Timing of Gene Activation in <i>Xenopus laevis</i> Embryos. <i>Developmental Biology</i> , 2002, 243, 155-165.	0.9	96
29	ATM Deficiency Generating Genomic Instability Sensitizes Pancreatic Ductal Adenocarcinoma Cells to Therapy-Induced DNA Damage. <i>Cancer Research</i> , 2017, 77, 5576-5590.	0.4	94
30	A reassessment of DNA-immunoprecipitation-based genomic profiling. <i>Nature Methods</i> , 2018, 15, 499-504.	9.0	92
31	Monitoring of cellular senescence by DNA methylation at specific CpG sites. <i>Aging Cell</i> , 2012, 11, 366-369.	3.0	90
32	Loss of ATM accelerates pancreatic cancer formation and epithelial-mesenchymal transition. <i>Nature Communications</i> , 2015, 6, 7677.	5.8	90
33	DNA methylation in animal development. <i>Seminars in Cell and Developmental Biology</i> , 2003, 14, 53-65.	2.3	86
34	Neutrophils Fuel Effective Immune Responses through Gluconeogenesis and Glycogenesis. <i>Cell Metabolism</i> , 2021, 33, 411-423.e4.	7.2	84
35	Dynamic changes in 5-hydroxymethylation signatures underpin early and late events in drug exposed liver. <i>Nucleic Acids Research</i> , 2013, 41, 5639-5654.	6.5	78
36	DNA Methylation Directs Polycomb-Dependent 3D Genome Re-organization in Naive Pluripotency. <i>Cell Reports</i> , 2019, 29, 1974-1985.e6.	2.9	76

#	ARTICLE	IF	CITATIONS
37	Non-canonical functions of the DNA methylome in gene regulation. <i>Biochemical Journal</i> , 2013, 451, 13-23.	1.7	75
38	Non-genotoxic carcinogen exposure induces defined changes in the 5-hydroxymethylome. <i>Genome Biology</i> , 2012, 13, R93.	13.9	74
39	Multigenerational programming in the glucocorticoid programmed rat is associated with generation-specific and parent of origin effects. <i>Epigenetics</i> , 2011, 6, 1334-1343.	1.3	72
40	Loss of Tet1-Associated 5-Hydroxymethylcytosine Is Concomitant with Aberrant Promoter Hypermethylation in Liver Cancer. <i>Cancer Research</i> , 2016, 76, 3097-3108.	0.4	71
41	Potential and suppression of mouse liver cytochrome P-450 isozymes during the acute-phase response induced by bacterial endotoxin. <i>FEBS Journal</i> , 1988, 174, 31-36.	0.2	67
42	Reduced levels of two modifiers of epigenetic gene silencing, Dnmt3a and Trim28, cause increased phenotypic noise. <i>Genome Biology</i> , 2010, 11, R111.	3.8	66
43	A Cell/Cilia Cycle Biosensor for Single-Cell Kinetics Reveals Persistence of Cilia after G1/S Transition Is a General Property in Cells and Mice. <i>Developmental Cell</i> , 2018, 47, 509-523.e5.	3.1	66
44	xDnmt1 regulates transcriptional silencing in pre-MBT <i>Xenopus</i> embryos independently of its catalytic function. <i>Development (Cambridge)</i> , 2008, 135, 1295-1302.	1.2	65
45	Microarray Analysis of LTR Retrotransposon Silencing Identifies Hdac1 as a Regulator of Retrotransposon Expression in Mouse Embryonic Stem Cells. <i>PLoS Computational Biology</i> , 2012, 8, e1002486.	1.5	64
46	DNMT1 deficiency triggers mismatch repair defects in human cells through depletion of repair protein levels in a process involving the DNA damage response. <i>Human Molecular Genetics</i> , 2011, 20, 3241-3255.	1.4	63
47	Identification of Dlk1-Dio3 Imprinted Gene Cluster Noncoding RNAs as Novel Candidate Biomarkers for Liver Tumor Promotion. <i>Toxicological Sciences</i> , 2013, 131, 375-386.	1.4	62
48	Epigenetic program and transcription factor circuitry of dendritic cell development. <i>Nucleic Acids Research</i> , 2015, 43, gkv1056.	6.5	62
49	Hypoxia determines survival outcomes of bacterial infection through HIF-1 α -dependent reprogramming of leukocyte metabolism. <i>Science Immunology</i> , 2017, 2, .	5.6	61
50	A Dynamic Role of TBX3 in the Pluripotency Circuitry. <i>Stem Cell Reports</i> , 2015, 5, 1155-1170.	2.3	57
51	5-Hydroxymethylcytosine Remodeling Precedes Lineage Specification during Differentiation of Human CD4+ T Cells. <i>Cell Reports</i> , 2016, 16, 559-570.	2.9	56
52	DNA methylation as a genomic marker of exposure to chemical and environmental agents. <i>Current Opinion in Chemical Biology</i> , 2018, 45, 48-56.	2.8	55
53	Expression of a large LINE-1-driven antisense RNA is linked to epigenetic silencing of the metastasis suppressor gene TFPI-2 in cancer. <i>Nucleic Acids Research</i> , 2013, 41, 6857-6869.	6.5	54
54	Epigenetic profiles as defined signatures of xenobiotic exposure. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2014, 764-765, 3-9.	0.9	53

#	ARTICLE	IF	CITATIONS
55	5-hydroxymethylcytosine profiling as an indicator of cellular state. <i>Epigenomics</i> , 2013, 5, 655-669.	1.0	52
56	Epigenetic modification of the PD-1 (<i>Pdcd1</i>) promoter in effector CD4+ T cells tolerized by peptide immunotherapy. <i>ELife</i> , 2014, 3, .	2.8	52
57	The interaction of χ Kaiso with χ Tcf3: a revised model for integration of epigenetic and Wnt signalling pathways. <i>Development (Cambridge)</i> , 2009, 136, 723-727.	1.2	48
58	The non-methylated DNA-binding function of Kaiso is not required in early <i>Xenopus laevis</i> development. <i>Development (Cambridge)</i> , 2009, 136, 729-738.	1.2	47
59	An In Vitro Model That Recapitulates the Epithelial to Mesenchymal Transition (EMT) in Human Breast Cancer. <i>PLoS ONE</i> , 2011, 6, e17083.	1.1	45
60	Binding of Histone H1 to DNA Is Indifferent to Methylation at CpG Sequences. <i>Journal of Biological Chemistry</i> , 1995, 270, 26473-26481.	1.6	44
61	Comparative analysis of affinity-based 5-hydroxymethylation enrichment techniques. <i>Nucleic Acids Research</i> , 2013, 41, e206-e206.	6.5	44
62	Mobilization of LINE-1 retrotransposons is restricted by Tex19.1 in mouse embryonic stem cells. <i>ELife</i> , 2017, 6, .	2.8	43
63	The application of genome-wide 5-hydroxymethylcytosine studies in cancer research. <i>Epigenomics</i> , 2017, 9, 77-91.	1.0	42
64	A determining influence for CpG dinucleotides on nucleosome positioning in vitro. <i>Nucleic Acids Research</i> , 2004, 32, 4322-4331.	6.5	39
65	Increased DNA methylation of <i>Dnmt3b</i> targets impairs leukemogenesis. <i>Blood</i> , 2016, 127, 1575-1586.	0.6	38
66	The genome-defence gene <i>Tex19.1</i> suppresses LINE-1 retrotransposons in the placenta and prevents intra-uterine growth retardation in mice. <i>Human Molecular Genetics</i> , 2013, 22, 1791-1806.	1.4	37
67	Detecting differential peaks in ChIP-seq signals with ODIN. <i>Bioinformatics</i> , 2014, 30, 3467-3475.	1.8	36
68	Bivalent promoter hypermethylation in cancer is linked to the H327me3/H3K4me3 ratio in embryonic stem cells. <i>BMC Biology</i> , 2020, 18, 25.	1.7	35
69	Hematopoietic Stem and Progenitor Cells Acquire Distinct DNA-Hypermethylation During in vitro Culture. <i>Scientific Reports</i> , 2013, 3, 3372.	1.6	31
70	Non-alcoholic fatty liver disease (NAFLD) is associated with dynamic changes in DNA hydroxymethylation. <i>Epigenetics</i> , 2020, 15, 61-71.	1.3	31
71	MBD4 and MLH1 are required for apoptotic induction in χ DNMT1-depleted embryos. <i>Development (Cambridge)</i> , 2009, 136, 2277-2286.	1.2	30
72	Modelling non-alcoholic fatty liver disease in human hepatocyte-like cells. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170362.	1.8	29

#	ARTICLE	IF	CITATIONS
73	Hydroxymethylated DNA Immunoprecipitation (hmeDIP). <i>Methods in Molecular Biology</i> , 2014, 1094, 259-267.	0.4	27
74	Tbx3 fosters pancreatic cancer growth by increased angiogenesis and activin/nodal-dependent induction of stemness. <i>Stem Cell Research</i> , 2016, 17, 367-378.	0.3	27
75	Apoptosis and DNA Methylation. <i>Cancers</i> , 2011, 3, 1798-1820.	1.7	25
76	Epigenetic silencing in embryogenesis. <i>Experimental Cell Research</i> , 2005, 309, 241-249.	1.2	24
77	Do age-associated DNA methylation changes increase the risk of malignant transformation?. <i>BioEssays</i> , 2015, 37, 20-24.	1.2	22
78	Cloning and expression of sheep DNA methyltransferase 1 and its development-specific isoform. <i>Molecular Reproduction and Development</i> , 2009, 76, 501-513.	1.0	20
79	Investigation into the role of the germline epigenome in the transmission of glucocorticoid-programmed effects across generations. <i>Genome Biology</i> , 2018, 19, 50.	3.8	20
80	A human pluripotent stem cell model for the analysis of metabolic dysfunction in hepatic steatosis. <i>IScience</i> , 2021, 24, 101931.	1.9	19
81	Epigenetic reprogramming: preparing the epigenome for the next generation. <i>Biochemical Society Transactions</i> , 2013, 41, 809-814.	1.6	16
82	Investigating 5-Hydroxymethylcytosine (5hmC): The State of the Art. <i>Methods in Molecular Biology</i> , 2014, 1094, 243-258.	0.4	16
83	DNA-methylation in C1R is a prognostic biomarker for acute myeloid leukemia. <i>Clinical Epigenetics</i> , 2015, 7, 116.	1.8	16
84	Methyl donor deficient diets cause distinct alterations in lipid metabolism but are poorly representative of human NAFLD. <i>Wellcome Open Research</i> , 2017, 2, 67.	0.9	15
85	Molecular cloning and developmental expression of two Chloride Intracellular Channel (CLIC) genes in <i>Xenopus laevis</i> . <i>Development Genes and Evolution</i> , 2003, 213, 514-518.	0.4	13
86	Dynamic changes in DNA modification states during late gestation male germ line development in the rat. <i>Epigenetics and Chromatin</i> , 2014, 7, 19.	1.8	12
87	Lsh Is Essential for Maintaining Global DNA Methylation Levels in Amphibia and Fish and Interacts Directly with Dnmt1. <i>BioMed Research International</i> , 2015, 2015, 1-12.	0.9	12
88	Deep C diving: mapping the low-abundance modifications of the DNA demethylation pathway. <i>Genome Biology</i> , 2013, 14, 118.	3.8	10
89	Shoring up <scp>DNA</scp> methylation and H3K27me3 domain demarcation at developmental genes. <i>EMBO Journal</i> , 2017, 36, 3407-3408.	3.5	9
90	From Paramutation to Paradigm. <i>PLoS Genetics</i> , 2013, 9, e1003537.	1.5	8

#	ARTICLE	IF	CITATIONS
91	Cloning and developmental expression of MARK/Par-1/MELK-related protein kinase xMAK-V in <i>Xenopus laevis</i> . <i>Development Genes and Evolution</i> , 2004, 214, 139-143.	0.4	7
92	Decoupling of DNA methylation and activity of intergenic LINE-1 promoters in colorectal cancer. <i>Epigenetics</i> , 2017, 12, 465-475.	1.3	7
93	The CXXC-TET bridge "mind the methylation gap!". <i>Cell Research</i> , 2013, 23, 973-974.	5.7	5
94	PRC2 inhibition counteracts the culture-associated loss of engraftment potential of human cord blood-derived hematopoietic stem and progenitor cells. <i>Scientific Reports</i> , 2015, 5, 12319.	1.6	5
95	Defining baseline epigenetic landscapes in the rat liver. <i>Epigenomics</i> , 2017, 9, 1503-1527.	1.0	5
96	Activation of transcription factor circuitry in 2i-induced ground state pluripotency is independent of repressive global epigenetic landscapes. <i>Nucleic Acids Research</i> , 2020, 48, 7748-7766.	6.5	5
97	Methylation-Sensitive Polymerase Chain Reaction. , 2006, 325, 239-250.		4
98	5-Hydroxymethylcytosine Profiling in Human DNA. <i>Methods in Molecular Biology</i> , 2015, 1589, 89-98.	0.4	4
99	Affinity-Based Enrichment Techniques for the Genome-Wide Analysis of 5-Hydroxymethylcytosine. <i>Methods in Molecular Biology</i> , 2018, 1708, 679-696.	0.4	3
100	Genes V. <i>Trends in Genetics</i> , 1994, 10, 258-259.	2.9	0
101	Putting muscle in DNA methylation. <i>Cell Research</i> , 2011, 21, 1531-1533.	5.7	0
102	Dynamics and Mechanisms of DNA Methylation Reprogramming. , 2019, , 19-45.		0