

Richard Meehan

List of Publications by Year in descending order

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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	Neutrophils Fuel Effective Immune Responses through Gluconeogenesis and Glycogenesis. <i>Cell Metabolism</i> , 2021, 33, 411-423.e4.	7.2	84
2	A human pluripotent stem cell model for the analysis of metabolic dysfunction in hepatic steatosis. <i>IScience</i> , 2021, 24, 101931.	1.9	19
3	Non-alcoholic fatty liver disease (NAFLD) is associated with dynamic changes in DNA hydroxymethylation. <i>Epigenetics</i> , 2020, 15, 61-71.	1.3	31
4	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
5	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
6	DNA Methylation Directs Polycomb-Dependent 3D Genome Re-organization in Naive Pluripotency. <i>Cell Reports</i> , 2019, 29, 1974-1985.e6.	2.9	76
7	Dynamics and Mechanisms of DNA Methylation Reprogramming. , 2019, , 19-45.		0
8	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
9	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
10	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
11	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
12	A reassessment of DNA-immunoprecipitation-based genomic profiling. <i>Nature Methods</i> , 2018, 15, 499-504.	9.0	92
13	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
14	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
15	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
16	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
17	Decoupling of DNA methylation and activity of intergenic LINE-1 promoters in colorectal cancer. <i>Epigenetics</i> , 2017, 12, 465-475.	1.3	7
18	The application of genome-wide 5-hydroxymethylcytosine studies in cancer research. <i>Epigenomics</i> , 2017, 9, 77-91.	1.0	42

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19	Applying 'omics technologies in chemicals risk assessment: Report of an ECETOC workshop. Regulatory Toxicology and Pharmacology, 2017, 91, S3-S13.	1.3	102
20	ATM Deficiency Generating Genomic Instability Sensitizes Pancreatic Ductal Adenocarcinoma Cells to Therapy-Induced DNA Damage. Cancer Research, 2017, 77, 5576-5590.	0.4	94
21	Shoring up <scp>DNA</scp> methylation and H3K27me3 domain demarcation at developmental genes. EMBO Journal, 2017, 36, 3407-3408.	3.5	9
22	Cholangiocytes act as facultative liver stem cells during impaired hepatocyte regeneration. Nature, 2017, 547, 350-354.	13.7	405
23	Diverse interventions that extend mouse lifespan suppress shared age-associated epigenetic changes at critical gene regulatory regions. Genome Biology, 2017, 18, 58.	3.8	147
24	Defining baseline epigenetic landscapes in the rat liver. Epigenomics, 2017, 9, 1503-1527.	1.0	5
25	Methyl donor deficient diets cause distinct alterations in lipid metabolism but are poorly representative of human NAFLD. Wellcome Open Research, 2017, 2, 67.	0.9	15
26	Mobilization of LINE-1 retrotransposons is restricted by Tex19.1 in mouse embryonic stem cells. ELife, 2017, 6, .	2.8	43
27	5-Hydroxymethylcytosine Remodeling Precedes Lineage Specification during Differentiation of Human CD4+ T Cells. Cell Reports, 2016, 16, 559-570.	2.9	56
28	Loss of Tet1-Associated 5-Hydroxymethylcytosine Is Concomitant with Aberrant Promoter Hypermethylation in Liver Cancer. Cancer Research, 2016, 76, 3097-3108.	0.4	71
29	Increased DNA methylation of Dnmt3b targets impairs leukemogenesis. Blood, 2016, 127, 1575-1586.	0.6	38
30	Tbx3 fosters pancreatic cancer growth by increased angiogenesis and activin/nodal-dependent induction of stemness. Stem Cell Research, 2016, 17, 367-378.	0.3	27
31	PRC2 inhibition counteracts the culture-associated loss of engraftment potential of human cord blood-derived hematopoietic stem and progenitor cells. Scientific Reports, 2015, 5, 12319.	1.6	5
32	A Dynamic Role of TBX3 in the Pluripotency Circuitry. Stem Cell Reports, 2015, 5, 1155-1170.	2.3	57
33	DNA-methylation in C1R is a prognostic biomarker for acute myeloid leukemia. Clinical Epigenetics, 2015, 7, 116.	1.8	16
34	Lsh Is Essential for Maintaining Global DNA Methylation Levels in Amphibia and Fish and Interacts Directly with Dnmt1. BioMed Research International, 2015, 2015, 1-12.	0.9	12
35	Rapid reprogramming of epigenetic and transcriptional profiles in mammalian culture systems. Genome Biology, 2015, 16, 11.	3.8	137
36	Loss of ATM accelerates pancreatic cancer formation and epithelialâ€mesenchymal transition. Nature Communications, 2015, 6, 7677.	5.8	90

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37	Epigenetic program and transcription factor circuitry of dendritic cell development. <i>Nucleic Acids Research</i> , 2015, 43, gkv1056.	6.5	62
38	5-Hydroxymethylcytosine Profiling in Human DNA. <i>Methods in Molecular Biology</i> , 2015, 1589, 89-98.	0.4	4
39	Do age-associated DNA methylation changes increase the risk of malignant transformation?. <i>BioEssays</i> , 2015, 37, 20-24.	1.2	22
40	Epigenetic Aging Signatures Are Coherently Modified in Cancer. <i>PLoS Genetics</i> , 2015, 11, e1005334.	1.5	99
41	Modules, networks and systems medicine for understanding disease and aiding diagnosis. <i>Genome Medicine</i> , 2014, 6, 82.	3.6	169
42	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
43	Aging of blood can be tracked by DNA methylation changes at just three CpG sites. <i>Genome Biology</i> , 2014, 15, R24.	13.9	709
44	Investigating 5-Hydroxymethylcytosine (5hmC): The State of the Art. <i>Methods in Molecular Biology</i> , 2014, 1094, 243-258.	0.4	16
45	Hydroxymethylated DNA Immunoprecipitation (hmeDIP). <i>Methods in Molecular Biology</i> , 2014, 1094, 259-267.	0.4	27
46	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
47	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
48	Detecting differential peaks in ChIP-seq signals with ODIN. <i>Bioinformatics</i> , 2014, 30, 3467-3475.	1.8	36
49	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
50	Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. <i>Genome Biology</i> , 2013, 14, R25.	13.9	200
51	Genomic insights into cancer-associated aberrant CpG island hypermethylation. <i>Briefings in Functional Genomics</i> , 2013, 12, 174-190.	1.3	105
52	Senescent cells harbour features of the cancer epigenome. <i>Nature Cell Biology</i> , 2013, 15, 1495-1506.	4.6	300
53	Deep C diving: mapping the low-abundance modifications of the DNA demethylation pathway. <i>Genome Biology</i> , 2013, 14, 118.	3.8	10
54	Comparative analysis of affinity-based 5-hydroxymethylation enrichment techniques. <i>Nucleic Acids Research</i> , 2013, 41, e206-e206.	6.5	44

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55	Non-canonical functions of the DNA methylome in gene regulation. <i>Biochemical Journal</i> , 2013, 451, 13-23.	1.7	75
56	Pluripotent stem cells escape from senescence-associated DNA methylation changes. <i>Genome Research</i> , 2013, 23, 248-259.	2.4	107
57	5-hydroxymethylcytosine profiling as an indicator of cellular state. <i>Epigenomics</i> , 2013, 5, 655-669.	1.0	52
58	The CXXC-TET bridge "mind the methylation gap!". <i>Cell Research</i> , 2013, 23, 973-974.	5.7	5
59	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
60	From Paramutation to Paradigm. <i>PLoS Genetics</i> , 2013, 9, e1003537.	1.5	8
61	Epigenetic reprogramming: preparing the epigenome for the next generation. <i>Biochemical Society Transactions</i> , 2013, 41, 809-814.	1.6	16
62	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
63	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
64	The genome-defence gene Tex19.1 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
65	Hematopoietic Stem and Progenitor Cells Acquire Distinct DNA-Hypermethylation During in vitro Culture. <i>Scientific Reports</i> , 2013, 3, 3372.	1.6	31
66	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
67	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
68	Tissue of origin determines cancer-associated CpG island promoter hypermethylation patterns. <i>Genome Biology</i> , 2012, 13, R84.	13.9	140
69	Non-genotoxic carcinogen exposure induces defined changes in the 5-hydroxymethylome. <i>Genome Biology</i> , 2012, 13, R93.	13.9	74
70	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
71	Monitoring of cellular senescence by DNA-methylation at specific CpG sites. <i>Aging Cell</i> , 2012, 11, 366-369.	3.0	90
72	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

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73	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
74	Putting muscle in DNA methylation. <i>Cell Research</i> , 2011, 21, 1531-1533.	5.7	0
75	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
76	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
77	Apoptosis and DNA Methylation. <i>Cancers</i> , 2011, 3, 1798-1820.	1.7	25
78	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
79	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
80	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
81	MBD4 and MLH1 are required for apoptotic induction in xDNMT1-depleted embryos. <i>Development (Cambridge)</i> , 2009, 136, 2277-2286.	1.2	30
82	The interaction of xKaiso with xTcf3: a revised model for integration of epigenetic and Wnt signalling pathways. <i>Development (Cambridge)</i> , 2009, 136, 723-727.	1.2	48
83	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
84	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
85	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
86	Methylation-Sensitive Polymerase Chain Reaction. , 2006, 325, 239-250.		4
87	Epigenetic silencing in embryogenesis. <i>Experimental Cell Research</i> , 2005, 309, 241-249.	1.2	24
88	A determining influence for CpG dinucleotides on nucleosome positioning in vitro. <i>Nucleic Acids Research</i> , 2004, 32, 4322-4331.	6.5	39
89	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
90	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

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91	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
92	Non-conservation of mammalian preimplantation methylation dynamics. <i>Current Biology</i> , 2004, 14, R266-R267.	1.8	207
93	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
94	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
95	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
96	DNA methylation in animal development. <i>Seminars in Cell and Developmental Biology</i> , 2003, 14, 53-65.	2.3	86
97	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
98	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
99	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
100	Genes V. <i>Trends in Genetics</i> , 1994, 10, 258-259.	2.9	0
101	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
102	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