

# Hendrik Marks

## List of Publications by Year in descending order

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Version: 2024-02-01

55  
papers

5,074  
citations

201674

27  
h-index

168389

53  
g-index

61  
all docs

61  
docs citations

61  
times ranked

8024  
citing authors

#	ARTICLE	IF	CITATIONS
1	There is another: H3K27me3-mediated genomic imprinting. Trends in Genetics, 2022, 38, 82-96.	6.7	16
2	Human branching cholangiocyte organoids recapitulate functional bile duct formation. Cell Stem Cell, 2022, 29, 776-794.e13.	11.1	17
3	PRC1 uncomplexed. Stem Cell Reports, 2022, 17, 1009-1011.	4.8	0
4	Integrated multi-omics reveal polycomb repressive complex 2 restricts human trophoblast induction. Nature Cell Biology, 2022, 24, 858-871.	10.3	30
5	Terminal keratinocyte differentiation in vitro is associated with a stable DNA methylome. Experimental Dermatology, 2021, 30, 1023-1032.	2.9	8
6	Overcoming epigenetic roadblocks. Nature Chemical Biology, 2021, 17, 6-7.	8.0	0
7	Developments in pluripotency: a new formative state. Cell Research, 2021, 31, 493-494.	12.0	8
8	A plug and play microfluidic platform for standardized sensitive low-input chromatin immunoprecipitation. Genome Research, 2021, 31, 919-933.	5.5	4
9	Cholangiocyte organoids from human bile retain a local phenotype and can repopulate bile ducts in vitro. Clinical and Translational Medicine, 2021, 11, e566.	4.0	12
10	Critical Role for P53 in Regulating the Cell Cycle of Ground State Embryonic Stem Cells. Stem Cell Reports, 2020, 14, 175-183.	4.8	22
11	STARR-seq identifies active, chromatin-masked, and dormant enhancers in pluripotent mouse embryonic stem cells. Genome Biology, 2020, 21, 243.	8.8	48
12	Two Functional Axes of Feedback-Enforced PRC2 Recruitment in Mouse Embryonic Stem Cells. Stem Cell Reports, 2020, 15, 1287-1300.	4.8	19
13	In vitro capture and characterization of embryonic rosette-stage pluripotency between naive and primed states. Nature Cell Biology, 2020, 22, 534-545.	10.3	91
14	Dynamic CpG methylation delineates subregions within super-enhancers selectively decommissioned at the exit from naive pluripotency. Nature Communications, 2020, 11, 1112.	12.8	25
15	A Mass Spectrometry Survey of Chromatin-Associated Proteins in Pluripotency and Early Lineage Commitment. Proteomics, 2019, 19, 1900047.	2.2	16
16	The Complexity of PRC2 Subcomplexes. Trends in Cell Biology, 2019, 29, 660-671.	7.9	178
17	Epigenetic modulation of a hardwired 3D chromatin landscape in two naive states of pluripotency. Nature Cell Biology, 2019, 21, 568-578.	10.3	55
18	Allele-specific RNA-seq expression profiling of imprinted genes in mouse isogenic pluripotent states. Epigenetics and Chromatin, 2019, 12, 14.	3.9	11

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19	Miniaturised interaction proteomics on a microfluidic platform with ultra-low input requirements. <i>Nature Communications</i> , 2019, 10, 1525.	12.8	29
20	Untargeted histone profiling during naive conversion uncovers conserved modification markers between mouse and human. <i>Scientific Reports</i> , 2019, 9, 17240.	3.3	14
21	Integrative Proteomic Profiling Reveals PRC2-Dependent Epigenetic Crosstalk Maintains Ground-State Pluripotency. <i>Cell Stem Cell</i> , 2019, 24, 123-137.e8.	11.1	90
22	Quantitative subcellular proteomics using SILAC reveals enhanced metabolic buffering in the pluripotent ground state. <i>Stem Cell Research</i> , 2018, 33, 135-145.	0.7	8
23	MTF2 recruits Polycomb Repressive Complex 2 by helical-shape-selective DNA binding. <i>Nature Genetics</i> , 2018, 50, 1002-1010.	21.4	147
24	Mammalian embryo comparison identifies novel pluripotency genes associated with the naïve or primed state. <i>Biology Open</i> , 2018, 7, .	1.2	32
25	Tracking the embryonic stem cell transition from ground state pluripotency. <i>Development (Cambridge)</i> , 2017, 144, 1221-1234.	2.5	226
26	An efficient method for generation of bi-allelic null mutant mouse embryonic stem cells and its application for investigating epigenetic modifiers. <i>Nucleic Acids Research</i> , 2017, 45, e174-e174.	14.5	7
27	PRC1 Prevents Replication Stress during Chondrogenic Transit Amplification. <i>Epigenomes</i> , 2017, 1, 22.	1.8	0
28	Genome-wide epigenomic profiling for biomarker discovery. <i>Clinical Epigenetics</i> , 2016, 8, 122.	4.1	67
29	Dynamics of gene silencing during X inactivation using allele-specific RNA-seq. <i>Genome Biology</i> , 2015, 16, 149.	8.8	104
30	Mll2 is required for H3K4 trimethylation on bivalent promoters in embryonic stem cells, whereas Mll1 is redundant. <i>Development (Cambridge)</i> , 2014, 141, 526-537.	2.5	225
31	Transcription regulation and chromatin structure in the pluripotent ground state. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 129-137.	1.9	33
32	Otx2 and Oct4 Drive Early Enhancer Activation during Embryonic Stem Cell Transition from Naive Pluripotency. <i>Cell Reports</i> , 2014, 7, 1968-1981.	6.4	117
33	Stable Methylation at Promoters Distinguishes Epiblast Stem Cells from Embryonic Stem Cells and the In Vivo Epiblasts. <i>Stem Cells and Development</i> , 2014, 23, 2014-2029.	2.1	31
34	Whole-Genome Bisulfite Sequencing of Two Distinct Interconvertible DNA Methylomes of Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2013, 13, 360-369.	11.1	424
35	The PinkThing for analysing ChIP profiling data in their genomic context. <i>BMC Research Notes</i> , 2013, 6, 133.	1.4	4
36	The Transcriptional and Epigenomic Foundations of Ground State Pluripotency. <i>Cell</i> , 2012, 149, 590-604.	28.9	774

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37	Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. <i>Genome Research</i> , 2012, 22, 1128-1138.	5.5	344
38	An RNA-Seq Strategy to Detect the Complete Coding and Non-Coding Transcriptome Including Full-Length Imprinted Macro ncRNAs. <i>PLoS ONE</i> , 2011, 6, e27288.	2.5	97
39	A role for cohesin in T-cell-receptor rearrangement and thymocyte differentiation. <i>Nature</i> , 2011, 476, 467-471.	27.8	217
40	In vitro culture and characterization of putative porcine embryonic germ cells derived from domestic breeds and Yucatan mini pig embryos at Days 20-24 of gestation. <i>Stem Cell Research</i> , 2011, 6, 226-237.	0.7	28
41	Epigenetic Regulation of Learning and Memory by <i>Drosophila</i> EHMT/G9a. <i>PLoS Biology</i> , 2011, 9, e1000569.	5.6	185
42	Evaluation of white spot syndrome virus variable DNA loci as molecular markers of virus spread at intermediate spatiotemporal scales. <i>Journal of General Virology</i> , 2010, 91, 1164-1172.	2.9	23
43	Quantitative Interaction Proteomics and Genome-wide Profiling of Epigenetic Histone Marks and Their Readers. <i>Cell</i> , 2010, 142, 967-980.	28.9	710
44	Insightful Tales from Single Embryonic Cells. <i>Cell Stem Cell</i> , 2010, 6, 397-398.	11.1	7
45	High-resolution analysis of epigenetic changes associated with X inactivation. <i>Genome Research</i> , 2009, 19, 1361-1373.	5.5	122
46	Diminished expression of multidrug resistance-associated protein 1 (MRP1) in bronchial epithelium of COPD patients. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2006, 449, 682-688.	2.8	57
47	In silico identification of putative promoter motifs of White Spot Syndrome Virus. <i>BMC Bioinformatics</i> , 2006, 7, 309.	2.6	17
48	Fitness and virulence of an ancestral White Spot Syndrome Virus isolate from shrimp. <i>Virus Research</i> , 2005, 110, 9-20.	2.2	70
49	Gene-expression profiling of White spot syndrome virus in vivo. <i>Journal of General Virology</i> , 2005, 86, 2081-2100.	2.9	62
50	Molecular epidemiology of white spot syndrome virus within Vietnam. <i>Journal of General Virology</i> , 2004, 85, 3607-3618.	2.9	66
51	Genetic variation among isolates of White spot syndrome virus. <i>Archives of Virology</i> , 2004, 149, 673-697.	2.1	82
52	Virus-Host Interactions of White Spot Syndrome Virus. <i>Molecular Aspects of Fish and Marine Biology</i> , 2004, , 237-255.	0.2	4
53	Intracellular distribution of cowpea mosaic virus movement protein as visualised by green fluorescent protein fusions. <i>Archives of Virology</i> , 2003, 148, 2099-2114.	2.1	14
54	Promoter analysis of the Chilo iridescent virus DNA polymerase and major capsid protein genes. <i>Virology</i> , 2003, 317, 321-329.	2.4	30

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55	Transcriptional analysis of the white spot syndrome virus major virion protein genes. Journal of General Virology, 2003, 84, 1517-1523.	2.9	36