

# Hendrik Marks

## List of Publications by Year in descending order

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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	The Transcriptional and Epigenomic Foundations of Ground State Pluripotency. <i>Cell</i> , 2012, 149, 590-604.	28.9	774
2	Quantitative Interaction Proteomics and Genome-wide Profiling of Epigenetic Histone Marks and Their Readers. <i>Cell</i> , 2010, 142, 967-980.	28.9	710
3	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
4	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
5	Tracking the embryonic stem cell transition from ground state pluripotency. <i>Development (Cambridge)</i> , 2017, 144, 1221-1234.	2.5	226
6	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
7	A role for cohesin in T-cell-receptor rearrangement and thymocyte differentiation. <i>Nature</i> , 2011, 476, 467-471.	27.8	217
8	Epigenetic Regulation of Learning and Memory by Drosophila EHMT/G9a. <i>PLoS Biology</i> , 2011, 9, e1000569.	5.6	185
9	The Complexity of PRC2 Subcomplexes. <i>Trends in Cell Biology</i> , 2019, 29, 660-671.	7.9	178
10	MTF2 recruits Polycomb Repressive Complex 2 by helical-shape-selective DNA binding. <i>Nature Genetics</i> , 2018, 50, 1002-1010.	21.4	147
11	High-resolution analysis of epigenetic changes associated with X inactivation. <i>Genome Research</i> , 2009, 19, 1361-1373.	5.5	122
12	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
13	Dynamics of gene silencing during X inactivation using allele-specific RNA-seq. <i>Genome Biology</i> , 2015, 16, 149.	8.8	104
14	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
15	In vitro capture and characterization of embryonic rosette-stage pluripotency between naive and primed states. <i>Nature Cell Biology</i> , 2020, 22, 534-545.	10.3	91
16	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
17	Genetic variation among isolates of White spot syndrome virus. <i>Archives of Virology</i> , 2004, 149, 673-697.	2.1	82
18	Fitness and virulence of an ancestral White Spot Syndrome Virus isolate from shrimp. <i>Virus Research</i> , 2005, 110, 9-20.	2.2	70

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19	Genome-wide epigenomic profiling for biomarker discovery. <i>Clinical Epigenetics</i> , 2016, 8, 122.	4.1	67
20	Molecular epidemiology of white spot syndrome virus within Vietnam. <i>Journal of General Virology</i> , 2004, 85, 3607-3618.	2.9	66
21	Gene-expression profiling of White spot syndrome virus in vivo. <i>Journal of General Virology</i> , 2005, 86, 2081-2100.	2.9	62
22	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
23	Epigenetic modulation of a hardwired 3D chromatin landscape in two naive states of pluripotency. <i>Nature Cell Biology</i> , 2019, 21, 568-578.	10.3	55
24	STARR-seq identifies active, chromatin-masked, and dormant enhancers in pluripotent mouse embryonic stem cells. <i>Genome Biology</i> , 2020, 21, 243.	8.8	48
25	Transcriptional analysis of the white spot syndrome virus major virion protein genes. <i>Journal of General Virology</i> , 2003, 84, 1517-1523.	2.9	36
26	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
27	Mammalian embryo comparison identifies novel pluripotency genes associated with the naïve or primed state. <i>Biology Open</i> , 2018, 7, .	1.2	32
28	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
29	Promoter analysis of the Chilo iridescent virus DNA polymerase and major capsid protein genes. <i>Virology</i> , 2003, 317, 321-329.	2.4	30
30	Integrated multi-omics reveal polycomb repressive complex 2 restricts human trophoblast induction. <i>Nature Cell Biology</i> , 2022, 24, 858-871.	10.3	30
31	Miniaturised interaction proteomics on a microfluidic platform with ultra-low input requirements. <i>Nature Communications</i> , 2019, 10, 1525.	12.8	29
32	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
33	Dynamic CpG methylation delineates subregions within super-enhancers selectively decommissioned at the exit from naive pluripotency. <i>Nature Communications</i> , 2020, 11, 1112.	12.8	25
34	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
35	Critical Role for P53 in Regulating the Cell Cycle of Ground State Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2020, 14, 175-183.	4.8	22
36	Two Functional Axes of Feedback-Enforced PRC2 Recruitment in Mouse Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2020, 15, 1287-1300.	4.8	19

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37	In silico identification of putative promoter motifs of White Spot Syndrome Virus. BMC Bioinformatics, 2006, 7, 309.	2.6	17
38	Human branching cholangiocyte organoids recapitulate functional bile duct formation. Cell Stem Cell, 2022, 29, 776-794.e13.	11.1	17
39	A Mass Spectrometry Survey of Chromatin-Associated Proteins in Pluripotency and Early Lineage Commitment. Proteomics, 2019, 19, 1900047.	2.2	16
40	There is another: H3K27me3-mediated genomic imprinting. Trends in Genetics, 2022, 38, 82-96.	6.7	16
41	Intracellular distribution of cowpea mosaic virus movement protein as visualised by green fluorescent protein fusions. Archives of Virology, 2003, 148, 2099-2114.	2.1	14
42	Untargeted histone profiling during naive conversion uncovers conserved modification markers between mouse and human. Scientific Reports, 2019, 9, 17240.	3.3	14
43	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
44	Allele-specific RNA-seq expression profiling of imprinted genes in mouse isogenic pluripotent states. Epigenetics and Chromatin, 2019, 12, 14.	3.9	11
45	Quantitative subcellular proteomics using SILAC reveals enhanced metabolic buffering in the pluripotent ground state. Stem Cell Research, 2018, 33, 135-145.	0.7	8
46	Terminal keratinocyte differentiation in vitro is associated with a stable DNA methylome. Experimental Dermatology, 2021, 30, 1023-1032.	2.9	8
47	Developments in pluripotency: a new formative state. Cell Research, 2021, 31, 493-494.	12.0	8
48	Insightful Tales from Single Embryonic Cells. Cell Stem Cell, 2010, 6, 397-398.	11.1	7
49	An efficient method for generation of bi-allelic null mutant mouse embryonic stem cells and its application for investigating epigenetic modifiers. Nucleic Acids Research, 2017, 45, e174-e174.	14.5	7
50	The PinkThing for analysing ChIP profiling data in their genomic context. BMC Research Notes, 2013, 6, 133.	1.4	4
51	A plug and play microfluidic platform for standardized sensitive low-input chromatin immunoprecipitation. Genome Research, 2021, 31, 919-933.	5.5	4
52	Virus-Host Interactions of White Spot Syndrome Virus. Molecular Aspects of Fish and Marine Biology, 2004, , 237-255.	0.2	4
53	PRC1 Prevents Replication Stress during Chondrogenic Transit Amplification. Epigenomes, 2017, 1, 22.	1.8	0
54	Overcoming epigenetic roadblocks. Nature Chemical Biology, 2021, 17, 6-7.	8.0	0

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55	PRC1 uncomplexed. Stem Cell Reports, 2022, 17, 1009-1011.	4.8	0