

Hendrik Marks

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

5,074
citations

201385

27
h-index

168136

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.	13.5	774
2	Quantitative Interaction Proteomics and Genome-wide Profiling of Epigenetic Histone Marks and Their Readers. <i>Cell</i> , 2010, 142, 967-980.	13.5	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.	5.2	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.	2.4	344
5	Tracking the embryonic stem cell transition from ground state pluripotency. <i>Development (Cambridge)</i> , 2017, 144, 1221-1234.	1.2	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.	1.2	225
7	A role for cohesin in T-cell-receptor rearrangement and thymocyte differentiation. <i>Nature</i> , 2011, 476, 467-471.	13.7	217
8	Epigenetic Regulation of Learning and Memory by Drosophila EHMT/G9a. <i>PLoS Biology</i> , 2011, 9, e1000569.	2.6	185
9	The Complexity of PRC2 Subcomplexes. <i>Trends in Cell Biology</i> , 2019, 29, 660-671.	3.6	178
10	MTF2 recruits Polycomb Repressive Complex 2 by helical-shape-selective DNA binding. <i>Nature Genetics</i> , 2018, 50, 1002-1010.	9.4	147
11	High-resolution analysis of epigenetic changes associated with X inactivation. <i>Genome Research</i> , 2009, 19, 1361-1373.	2.4	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.	2.9	117
13	Dynamics of gene silencing during X inactivation using allele-specific RNA-seq. <i>Genome Biology</i> , 2015, 16, 149.	3.8	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.	1.1	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.	4.6	91
16	Integrative Proteomic Profiling Reveals PRC2-Dependent Epigenetic Crosstalk Maintains Ground-State Pluripotency. <i>Cell Stem Cell</i> , 2019, 24, 123-137.e8.	5.2	90
17	Genetic variation among isolates of White spot syndrome virus. <i>Archives of Virology</i> , 2004, 149, 673-697.	0.9	82
18	Fitness and virulence of an ancestral White Spot Syndrome Virus isolate from shrimp. <i>Virus Research</i> , 2005, 110, 9-20.	1.1	70

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19	Genome-wide epigenomic profiling for biomarker discovery. <i>Clinical Epigenetics</i> , 2016, 8, 122.	1.8	67
20	Molecular epidemiology of white spot syndrome virus within Vietnam. <i>Journal of General Virology</i> , 2004, 85, 3607-3618.	1.3	66
21	Gene-expression profiling of White spot syndrome virus in vivo. <i>Journal of General Virology</i> , 2005, 86, 2081-2100.	1.3	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.	1.4	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.	4.6	55
24	STARR-seq identifies active, chromatin-masked, and dormant enhancers in pluripotent mouse embryonic stem cells. <i>Genome Biology</i> , 2020, 21, 243.	3.8	48
25	Transcriptional analysis of the white spot syndrome virus major virion protein genes. <i>Journal of General Virology</i> , 2003, 84, 1517-1523.	1.3	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.	0.9	33
27	Mammalian embryo comparison identifies novel pluripotency genes associated with the naïve or primed state. <i>Biology Open</i> , 2018, 7, .	0.6	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.	1.1	31
29	Promoter analysis of the Chilo iridescent virus DNA polymerase and major capsid protein genes. <i>Virology</i> , 2003, 317, 321-329.	1.1	30
30	Integrated multi-omics reveal polycomb repressive complex 2 restricts human trophoblast induction. <i>Nature Cell Biology</i> , 2022, 24, 858-871.	4.6	30
31	Miniaturised interaction proteomics on a microfluidic platform with ultra-low input requirements. <i>Nature Communications</i> , 2019, 10, 1525.	5.8	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.	0.3	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.	5.8	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.	1.3	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.	2.3	22
36	Two Functional Axes of Feedback-Enforced PRC2 Recruitment in Mouse Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2020, 15, 1287-1300.	2.3	19

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37	In silico identification of putative promoter motifs of White Spot Syndrome Virus. <i>BMC Bioinformatics</i> , 2006, 7, 309.	1.2	17
38	Human branching cholangiocyte organoids recapitulate functional bile duct formation. <i>Cell Stem Cell</i> , 2022, 29, 776-794.e13.	5.2	17
39	A Mass Spectrometry Survey of Chromatin-Associated Proteins in Pluripotency and Early Lineage Commitment. <i>Proteomics</i> , 2019, 19, 1900047.	1.3	16
40	There is another: H3K27me3-mediated genomic imprinting. <i>Trends in Genetics</i> , 2022, 38, 82-96.	2.9	16
41	Intracellular distribution of cowpea mosaic virus movement protein as visualised by green fluorescent protein fusions. <i>Archives of Virology</i> , 2003, 148, 2099-2114.	0.9	14
42	Untargeted histone profiling during naive conversion uncovers conserved modification markers between mouse and human. <i>Scientific Reports</i> , 2019, 9, 17240.	1.6	14
43	Cholangiocyte organoids from human bile retain a local phenotype and can repopulate bile ducts in vitro. <i>Clinical and Translational Medicine</i> , 2021, 11, e566.	1.7	12
44	Allele-specific RNA-seq expression profiling of imprinted genes in mouse isogenic pluripotent states. <i>Epigenetics and Chromatin</i> , 2019, 12, 14.	1.8	11
45	Quantitative subcellular proteomics using SILAC reveals enhanced metabolic buffering in the pluripotent ground state. <i>Stem Cell Research</i> , 2018, 33, 135-145.	0.3	8
46	Terminal keratinocyte differentiation in vitro is associated with a stable DNA methylome. <i>Experimental Dermatology</i> , 2021, 30, 1023-1032.	1.4	8
47	Developments in pluripotency: a new formative state. <i>Cell Research</i> , 2021, 31, 493-494.	5.7	8
48	Insightful Tales from Single Embryonic Cells. <i>Cell Stem Cell</i> , 2010, 6, 397-398.	5.2	7
49	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.	6.5	7
50	The PinkThing for analysing ChIP profiling data in their genomic context. <i>BMC Research Notes</i> , 2013, 6, 133.	0.6	4
51	A plug and play microfluidic platform for standardized sensitive low-input chromatin immunoprecipitation. <i>Genome Research</i> , 2021, 31, 919-933.	2.4	4
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	PRC1 Prevents Replication Stress during Chondrogenic Transit Amplification. <i>Epigenomes</i> , 2017, 1, 22.	0.8	0
54	Overcoming epigenetic roadblocks. <i>Nature Chemical Biology</i> , 2021, 17, 6-7.	3.9	0

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55	PRC1 uncomplexed. Stem Cell Reports, 2022, 17, 1009-1011.	2.3	0