

# Holger Heyn

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

83  
papers

9,190  
citations

44  
h-index

95  
g-index

95  
ext. papers

11,711  
ext. citations

14.9  
avg, IF

6.03  
L-index

#	Paper	IF	Citations
83	Global epigenomic reconfiguration during mammalian brain development. <i>Science</i> , <b>2013</b> , 341, 1237905	33.3	1283
82	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , <b>2016</b> , 166, 740-754	56.2	892
81	Validation of a DNA methylation microarray for 450,000 CpG sites in the human genome. <i>Epigenetics</i> , <b>2011</b> , 6, 692-702	5.7	767
80	Comparative Analysis of Single-Cell RNA Sequencing Methods. <i>Molecular Cell</i> , <b>2017</b> , 65, 631-643.e4	17.6	761
79	DNA methylation profiling in the clinic: applications and challenges. <i>Nature Reviews Genetics</i> , <b>2012</b> , 13, 679-92	30.1	579
78	Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 10522-7	11.5	563
77	DNA methylation contributes to natural human variation. <i>Genome Research</i> , <b>2013</b> , 23, 1363-72	9.7	272
76	Epigenetic profiling to classify cancer of unknown primary: a multicentre, retrospective analysis. <i>Lancet Oncology</i> , <b>2016</b> , 17, 1386-1395	21.7	251
75	A prognostic DNA methylation signature for stage I non-small-cell lung cancer. <i>Journal of Clinical Oncology</i> , <b>2013</b> , 31, 4140-7	2.2	210
74	Mutations in neutrophil elastase causing congenital neutropenia lead to cytoplasmic protein accumulation and induction of the unfolded protein response. <i>Blood</i> , <b>2006</b> , 108, 493-500	2.2	166
73	DNA methylation map of human atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , <b>2014</b> , 7, 692-700		157
72	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 747-755	44.5	142
71	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , <b>2016</b> , 17, 11	18.3	141
70	An Adenine Code for DNA: A Second Life for N6-Methyladenine. <i>Cell</i> , <b>2015</b> , 161, 710-3	56.2	117
69	DNA methylation profiling in breast cancer discordant identical twins identifies DOK7 as novel epigenetic biomarker. <i>Carcinogenesis</i> , <b>2013</b> , 34, 102-8	4.6	117
68	Epigenetic inactivation of the p53-induced long noncoding RNA TP53 target 1 in human cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E7535-E7544	11.5	106
67	Mex3a Marks a Slowly Dividing Subpopulation of Lgr5+ Intestinal Stem Cells. <i>Cell Stem Cell</i> , <b>2017</b> , 20, 801-816.e7	18	101

66	Single-cell transcriptome conservation in cryopreserved cells and tissues. <i>Genome Biology</i> , <b>2017</b> , 18, 45	18.3	101
65	Human DNA methylomes of neurodegenerative diseases show common epigenomic patterns. <i>Translational Psychiatry</i> , <b>2016</b> , 6, e718	8.6	101
64	RANKL/RANK control Brca1 mutation-. <i>Cell Research</i> , <b>2016</b> , 26, 761-74	24.7	96
63	MicroRNA miR-335 is crucial for the BRCA1 regulatory cascade in breast cancer development. <i>International Journal of Cancer</i> , <b>2011</b> , 129, 2797-806	7.5	95
62	Dynamics of DNA methylation in recent human and great ape evolution. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003763		92
61	Identity Noise and Adipogenic Traits Characterize Dermal Fibroblast Aging. <i>Cell</i> , <b>2018</b> , 175, 1575-1590.e23	26.2	91
60	Epigenetic inactivation of the putative DNA/RNA helicase SLFN11 in human cancer confers resistance to platinum drugs. <i>Oncotarget</i> , <b>2016</b> , 7, 3084-97	3.3	88
59	Tutorial: guidelines for the experimental design of single-cell RNA sequencing studies. <i>Nature Protocols</i> , <b>2018</b> , 13, 2742-2757	18.8	87
58	Aberrant DNA methylation profiles in the premature aging disorders Hutchinson-Gilford Progeria and Werner syndrome. <i>Epigenetics</i> , <b>2013</b> , 8, 28-33	5.7	84
57	A DERL3-associated defect in the degradation of SLC2A1 mediates the Warburg effect. <i>Nature Communications</i> , <b>2014</b> , 5, 3608	17.4	77
56	Single-cell transcriptomics unveils gene regulatory network plasticity. <i>Genome Biology</i> , <b>2019</b> , 20, 110	18.3	75
55	Epigenetic activation of a cryptic TBC1D16 transcript enhances melanoma progression by targeting EGFR. <i>Nature Medicine</i> , <b>2015</b> , 21, 741-50	50.5	75
54	Promoter hypermethylation of the phosphatase DUSP22 mediates PKA-dependent TAU phosphorylation and CREB activation in Alzheimer's disease. <i>Hippocampus</i> , <b>2014</b> , 24, 363-8	3.5	75
53	SPOTlight: seeded NMF regression to deconvolute spatial transcriptomics spots with single-cell transcriptomes. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, e50	20.1	75
52	The DNA methylation drift of the atherosclerotic aorta increases with lesion progression. <i>BMC Medical Genomics</i> , <b>2015</b> , 8, 7	3.7	73
51	Epigenetic loss of the PIWI/piRNA machinery in human testicular tumorigenesis. <i>Epigenetics</i> , <b>2014</b> , 9, 113-8	5.7	73
50	Epigenetic disruption of the PIWI pathway in human spermatogenic disorders. <i>PLoS ONE</i> , <b>2012</b> , 7, e47893	3.7	73
49	Novel insights into DNA methylation features in spermatozoa: stability and peculiarities. <i>PLoS ONE</i> , <b>2012</b> , 7, e44479	3.7	65

48	Linkage of DNA methylation quantitative trait loci to human cancer risk. <i>Cell Reports</i> , <b>2014</b> , 7, 331-338	10.6	60
47	Impaired DICER1 function promotes stemness and metastasis in colon cancer. <i>Oncogene</i> , <b>2014</b> , 33, 4003-45	15	60
46	Whole-genome bisulfite DNA sequencing of a DNMT3B mutant patient. <i>Epigenetics</i> , <b>2012</b> , 7, 542-50	5.7	59
45	Robustness and applicability of transcription factor and pathway analysis tools on single-cell RNA-seq data. <i>Genome Biology</i> , <b>2020</b> , 21, 36	18.3	57
44	A comprehensive DNA methylation profile of epithelial-to-mesenchymal transition. <i>Cancer Research</i> , <b>2014</b> , 74, 5608-19	10.1	54
43	The interplay between DNA methylation and sequence divergence in recent human evolution. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 8204-14	20.1	51
42	KAT6B Is a Tumor Suppressor Histone H3 Lysine 23 Acetyltransferase Undergoing Genomic Loss in Small Cell Lung Cancer. <i>Cancer Research</i> , <b>2015</b> , 75, 3936-45	10.1	48
41	bigSCale: an analytical framework for big-scale single-cell data. <i>Genome Research</i> , <b>2018</b> , 28, 878-890	9.7	45
40	CpG island hypermethylation-associated silencing of small nucleolar RNAs in human cancer. <i>RNA Biology</i> , <b>2012</b> , 9, 881-90	4.8	45
39	DNMT3A mutations mediate the epigenetic reactivation of the leukemogenic factor MEIS1 in acute myeloid leukemia. <i>Oncogene</i> , <b>2016</b> , 35, 3079-82	9.2	41
38	PM20D1 is a quantitative trait locus associated with Alzheimer's disease. <i>Nature Medicine</i> , <b>2018</b> , 24, 598-603	5.3	38
37	The NCI-60 Methylome and Its Integration into CellMiner. <i>Cancer Research</i> , <b>2017</b> , 77, 601-612	10.1	34
36	TRIM28 and Interacting KRAB-ZNFs Control Self-Renewal of Human Pluripotent Stem Cells through Epigenetic Repression of Pro-differentiation Genes. <i>Stem Cell Reports</i> , <b>2017</b> , 9, 2065-2080	8	34
35	Epigenetic profiling joins personalized cancer medicine. <i>Expert Review of Molecular Diagnostics</i> , <b>2013</b> , 13, 473-9	3.8	30
34	DNA methylation dynamics in human carotid plaques after cerebrovascular events. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2015</b> , 35, 1835-42	9.4	28
33	Genome-wide DNA methylation profiling predicts relapse in childhood B-cell acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , <b>2013</b> , 160, 406-9	4.5	28
32	Dietary palmitic acid promotes a prometastatic memory via Schwann cells. <i>Nature</i> , <b>2021</b> , 599, 485-490	50.4	27
31	Assessing associations between the AURKA-HMMR-TPX2-TUBG1 functional module and breast cancer risk in BRCA1/2 mutation carriers. <i>PLoS ONE</i> , <b>2015</b> , 10, e0120020	3.7	26

30	Sampling time-dependent artifacts in single-cell genomics studies. <i>Genome Biology</i> , <b>2020</b> , 21, 112	18.3	25
29	A symbiotic liaison between the genetic and epigenetic code. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 113	4.5	20
28	MicroRNA miR-548d is a superior regulator in pancreatic cancer. <i>Pancreas</i> , <b>2012</b> , 41, 218-21	2.6	19
27	Single cell RNA-seq identifies the origins of heterogeneity in efficient cell transdifferentiation and reprogramming. <i>ELife</i> , <b>2019</b> , 8,	8.9	19
26	Copy number rather than epigenetic alterations are the major dictator of imprinted methylation in tumors. <i>Nature Communications</i> , <b>2017</b> , 8, 467	17.4	18
25	Immune cell profiling of the cerebrospinal fluid enables the characterization of the brain metastasis microenvironment. <i>Nature Communications</i> , <b>2021</b> , 12, 1503	17.4	18
24	SPOTlight: Seeded NMF regression to Deconvolute Spatial Transcriptomics Spots with Single-Cell Transcriptomes		17
23	Modeling Human TBX5 Haploinsufficiency Predicts Regulatory Networks for Congenital Heart Disease. <i>Developmental Cell</i> , <b>2021</b> , 56, 292-309.e9	10.2	17
22	Metformin pharmacogenomics: a genome-wide association study to identify genetic and epigenetic biomarkers involved in metformin anticancer response using human lymphoblastoid cell lines. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 4819-4834	5.6	16
21	EZH2: an epigenetic gatekeeper promoting lymphomagenesis. <i>Cancer Cell</i> , <b>2013</b> , 23, 563-5	24.3	15
20	Benchmarking Single-Cell RNA Sequencing Protocols for Cell Atlas Projects		13
19	Building a high-quality Human Cell Atlas. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 149-153	44.5	13
18	GATA2 Promotes Hematopoietic Development and Represses Cardiac Differentiation of Human Mesoderm. <i>Stem Cell Reports</i> , <b>2019</b> , 13, 515-529	8	12
17	Whole genome grey and white matter DNA methylation profiles in dorsolateral prefrontal cortex. <i>Synapse</i> , <b>2017</b> , 71, e21959	2.4	10
16	The Polycomb-associated factor PHF19 controls hematopoietic stem cell state and differentiation. <i>Science Advances</i> , <b>2020</b> , 6, eabb2745	14.3	10
15	Single human oocyte transcriptome analysis reveals distinct maturation stage-dependent pathways impacted by age. <i>Aging Cell</i> , <b>2021</b> , 20, e13360	9.9	9
14	The order and logic of CD4 versus CD8 lineage choice and differentiation in mouse thymus. <i>Nature Communications</i> , <b>2021</b> , 12, 99	17.4	9
13	A Single-Cell Tumor Immune Atlas for Precision Oncology		7

12	A single-cell tumor immune atlas for precision oncology. <i>Genome Research</i> , <b>2021</b> , 31, 1913-1926	9.7	7
11	bigScale: An Analytical Framework for Big-Scale Single-Cell Data		6
10	Quantitative Trait Loci Identify Functional Noncoding Variation in Cancer. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1005826	5.8	5
9	Cancer network activity associated with therapeutic response and synergism. <i>Genome Medicine</i> , <b>2016</b> , 8, 88	14.4	5
8	SARS-CoV-2 interaction with Siglec-1 mediates trans-infection by dendritic cells. <i>Cellular and Molecular Immunology</i> , <b>2021</b> , 18, 2676-2678	15.4	3
7	Sampling artifacts in single-cell genomics cohort studies		2
6	Use of patient derived orthotopic xenograft models for real-time therapy guidance in a pediatric sporadic malignant peripheral nerve sheath tumor. <i>Therapeutic Advances in Medical Oncology</i> , <b>2020</b> , 12, 1758835920929579	5.4	2
5	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses.. <i>Nature Communications</i> , <b>2022</b> , 13, 1779	17.4	2
4	Personalized Therapy Epigenetic Profiling as Predictors of Prognosis and Response <b>2015</b> , 677-698		1
3	Single-Cell Transcriptomics Unveils Gene Regulatory Network Plasticity		1
2	The Role of the Genetic Code in the DNA Methylation Landscape Formation <b>2016</b> , 1-18		0
1	Modeling iPSC-derived human neurofibroma-like tumors in mice uncovers the heterogeneity of Schwann cells within plexiform neurofibromas.. <i>Cell Reports</i> , <b>2022</b> , 38, 110385	10.6	0