Holger Heyn

List of Publications by Year in Descending Order

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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	9,190	44	95
papers	citations	h-index	g-index
95	11,711	14.9	6.03
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
83	Modeling iPSC-derived human neurofibroma-like tumors in mice uncovers the heterogeneity of Schwann cells within plexiform neurofibromas.. *Cell Reports*, **2022**, 38, 110385	10.6	0
82	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses.. *Nature Communications*, **2022**, 13, 1779	17.4	2
81	Dietary palmitic acid promotes a prometastatic memory via Schwann cells. *Nature*, **2021**, 599, 485-490	50.4	27
80	SARS-CoV-2 interaction with Siglec-1 mediates trans-infection by dendritic cells. *Cellular and Molecular Immunology*, **2021**, 18, 2676-2678	15.4	3
79	Immune cell profiling of the cerebrospinal fluid enables the characterization of the brain metastasis microenvironment. *Nature Communications*, **2021**, 12, 1503	17.4	18
78	Single human oocyte transcriptome analysis reveals distinct maturation stage-dependent pathways impacted by age. *Aging Cell*, **2021**, 20, e13360	9.9	9
77	Modeling Human TBX5 Haploinsufficiency Predicts Regulatory Networks for Congenital Heart Disease. *Developmental Cell*, **2021**, 56, 292-309.e9	10.2	17
76	Building a high-quality Human Cell Atlas. *Nature Biotechnology*, **2021**, 39, 149-153	44.5	13
75	The order and logic of CD4 versus CD8 lineage choice and differentiation in mouse thymus. *Nature Communications*, **2021**, 12, 99	17.4	9
74	SPOTlight: seeded NMF regression to deconvolute spatial transcriptomics spots with single-cell transcriptomes. *Nucleic Acids Research*, **2021**, 49, e50	20.1	75
73	A single-cell tumor immune atlas for precision oncology. *Genome Research*, **2021**, 31, 1913-1926	9.7	7
72	Sampling time-dependent artifacts in single-cell genomics studies. *Genome Biology*, **2020**, 21, 112	18.3	25
71	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. *Nature Biotechnology*, **2020**, 38, 747-755	44.5	142
70	Robustness and applicability of transcription factor and pathway analysis tools on single-cell RNA-seq data. *Genome Biology*, **2020**, 21, 36	18.3	57
69	Use of patient derived orthotopic xenograft models for real-time therapy guidance in a pediatric sporadic malignant peripheral nerve sheath tumor. *Therapeutic Advances in Medical Oncology*, **2020**, 12, 1758835920929579	5.4	2
68	The Polycomb-associated factor PHF19 controls hematopoietic stem cell state and differentiation. *Science Advances*, **2020**, 6, eabb2745	14.3	10
67	Single-cell transcriptomics unveils gene regulatory network plasticity. *Genome Biology*, **2019**, 20, 110	18.3	75

66	GATA2 Promotes Hematopoietic Development and Represses Cardiac Differentiation of Human Mesoderm. *Stem Cell Reports*, **2019**, 13, 515-529	8	12
65	Single cell RNA-seq identifies the origins of heterogeneity in efficient cell transdifferentiation and reprogramming. *ELife*, **2019**, 8,	8.9	19
64	bigSCale: an analytical framework for big-scale single-cell data. *Genome Research*, **2018**, 28, 878-890	9.7	45
63	PM20D1 is a quantitative trait locus associated with Alzheimer's disease. *Nature Medicine*, **2018**, 24, 598-603	50.5	38
62	Tutorial: guidelines for the experimental design of single-cell RNA sequencing studies. *Nature Protocols*, **2018**, 13, 2742-2757	18.8	87
61	Identity Noise and Adipogenic Traits Characterize Dermal Fibroblast Aging. *Cell*, **2018**, 175, 1575-1590.e22	56.2	91
60	Whole genome grey and white matter DNA methylation profiles in dorsolateral prefrontal cortex. *Synapse*, **2017**, 71, e21959	2.4	10
59	Comparative Analysis of Single-Cell RNA Sequencing Methods. *Molecular Cell*, **2017**, 65, 631-643.e4	17.6	761
58	Mex3a Marks a Slowly Dividing Subpopulation of Lgr5+ Intestinal Stem Cells. *Cell Stem Cell*, **2017**, 20, 801-816.e7	18	101
57	Single-cell transcriptome conservation in cryopreserved cells and tissues. *Genome Biology*, **2017**, 18, 45	18.3	101
56	The NCI-60 Methylome and Its Integration into CellMiner. *Cancer Research*, **2017**, 77, 601-612	10.1	34
55	Copy number rather than epigenetic alterations are the major dictator of imprinted methylation in tumors. *Nature Communications*, **2017**, 8, 467	17.4	18
54	TRIM28 and Interacting KRAB-ZNFs Control Self-Renewal of Human Pluripotent Stem Cells through Epigenetic Repression of Pro-differentiation Genes. *Stem Cell Reports*, **2017**, 9, 2065-2080	8	34
53	DNMT3A mutations mediate the epigenetic reactivation of the leukemogenic factor MEIS1 in acute myeloid leukemia. *Oncogene*, **2016**, 35, 3079-82	9.2	41
52	Epigenetic profiling to classify cancer of unknown primary: a multicentre, retrospective analysis. *Lancet Oncology, The*, **2016**, 17, 1386-1395	21.7	251
51	Metformin pharmacogenomics: a genome-wide association study to identify genetic and epigenetic biomarkers involved in metformin anticancer response using human lymphoblastoid cell lines. *Human Molecular Genetics*, **2016**, 25, 4819-4834	5.6	16
50	Epigenetic inactivation of the p53-induced long noncoding RNA TP53 target 1 in human cancer. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E7535-E7544	11.5	106
49	RANKL/RANK control Brca1 mutation-. *Cell Research*, **2016**, 26, 761-74	24.7	96

48	Human DNA methylomes of neurodegenerative diseases show common epigenomic patterns. *Translational Psychiatry*, **2016**, 6, e718	8.6	101
47	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. *Genome Biology*, **2016**, 17, 11	18.3	141
46	The Role of the Genetic Code in the DNA Methylation Landscape Formation **2016**, 1-18		0
45	Epigenetic inactivation of the putative DNA/RNA helicase SLFN11 in human cancer confers resistance to platinum drugs. *Oncotarget*, **2016**, 7, 3084-97	3.3	88
44	Quantitative Trait Loci Identify Functional Noncoding Variation in Cancer. *PLoS Genetics*, **2016**, 12, e1005826	6	5
43	A Landscape of Pharmacogenomic Interactions in Cancer. *Cell*, **2016**, 166, 740-754	56.2	892
42	Cancer network activity associated with therapeutic response and synergism. *Genome Medicine*, **2016**, 8, 88	14.4	5
41	Personalized TherapyEpigenetic Profiling as Predictors of Prognosis and Response **2015**, 677-698		1
40	DNA methylation dynamics in human carotid plaques after cerebrovascular events. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 1835-42	9.4	28
39	An Adenine Code for DNA: A Second Life for N6-Methyladenine. *Cell*, **2015**, 161, 710-3	56.2	117
38	The DNA methylation drift of the atherosclerotic aorta increases with lesion progression. *BMC Medical Genomics*, **2015**, 8, 7	3.7	73
37	The interplay between DNA methylation and sequence divergence in recent human evolution. *Nucleic Acids Research*, **2015**, 43, 8204-14	20.1	51
36	KAT6B Is a Tumor Suppressor Histone H3 Lysine 23 Acetyltransferase Undergoing Genomic Loss in Small Cell Lung Cancer. *Cancer Research*, **2015**, 75, 3936-45	10.1	48
35	Assessing associations between the AURKA-HMMR-TPX2-TUBG1 functional module and breast cancer risk in BRCA1/2 mutation carriers. *PLoS ONE*, **2015**, 10, e0120020	3.7	26
34	Epigenetic activation of a cryptic TBC1D16 transcript enhances melanoma progression by targeting EGFR. *Nature Medicine*, **2015**, 21, 741-50	50.5	75
33	DNA methylation map of human atherosclerosis. *Circulation: Cardiovascular Genetics*, **2014**, 7, 692-700		157
32	Linkage of DNA methylation quantitative trait loci to human cancer risk. *Cell Reports*, **2014**, 7, 331-338	10.6	60
31	A comprehensive DNA methylation profile of epithelial-to-mesenchymal transition. *Cancer Research* , **2014**, 74, 5608-19	10.1	54

30	A DERL3-associated defect in the degradation of SLC2A1 mediates the Warburg effect. *Nature Communications*, **2014**, 5, 3608	17.4	77
29	Epigenetic loss of the PIWI/piRNA machinery in human testicular tumorigenesis. *Epigenetics*, **2014**, 9, 113-8	5.7	73
28	Impaired DICER1 function promotes stemness and metastasis in colon cancer. *Oncogene*, **2014**, 33, 4003-15	9.2	60
27	A symbiotic liaison between the genetic and epigenetic code. *Frontiers in Genetics*, **2014**, 5, 113	4.5	20
26	Promoter hypermethylation of the phosphatase DUSP22 mediates PKA-dependent TAU phosphorylation and CREB activation in Alzheimer's disease. *Hippocampus*, **2014**, 24, 363-8	3.5	75
25	A prognostic DNA methylation signature for stage I non-small-cell lung cancer. *Journal of Clinical Oncology*, **2013**, 31, 4140-7	2.2	210
24	Global epigenomic reconfiguration during mammalian brain development. *Science*, **2013**, 341, 1237905	33.3	1283
23	Genome-wide DNA methylation profiling predicts relapse in childhood B-cell acute lymphoblastic leukaemia. *British Journal of Haematology*, **2013**, 160, 406-9	4.5	28
22	Epigenetic profiling joins personalized cancer medicine. *Expert Review of Molecular Diagnostics*, **2013**, 13, 473-9	3.8	30
21	EZH2: an epigenetic gatekeeper promoting lymphomagenesis. *Cancer Cell*, **2013**, 23, 563-5	24.3	15
20	Dynamics of DNA methylation in recent human and great ape evolution. *PLoS Genetics*, **2013**, 9, e1003763	6	92
19	Aberrant DNA methylation profiles in the premature aging disorders Hutchinson-Gilford Progeria and Werner syndrome. *Epigenetics*, **2013**, 8, 28-33	5.7	84
18	DNA methylation contributes to natural human variation. *Genome Research*, **2013**, 23, 1363-72	9.7	272
17	DNA methylation profiling in breast cancer discordant identical twins identifies DOK7 as novel epigenetic biomarker. *Carcinogenesis*, **2013**, 34, 102-8	4.6	117
16	DNA methylation profiling in the clinic: applications and challenges. *Nature Reviews Genetics*, **2012**, 13, 679-92	30.1	579
15	Distinct DNA methylomes of newborns and centenarians. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 10522-7	11.5	563
14	CpG island hypermethylation-associated silencing of small nucleolar RNAs in human cancer. *RNA Biology*, **2012**, 9, 881-90	4.8	45
13	Whole-genome bisulfite DNA sequencing of a DNMT3B mutant patient. *Epigenetics*, **2012**, 7, 542-50	5.7	59

12	MicroRNA miR-548d is a superior regulator in pancreatic cancer. *Pancreas*, **2012**, 41, 218-21	2.6	19
11	Novel insights into DNA methylation features in spermatozoa: stability and peculiarities. *PLoS ONE*, **2012**, 7, e44479	3.7	65
10	Epigenetic disruption of the PIWI pathway in human spermatogenic disorders. *PLoS ONE*, **2012**, 7, e47892	3.7	73
9	MicroRNA miR-335 is crucial for the BRCA1 regulatory cascade in breast cancer development. *International Journal of Cancer*, **2011**, 129, 2797-806	7.5	95
8	Validation of a DNA methylation microarray for 450,000 CpG sites in the human genome. *Epigenetics*, **2011**, 6, 692-702	5.7	767
7	Mutations in neutrophil elastase causing congenital neutropenia lead to cytoplasmic protein accumulation and induction of the unfolded protein response. *Blood*, **2006**, 108, 493-500	2.2	166
6	bigSCale: An Analytical Framework for Big-Scale Single-Cell Data		6
5	Sampling artifacts in single-cell genomics cohort studies		2
4	SPOTlight: Seeded NMF regression to Deconvolute Spatial Transcriptomics Spots with Single-Cell Transcriptomes		17
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1	Benchmarking Single-Cell RNA Sequencing Protocols for Cell Atlas Projects		13