

Holger Heyn

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3964261/publications.pdf>

Version: 2024-02-01

80
papers

13,351
citations

44069

48
h-index

66911

78
g-index

95
all docs

95
docs citations

95
times ranked

24208
citing authors

#	ARTICLE	IF	CITATIONS
1	Modeling iPSC-derived human neurofibroma-like tumors in mice uncovers the heterogeneity of Schwann cells within plexiform neurofibromas. <i>Cell Reports</i> , 2022, 38, 110385.	6.4	19
2	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses. <i>Nature Communications</i> , 2022, 13, 1779.	12.8	25
3	Controlled X-chromosome dynamics defines meiotic potential of female mouse <i>in vitro</i> germ cells. <i>EMBO Journal</i> , 2022, 41, .	7.8	13
4	ATM germline variants in a young adult with chronic lymphocytic leukemia: 8% years of genomic evolution. <i>Blood Cancer Journal</i> , 2022, 12, .	6.2	2
5	Mex3a marks drug-tolerant persister colorectal cancer cells that mediate relapse after chemotherapy. <i>Nature Cancer</i> , 2022, 3, 1052-1070.	13.2	36
6	Modeling Human TBX5 Haploinsufficiency Predicts Regulatory Networks for Congenital Heart Disease. <i>Developmental Cell</i> , 2021, 56, 292-309.e9.	7.0	63
7	Building a high-quality Human Cell Atlas. <i>Nature Biotechnology</i> , 2021, 39, 149-153.	17.5	48
8	The order and logic of CD4 versus CD8 lineage choice and differentiation in mouse thymus. <i>Nature Communications</i> , 2021, 12, 99.	12.8	21
9	SPOTlight: seeded NMF regression to deconvolute spatial transcriptomics spots with single-cell transcriptomes. <i>Nucleic Acids Research</i> , 2021, 49, e50-e50.	14.5	338
10	Immune cell profiling of the cerebrospinal fluid enables the characterization of the brain metastasis microenvironment. <i>Nature Communications</i> , 2021, 12, 1503.	12.8	45
11	Single human oocyte transcriptome analysis reveals distinct maturation stage-dependent pathways impacted by age. <i>Aging Cell</i> , 2021, 20, e13360.	6.7	43
12	A single-cell tumor immune atlas for precision oncology. <i>Genome Research</i> , 2021, 31, 1913-1926.	5.5	87
13	Dietary palmitic acid promotes a prometastatic memory via Schwann cells. <i>Nature</i> , 2021, 599, 485-490.	27.8	126
14	SARS-CoV-2 interaction with Siglec-1 mediates trans-infection by dendritic cells. <i>Cellular and Molecular Immunology</i> , 2021, 18, 2676-2678.	10.5	36
15	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> , 2020, 12, 175883592092957.	3.2	5
16	The Polycomb-associated factor PHF19 controls hematopoietic stem cell state and differentiation. <i>Science Advances</i> , 2020, 6, eabb2745.	10.3	20
17	Sampling time-dependent artifacts in single-cell genomics studies. <i>Genome Biology</i> , 2020, 21, 112.	8.8	55
18	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , 2020, 38, 747-755.	17.5	313

#	ARTICLE	IF	CITATIONS
19	Robustness and applicability of transcription factor and pathway analysis tools on single-cell RNA-seq data. <i>Genome Biology</i> , 2020, 21, 36.	8.8	216
20	GATA2 Promotes Hematopoietic Development and Represses Cardiac Differentiation of Human Mesoderm. <i>Stem Cell Reports</i> , 2019, 13, 515-529.	4.8	27
21	Single-cell transcriptomics unveils gene regulatory network plasticity. <i>Genome Biology</i> , 2019, 20, 110.	8.8	170
22	Single cell RNA-seq identifies the origins of heterogeneity in efficient cell transdifferentiation and reprogramming. <i>ELife</i> , 2019, 8, .	6.0	44
23	bigSCale: an analytical framework for big-scale single-cell data. <i>Genome Research</i> , 2018, 28, 878-890.	5.5	76
24	Tutorial: guidelines for the experimental design of single-cell RNA sequencing studies. <i>Nature Protocols</i> , 2018, 13, 2742-2757.	12.0	153
25	Identity Noise and Adipogenic Traits Characterize Dermal Fibroblast Aging. <i>Cell</i> , 2018, 175, 1575-1590.e22.	28.9	168
26	PM20D1 is a quantitative trait locus associated with Alzheimer's disease. <i>Nature Medicine</i> , 2018, 24, 598-603.	30.7	73
27	Whole genome grey and white matter DNA methylation profiles in dorsolateral prefrontal cortex. <i>Synapse</i> , 2017, 71, e21959.	1.2	13
28	Comparative Analysis of Single-Cell RNA Sequencing Methods. <i>Molecular Cell</i> , 2017, 65, 631-643.e4.	9.7	1,131
29	Mex3a Marks a Slowly Dividing Subpopulation of Lgr5+ Intestinal Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 801-816.e7.	11.1	158
30	Single-cell transcriptome conservation in cryopreserved cells and tissues. <i>Genome Biology</i> , 2017, 18, 45.	8.8	134
31	The NCI-60 Methylome and Its Integration into CellMiner. <i>Cancer Research</i> , 2017, 77, 601-612.	0.9	48
32	Copy number rather than epigenetic alterations are the major dictator of imprinted methylation in tumors. <i>Nature Communications</i> , 2017, 8, 467.	12.8	27
33	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> , 2017, 9, 2065-2080.	4.8	62
34	Epigenetic inactivation of the putative DNA/RNA helicase SLFN11 in human cancer confers resistance to platinum drugs. <i>Oncotarget</i> , 2016, 7, 3084-3097.	1.8	120
35	Quantitative Trait Loci Identify Functional Noncoding Variation in Cancer. <i>PLoS Genetics</i> , 2016, 12, e1005826.	3.5	7
36	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016, 166, 740-754.	28.9	1,518

#	ARTICLE	IF	CITATIONS
37	Cancer network activity associated with therapeutic response and synergism. <i>Genome Medicine</i> , 2016, 8, 88.	8.2	7
38	Epigenetic profiling to classify cancer of unknown primary: a multicentre, retrospective analysis. <i>Lancet Oncology</i> , The, 2016, 17, 1386-1395.	10.7	357
39	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> , 2016, 25, ddw301.	2.9	18
40	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> , 2016, 113, E7535-E7544.	7.1	140
41	RANKL/RANK control Brca1 mutation-driven mammary tumors. <i>Cell Research</i> , 2016, 26, 761-774.	12.0	128
42	Human DNA methylomes of neurodegenerative diseases show common epigenomic patterns. <i>Translational Psychiatry</i> , 2016, 6, e718-e718.	4.8	137
43	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , 2016, 17, 11.	8.8	184
44	The Role of the Genetic Code in the DNA Methylation Landscape Formation. , 2016, , 1-18.		1
45	DNMT3A mutations mediate the epigenetic reactivation of the leukemogenic factor MEIS1 in acute myeloid leukemia. <i>Oncogene</i> , 2016, 35, 3079-3082.	5.9	54
46	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. <i>PLoS ONE</i> , 2015, 10, e0120020.	2.5	34
47	Epigenetic activation of a cryptic TBC1D16 transcript enhances melanoma progression by targeting EGFR. <i>Nature Medicine</i> , 2015, 21, 741-750.	30.7	107
48	Personalized Therapyâ€™Epigenetic Profiling as Predictors of Prognosis and Response. , 2015, , 677-698.		1
49	DNA Methylation Dynamics in Human Carotid Plaques After Cerebrovascular Events. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1835-1842.	2.4	34
50	An Adenine Code for DNA: A Second Life for N6-Methyladenine. <i>Cell</i> , 2015, 161, 710-713.	28.9	167
51	The DNA methylation drift of the atherosclerotic aorta increases with lesion progression. <i>BMC Medical Genomics</i> , 2015, 8, 7.	1.5	85
52	The interplay between DNA methylation and sequence divergence in recent human evolution. <i>Nucleic Acids Research</i> , 2015, 43, 8204-8214.	14.5	67
53	KAT6B Is a Tumor Suppressor Histone H3 Lysine 23 Acetyltransferase Undergoing Genomic Loss in Small Cell Lung Cancer. <i>Cancer Research</i> , 2015, 75, 3936-3945.	0.9	65
54	A Comprehensive DNA Methylation Profile of Epithelial-to-Mesenchymal Transition. <i>Cancer Research</i> , 2014, 74, 5608-5619.	0.9	69

#	ARTICLE	IF	CITATIONS
55	A DERL3-associated defect in the degradation of SLC2A1 mediates the Warburg effect. <i>Nature Communications</i> , 2014, 5, 3608.	12.8	94
56	Epigenetic loss of the PIWI/piRNA machinery in human testicular tumorigenesis. <i>Epigenetics</i> , 2014, 9, 113-118.	2.7	87
57	Impaired DICER1 function promotes stemness and metastasis in colon cancer. <i>Oncogene</i> , 2014, 33, 4003-4015.	5.9	78
58	A symbiotic liaison between the genetic and epigenetic code. <i>Frontiers in Genetics</i> , 2014, 5, 113.	2.3	25
59	Promoter hypermethylation of the phosphatase DUSP22 mediates PKA-dependent TAU phosphorylation and CREB activation in Alzheimer's disease. <i>Hippocampus</i> , 2014, 24, 363-368.	1.9	98
60	DNA Methylation Map of Human Atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 692-700.	5.1	207
61	Linkage of DNA Methylation Quantitative Trait Loci to Human Cancer Risk. <i>Cell Reports</i> , 2014, 7, 331-338.	6.4	76
62	A Prognostic DNA Methylation Signature for Stage I Non-Small-Cell Lung Cancer. <i>Journal of Clinical Oncology</i> , 2013, 31, 4140-4147.	1.6	250
63	Global Epigenomic Reconfiguration During Mammalian Brain Development. <i>Science</i> , 2013, 341, 1237905.	12.6	1,609
64	Genome-wide DNA methylation profiling predicts relapse in childhood B-cell acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , 2013, 160, 406-409.	2.5	33
65	Epigenetic profiling joins personalized cancer medicine. <i>Expert Review of Molecular Diagnostics</i> , 2013, 13, 473-479.	3.1	32
66	EZH2: An Epigenetic Gatekeeper Promoting Lymphomagenesis. <i>Cancer Cell</i> , 2013, 23, 563-565.	16.8	15
67	Dynamics of DNA Methylation in Recent Human and Great Ape Evolution. <i>PLoS Genetics</i> , 2013, 9, e1003763.	3.5	118
68	Aberrant DNA methylation profiles in the premature aging disorders Hutchinson-Gilford Progeria and Werner syndrome. <i>Epigenetics</i> , 2013, 8, 28-33.	2.7	95
69	DNA methylation contributes to natural human variation. <i>Genome Research</i> , 2013, 23, 1363-1372.	5.5	353
70	DNA methylation profiling in breast cancer discordant identical twins identifies DOK7 as novel epigenetic biomarker. <i>Carcinogenesis</i> , 2013, 34, 102-108.	2.8	135
71	CpG island hypermethylation-associated silencing of small nucleolar RNAs in human cancer. <i>RNA Biology</i> , 2012, 9, 881-890.	3.1	53
72	Whole-genome bisulfite DNA sequencing of a DNMT3B mutant patient. <i>Epigenetics</i> , 2012, 7, 542-550.	2.7	68

#	ARTICLE	IF	CITATIONS
73	MicroRNA miR-548d Is a Superior Regulator in Pancreatic Cancer. <i>Pancreas</i> , 2012, 41, 218-221.	1.1	24
74	DNA methylation profiling in the clinic: applications and challenges. <i>Nature Reviews Genetics</i> , 2012, 13, 679-692.	16.3	675
75	Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10522-10527.	7.1	687
76	Novel Insights into DNA Methylation Features in Spermatozoa: Stability and Peculiarities. <i>PLoS ONE</i> , 2012, 7, e44479.	2.5	68
77	Epigenetic Disruption of the PIWI Pathway in Human Spermatogenic Disorders. <i>PLoS ONE</i> , 2012, 7, e47892.	2.5	94
78	MicroRNA miR-335 is crucial for the BRCA1 regulatory cascade in breast cancer development. <i>International Journal of Cancer</i> , 2011, 129, 2797-2806.	5.1	112
79	Validation of a DNA methylation microarray for 450,000 CpG sites in the human genome. <i>Epigenetics</i> , 2011, 6, 692-702.	2.7	908
80	Mutations in neutrophil elastase causing congenital neutropenia lead to cytoplasmic protein accumulation and induction of the unfolded protein response. <i>Blood</i> , 2006, 108, 493-500.	1.4	185