

# Andrew Paul Hutchins

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1333409/publications.pdf>

Version: 2024-02-01

66  
papers

3,450  
citations

172386

29  
h-index

155592

55  
g-index

76  
all docs

76  
docs citations

76  
times ranked

6346  
citing authors

#	ARTICLE	IF	CITATIONS
1	CTCF functions as an insulator for somatic genes and a chromatin remodeler for pluripotency genes during reprogramming. <i>Cell Reports</i> , 2022, 39, 110626.	2.9	22
2	Metabolic and epigenetic dysfunctions underlie the arrest of in vitro fertilized human embryos in a senescent-like state. <i>PLoS Biology</i> , 2022, 20, e3001682.	2.6	12
3	The effects of sequencing depth on the assembly of coding and noncoding transcripts in the human genome. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
4	Chromatin and Epigenetic Rearrangements in Embryonic Stem Cell Fate Transitions. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 637309.	1.8	25
5	Identifying transposable element expression dynamics and heterogeneity during development at the single-cell level with a processing pipeline scTE. <i>Nature Communications</i> , 2021, 12, 1456.	5.8	74
6	The chromatin accessibility landscape reveals distinct transcriptional regulation in the induction of human primordial germ cell-like cells from pluripotent stem cells. <i>Stem Cell Reports</i> , 2021, 16, 1245-1261.	2.3	14
7	MIMIC: an optimization method to identify cell type-specific marker panel for cell sorting. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	1
8	Single cells and transposable element heterogeneity in stem cells and development. <i>Cell Regeneration</i> , 2021, 10, 23.	1.1	3
9	Transposable element sequence fragments incorporated into coding and noncoding transcripts modulate the transcriptome of human pluripotent stem cells. <i>Nucleic Acids Research</i> , 2021, 49, 9132-9153.	6.5	19
10	Unified Analysis of Multiple ChIP-Seq Datasets. <i>Methods in Molecular Biology</i> , 2021, 2198, 451-465.	0.4	2
11	JMJD3 acts in tandem with KLF4 to facilitate reprogramming to pluripotency. <i>Nature Communications</i> , 2020, 11, 5061.	5.8	24
12	Î2-Catenin safeguards the ground state of mouse pluripotency by strengthening the robustness of the transcriptional apparatus. <i>Science Advances</i> , 2020, 6, eaba1593.	4.7	10
13	DNA Damage Induces Dynamic Associations of BRD4/P-TEFb With Chromatin and Modulates Gene Transcription in a BRD4-Dependent and -Independent Manner. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 618088.	1.6	5
14	Systematic screening of CTCF binding partners identifies that BHLHE40 regulates CTCF genome-wide distribution and long-range chromatin interactions. <i>Nucleic Acids Research</i> , 2020, 48, 9606-9620.	6.5	30
15	Pluripotency reprogramming by competent and incompetent POU factors uncovers temporal dependency for Oct4 and Sox2. <i>Nature Communications</i> , 2019, 10, 3477.	5.8	60
16	DPre: computational identification of differentiation bias and genes underlying cell type conversions. <i>Bioinformatics</i> , 2019, 36, 1637-1639.	1.8	2
17	Computational Methods for Mapping, Assembly and Quantification for Coding and Non-coding Transcripts. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 628-637.	1.9	25
18	An alternative CTCF isoform antagonizes canonical CTCF occupancy and changes chromatin architecture to promote apoptosis. <i>Nature Communications</i> , 2019, 10, 1535.	5.8	39

#	ARTICLE	IF	CITATIONS
19	Resolving Cell Fate Decisions during Somatic Cell Reprogramming by Single-Cell RNA-Seq. <i>Molecular Cell</i> , 2019, 73, 815-829.e7.	4.5	79
20	Transposable elements are regulated by context-specific patterns of chromatin marks in mouse embryonic stem cells. <i>Nature Communications</i> , 2019, 10, 34.	5.8	104
21	Capturing the interactome of newly transcribed RNA. <i>Nature Methods</i> , 2018, 15, 213-220.	9.0	170
22	NCoR/SMRT co-repressors cooperate with c-MYC to create an epigenetic barrier to somatic cell reprogramming. <i>Nature Cell Biology</i> , 2018, 20, 400-412.	4.6	64
23	PCGF5 is required for neural differentiation of embryonic stem cells. <i>Nature Communications</i> , 2018, 9, 1463.	5.8	60
24	RNA Helicase DDX5 Inhibits Reprogramming to Pluripotency by miRNA-Based Repression of RYBP and its PRC1-Dependent and -Independent Functions. <i>Cell Stem Cell</i> , 2017, 20, 462-477.e6.	5.2	72
25	Generation of Human Liver Chimeric Mice with Hepatocytes from Familial Hypercholesterolemia Induced Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2017, 8, 605-618.	2.3	27
26	A sequential EMT-MET mechanism drives the differentiation of human embryonic stem cells towards hepatocytes. <i>Nature Communications</i> , 2017, 8, 15166.	5.8	106
27	Chromatin Accessibility Dynamics during iPSC Reprogramming. <i>Cell Stem Cell</i> , 2017, 21, 819-833.e6.	5.2	180
28	Kdm2b Regulates Somatic Reprogramming through Variant PRC1 Complex-Dependent Function. <i>Cell Reports</i> , 2017, 21, 2160-2170.	2.9	34
29	Predicting conformational ensembles and genome-wide transcription factor binding sites from DNA sequences. <i>Scientific Reports</i> , 2017, 7, 4071.	1.6	11
30	Genomic and molecular control of cell type and cell type conversions. <i>Cell Regeneration</i> , 2017, 6, 1-7.	1.1	12
31	Models of global gene expression define major domains of cell type and tissue identity. <i>Nucleic Acids Research</i> , 2017, 45, 2354-2367.	6.5	50
32	The cancer-associated CTCFL/BORIS protein targets multiple classes of genomic repeats, with a distinct binding and functional preference for humanoid-specific SVA transposable elements. <i>Epigenetics and Chromatin</i> , 2016, 9, 35.	1.8	33
33	Generation and Analysis of GATA2 w/eGFP Human ESCs Reveal ITGB3/CD61 as a Reliable Marker for Defining Hemogenic Endothelial Cells during Hematopoiesis. <i>Stem Cell Reports</i> , 2016, 7, 854-868.	2.3	22
34	TGF $\beta$ 2 signaling regulates the choice between pluripotent and neural fates during reprogramming of human urine derived cells. <i>Scientific Reports</i> , 2016, 6, 22484.	1.6	16
35	Transcriptional Control of Somatic Cell Reprogramming. <i>Trends in Cell Biology</i> , 2016, 26, 272-288.	3.6	35
36	Transient Activation of Mitoflashes Modulates Nanog at the Early Phase of Somatic Cell Reprogramming. <i>Cell Metabolism</i> , 2016, 23, 220-226.	7.2	28

#	ARTICLE	IF	CITATIONS
37	Remission for Loss of Odontogenic Potential in a New Micromilieu In Vitro. PLoS ONE, 2016, 11, e0152893.	1.1	13
38	The oncogene c-Jun impedes somatic cell reprogramming. Nature Cell Biology, 2015, 17, 856-867.	4.6	112
39	A <i>Drosophila</i> -centric view of protein tyrosine phosphatases. FEBS Letters, 2015, 589, 951-966.	1.3	20
40	Genomic analysis of LPS-stimulated myeloid cells identifies a common pro-inflammatory response but divergent IL-10 anti-inflammatory responses. Scientific Reports, 2015, 5, 9100.	1.6	43
41	Transcriptional Intricacies of Stem Cells. Cell Systems, 2015, 1, 100-101.	2.9	1
42	Transposable elements at the center of the crossroads between embryogenesis, embryonic stem cells, reprogramming, and long non-coding RNAs. Science Bulletin, 2015, 60, 1722-1733.	4.3	50
43	The p53-induced lincRNA-p21 derails somatic cell reprogramming by sustaining H3K9me3 and CpG methylation at pluripotency gene promoters. Cell Research, 2015, 25, 80-92.	5.7	160
44	Protein Tyrosine Phosphatase 1B Is a Regulator of the Interleukin-10-Induced Transcriptional Program in Macrophages. Science Signaling, 2014, 7, ra43.	1.6	49
45	Where cell fate conversions meet Chinese philosophy. Cell Research, 2014, 24, 1162-1163.	5.7	8
46	Transcriptional Pause Release Is a Rate-Limiting Step for Somatic Cell Reprogramming. Cell Stem Cell, 2014, 15, 574-588.	5.2	60
47	glbase: a framework for combining, analyzing and displaying heterogeneous genomic and high-throughput sequencing data. Cell Regeneration, 2014, 3, 3:1.	1.1	79
48	Systematic identification of transcriptional regulatory modules from protein-protein interaction networks. Nucleic Acids Research, 2014, 42, e6-e6.	6.5	27
49	PTP-central: A comprehensive resource of protein tyrosine phosphatases in eukaryotic genomes. Methods, 2014, 65, 156-164.	1.9	16
50	Characterization of PTPN2 and its use as a biomarker. Methods, 2014, 65, 239-246.	1.9	16
51	Oct4 switches partnering from Sox2 to Sox17 to reinterpret the enhancer code and specify endoderm. EMBO Journal, 2013, 32, 938-953.	3.5	161
52	The Repertoires of Ubiquitinating and Deubiquitinating Enzymes in Eukaryotic Genomes. Molecular Biology and Evolution, 2013, 30, 1172-1187.	3.5	70
53	The IL-10/STAT3-mediated anti-inflammatory response: recent developments and future challenges. Briefings in Functional Genomics, 2013, 12, 489-498.	1.3	320
54	Distinct transcriptional regulatory modules underlie STAT3's cell type-independent and cell type-specific functions. Nucleic Acids Research, 2013, 41, 2155-2170.	6.5	72

#	ARTICLE	IF	CITATIONS
55	Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. <i>Genome Biology</i> , 2013, 14, R11.	13.9	296
56	Co-Motif Discovery Identifies an Esrrb-Sox2-DNA Ternary Complex as a Mediator of Transcriptional Differences Between Mouse Embryonic and Epiblast Stem Cells. <i>Stem Cells</i> , 2013, 31, 269-281.	1.4	36
57	Genomic and computational approaches to dissect the mechanisms of STAT3's universal and cell type-specific functions. <i>Jak-stat</i> , 2013, 2, e25097.	2.2	26
58	Genome-wide analysis of STAT3 binding in vivo predicts effectors of the anti-inflammatory response in macrophages. <i>Blood</i> , 2012, 119, e110-e119.	0.6	103
59	Discovery and characterization of new transcripts from RNA-seq data in mouse CD4+ T cells. <i>Genomics</i> , 2012, 100, 303-313.	1.3	12
60	Conversion of Sox17 into a Pluripotency Reprogramming Factor by Reengineering Its Association with Oct4 on DNA. <i>Stem Cells</i> , 2011, 29, 940-951.	1.4	92
61	Selective recruitment of proteins to 5' cap complexes during the growth cycle in Arabidopsis. <i>Plant Journal</i> , 2009, 59, 400-412.	2.8	53
62	Unraveling the Human Embryonic Stem Cell Phosphoproteome. <i>Cell Stem Cell</i> , 2009, 5, 126-128.	5.2	10
63	In vivo interaction between CDKA and eIF4A: a possible mechanism linking translation and cell proliferation. <i>FEBS Letters</i> , 2004, 556, 91-94.	1.3	28
64	Resolving Cell Fate Decisions During Somatic Cell Reprogramming by Single-Cell RNA-Seq. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
65	Chromatin Accessibility Dynamics During Reprogramming. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
66	Transposable Elements in Pluripotent Stem Cells and Human Disease. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1