Andrew Paul Hutchins

List of Publications by Year
in descending order

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	The IL-10/STAT3-mediated anti-inflammatory response: recent developments and future challenges. Briefings in Functional Genomics, 2013, 12, 489-498.	1.3	320
2	Genome of Acanthamoeba castellanii highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. Genome Biology, 2013, 14, R11.	13.9	296
3	Chromatin Accessibility Dynamics during iPSC Reprogramming. Cell Stem Cell, 2017, 21, 819-833.e6.	5.2	180
4	Capturing the interactome of newly transcribed RNA. Nature Methods, 2018, 15, 213-220.	9.0	170
5	Oct4 switches partnering from Sox2 to Sox17 to reinterpret the enhancer code and specify endoderm. EMBO Journal, 2013, 32, 938-953.	3.5	161
6	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
7	The oncogene c-Jun impedes somatic cell reprogramming. Nature Cell Biology, 2015, 17, 856-867.	4.6	112
8	A sequential EMT-MET mechanism drives the differentiation of human embryonic stem cells towards hepatocytes. Nature Communications, 2017, 8, 15166.	5.8	106
9	Transposable elements are regulated by context-specific patterns of chromatin marks in mouse embryonic stem cells. Nature Communications, 2019, 10, 34.	5.8	104
10	Genome-wide analysis of STAT3 binding in vivo predicts effectors of the anti-inflammatory response in macrophages. Blood, 2012, 119, e110-e119.	0.6	103
11	Conversion of Sox17 into a Pluripotency Reprogramming Factor by Reengineering Its Association with Oct4 on DNA. Stem Cells, 2011, 29, 940-951.	1.4	92
12	glbase: a framework for combining, analyzing and displaying heterogeneous genomic and high-throughput sequencing data. Cell Regeneration, 2014, 3, 3:1.	1.1	79
13	Resolving Cell Fate Decisions during Somatic Cell Reprogramming by Single-Cell RNA-Seq. Molecular Cell, 2019, 73, 815-829.e7.	4.5	79
14	Identifying transposable element expression dynamics and heterogeneity during development at the single-cell level with a processing pipeline scTE. Nature Communications, 2021, 12, 1456.	5.8	74
15	Distinct transcriptional regulatory modules underlie STAT3â€™s cell type-independent and cell type-specific functions. Nucleic Acids Research, 2013, 41, 2155-2170.	6.5	72
16	RNA Helicase DDX5 Inhibits Reprogramming to Pluripotency by miRNA-Based Repression of RYBP and its PRC1-Dependent and -Independent Functions. Cell Stem Cell, 2017, 20, 462-477.e6.	5.2	72
17	The Repertoires of Ubiquitinating and Deubiquitinating Enzymes in Eukaryotic Genomes. Molecular Biology and Evolution, 2013, 30, 1172-1187.	3.5	70
18	NCoR/SMRT co-repressors cooperate with c-MYC to create an epigenetic barrier to somatic cell reprogramming. Nature Cell Biology, 2018, 20, 400-412.	4.6	64

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19	Transcriptional Pause Release Is a Rate-Limiting Step for Somatic Cell Reprogramming. Cell Stem Cell, 2014, 15, 574-588.	5.2	60
20	PCGF5 is required for neural differentiation of embryonic stem cells. Nature Communications, 2018, 9, 1463.	5.8	60
21	Pluripotency reprogramming by competent and incompetent POU factors uncovers temporal dependency for Oct4 and Sox2. Nature Communications, 2019, 10, 3477.	5.8	60
22	Selective recruitment of proteins to 5â€² cap complexes during the growth cycle in Arabidopsis. Plant Journal, 2009, 59, 400-412.	2.8	53
23	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
24	Models of global gene expression define major domains of cell type and tissue identity. Nucleic Acids Research, 2017, 45, 2354-2367.	6.5	50
25	Protein Tyrosine Phosphatase 1B Is a Regulator of the Interleukin-10â€“Induced Transcriptional Program in Macrophages. Science Signaling, 2014, 7, ra43.	1.6	49
26	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
27	An alternative CTCF isoform antagonizes canonical CTCF occupancy and changes chromatin architecture to promote apoptosis. Nature Communications, 2019, 10, 1535.	5.8	39
28	Co-Motif Discovery Identifies an Esrrb-Sox2-DNA Ternary Complex as a Mediator of Transcriptional Differences Between Mouse Embryonic and Epiblast Stem Cells. Stem Cells, 2013, 31, 269-281.	1.4	36
29	Transcriptional Control of Somatic Cell Reprogramming. Trends in Cell Biology, 2016, 26, 272-288.	3.6	35
30	Kdm2b Regulates Somatic Reprogramming through Variant PRC1 Complex-Dependent Function. Cell Reports, 2017, 21, 2160-2170.	2.9	34
31	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. Epigenetics and Chromatin, 2016, 9, 35.	1.8	33
32	Systematic screening of CTCF binding partners identifies that BHLHE40 regulates CTCF genome-wide distribution and long-range chromatin interactions. Nucleic Acids Research, 2020, 48, 9606-9620.	6.5	30
33	In vivo interaction between CDKA and eIF4A: a possible mechanism linking translation and cell proliferation. FEBS Letters, 2004, 556, 91-94.	1.3	28
34	Transient Activation of Mitoflashes Modulates Nanog at the Early Phase of Somatic Cell Reprogramming. Cell Metabolism, 2016, 23, 220-226.	7.2	28
35	Systematic identification of transcriptional regulatory modules from proteinâ€“protein interaction networks. Nucleic Acids Research, 2014, 42, e6-e6.	6.5	27
36	Generation of Human Liver Chimeric Mice with Hepatocytes from Familial Hypercholesterolemia Induced Pluripotent Stem Cells. Stem Cell Reports, 2017, 8, 605-618.	2.3	27

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37	Genomic and computational approaches to dissect the mechanisms of STAT3â€™s universal and cell type-specific functions. Jak-stat, 2013, 2, e25097.	2.2	26
38	Computational Methods for Mapping, Assembly and Quantification for Coding and Non-coding Transcripts. Computational and Structural Biotechnology Journal, 2019, 17, 628-637.	1.9	25
39	Chromatin and Epigenetic Rearrangements in Embryonic Stem Cell Fate Transitions. Frontiers in Cell and Developmental Biology, 2021, 9, 637309.	1.8	25
40	JMJD3 acts in tandem with KLF4 to facilitate reprogramming to pluripotency. Nature Communications, 2020, 11, 5061.	5.8	24
41	Generation and Analysis of GATA2 w/eGFP Human ESCs Reveal ITGB3/CD61 as a Reliable Marker for Defining Hemogenic Endothelial Cells during Hematopoiesis. Stem Cell Reports, 2016, 7, 854-868.	2.3	22
42	CTCF functions as an insulator for somatic genes and a chromatin remodeler for pluripotency genes during reprogramming. Cell Reports, 2022, 39, 110626.	2.9	22
43	A Drosophilaâ€centric view of protein tyrosine phosphatases. FEBS Letters, 2015, 589, 951-966.	1.3	20
44	Transposable element sequence fragments incorporated into coding and noncoding transcripts modulate the transcriptome of human pluripotent stem cells. Nucleic Acids Research, 2021, 49, 9132-9153.	6.5	19
45	PTP-central: A comprehensive resource of protein tyrosine phosphatases in eukaryotic genomes. Methods, 2014, 65, 156-164.	1.9	16
46	Characterization of PTPN2 and its use as a biomarker. Methods, 2014, 65, 239-246.	1.9	16
47	TGFÎ² signaling regulates the choice between pluripotent and neural fates during reprogramming of human urine derived cells. Scientific Reports, 2016, 6, 22484.	1.6	16
48	The chromatin accessibility landscape reveals distinct transcriptional regulation in the induction of human primordial germ cell-like cells from pluripotent stem cells. Stem Cell Reports, 2021, 16, 1245-1261.	2.3	14
49	Remission for Loss of Odontogenic Potential in a New Micromilieu In Vitro. PLoS ONE, 2016, 11, e0152893.	1.1	13
50	Discovery and characterization of new transcripts from RNA-seq data in mouse CD4+ T cells. Genomics, 2012, 100, 303-313.	1.3	12
51	Genomic and molecular control of cell type and cell type conversions. Cell Regeneration, 2017, 6, 1-7.	1.1	12
52	Metabolic and epigenetic dysfunctions underlie the arrest of in vitro fertilized human embryos in a senescent-like state. PLoS Biology, 2022, 20, e3001682.	2.6	12
53	Predicting conformational ensembles and genome-wide transcription factor binding sites from DNA sequences. Scientific Reports, 2017, 7, 4071.	1.6	11
54	Unraveling the Human Embryonic Stem Cell Phosphoproteome. Cell Stem Cell, 2009, 5, 126-128.	5.2	10

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55	Î²-Catenin safeguards the ground state of mousepluripotency by strengthening the robustness of the transcriptional apparatus. Science Advances, 2020, 6, eaba1593.	4.7	10
56	Where cell fate conversions meet Chinese philosophy. Cell Research, 2014, 24, 1162-1163.	5.7	8
57	DNA Damage Induces Dynamic Associations of BRD4/P-TEFb With Chromatin and Modulates Gene Transcription in a BRD4-Dependent and -Independent Manner. Frontiers in Molecular Biosciences, 2020, 7, 618088.	1.6	5
58	The effects of sequencing depth on the assembly of coding and noncoding transcripts in the human genome. BMC Genomics, 2022, 23, .	1.2	5
59	Single cells and transposable element heterogeneity in stem cells and development. Cell Regeneration, 2021, 10, 23.	1.1	3
60	DPre: computational identification of differentiation bias and genes underlying cell type conversions. Bioinformatics, 2019, 36, 1637-1639.	1.8	2
61	Unified Analysis of Multiple ChIP-Seq Datasets. Methods in Molecular Biology, 2021, 2198, 451-465.	0.4	2
62	Transcriptional Intricacies of Stem Cells. Cell Systems, 2015, 1, 100-101.	2.9	1
63	MIMIC: an optimization method to identify cell type-specific marker panel for cell sorting. Briefings in Bioinformatics, 2021, 22, .	3.2	1
64	Transposable Elements in Pluripotent Stem Cells and Human Disease. Frontiers in Genetics, 0, 13, .	1.1	1
65	Resolving Cell Fate Decisions During Somatic Cell Reprogramming by Single-Cell RNA-Seq. SSRN Electronic Journal, 0, , .	0.4	0
66	Chromatin Accessibility Dynamics During Reprogramming. SSRN Electronic Journal, 0, , .	0.4	0