

# Howard Y Chang

## List of Publications by Year in descending order

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255  
papers

89,109  
citations

1099

112  
h-index

693

253  
g-index

322  
all docs

322  
docs citations

322  
times ranked

80705  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position. <i>Nature Methods</i> , 2013, 10, 1213-1218.	19.0	5,209
2	Long non-coding RNA HOTAIR reprograms chromatin state to promote cancer metastasis. <i>Nature</i> , 2010, 464, 1071-1076.	27.8	4,648
3	Functional Demarcation of Active and Silent Chromatin Domains in Human HOX Loci by Noncoding RNAs. <i>Cell</i> , 2007, 129, 1311-1323.	28.9	3,835
4	Molecular Mechanisms of Long Noncoding RNAs. <i>Molecular Cell</i> , 2011, 43, 904-914.	9.7	3,833
5	Genome Regulation by Long Noncoding RNAs. <i>Annual Review of Biochemistry</i> , 2012, 81, 145-166.	11.1	3,665
6	Long Noncoding RNA as Modular Scaffold of Histone Modification Complexes. <i>Science</i> , 2010, 329, 689-693.	12.6	2,976
7	Unique features of long non-coding RNA biogenesis and function. <i>Nature Reviews Genetics</i> , 2016, 17, 47-62.	16.3	2,891
8	Long Noncoding RNAs in Cancer Pathways. <i>Cancer Cell</i> , 2016, 29, 452-463.	16.8	2,584
9	ATAC-seq: A Method for Assaying Chromatin Accessibility Genome-wide. <i>Current Protocols in Molecular Biology</i> , 2015, 109, 21.29.1-21.29.9.	2.9	2,391
10	Long Noncoding RNAs: Cellular Address Codes in Development and Disease. <i>Cell</i> , 2013, 152, 1298-1307.	28.9	2,279
11	Long noncoding RNAs and human disease. <i>Trends in Cell Biology</i> , 2011, 21, 354-361.	7.9	1,806
12	Single-cell chromatin accessibility reveals principles of regulatory variation. <i>Nature</i> , 2015, 523, 486-490.	27.8	1,798
13	A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. <i>Nature</i> , 2011, 472, 120-124.	27.8	1,760
14	An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. <i>Nature Methods</i> , 2017, 14, 959-962.	19.0	1,653
15	Genomic Maps of Long Noncoding RNA Occupancy Reveal Principles of RNA-Chromatin Interactions. <i>Molecular Cell</i> , 2011, 44, 667-678.	9.7	1,104
16	Extensive and coordinated transcription of noncoding RNAs within cell-cycle promoters. <i>Nature Genetics</i> , 2011, 43, 621-629.	21.4	1,080
17	m6A RNA Modification Controls Cell Fate Transition in Mammalian Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2014, 15, 707-719.	11.1	990
18	Diversity, topographic differentiation, and positional memory in human fibroblasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12877-12882.	7.1	983

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19	Clonal replacement of tumor-specific T cells following PD-1 blockade. <i>Nature Medicine</i> , 2019, 25, 1251-1259.	30.7	974
20	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. <i>Nature Genetics</i> , 2016, 48, 1193-1203.	21.4	952
21	Robustness, scalability, and integration of a wound-response gene expression signature in predicting breast cancer survival. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3738-3743.	7.1	934
22	Systematic Discovery of Xist RNA Binding Proteins. <i>Cell</i> , 2015, 161, 404-416.	28.9	886
23	CRISPR-engineered T cells in patients with refractory cancer. <i>Science</i> , 2020, 367, .	12.6	872
24	HiChIP: efficient and sensitive analysis of protein-directed genome architecture. <i>Nature Methods</i> , 2016, 13, 919-922.	19.0	853
25	Gene Expression Signature of Fibroblast Serum Response Predicts Human Cancer Progression: Similarities between Tumors and Wounds. <i>PLoS Biology</i> , 2004, 2, e7.	5.6	824
26	Control of somatic tissue differentiation by the long non-coding RNA TINCR. <i>Nature</i> , 2013, 493, 231-235.	27.8	810
27	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	12.6	781
28	Genome-wide measurement of RNA secondary structure in yeast. <i>Nature</i> , 2010, 467, 103-107.	27.8	713
29	Endothelial cell diversity revealed by global expression profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10623-10628.	7.1	679
30	Long Intergenic Noncoding RNAs: New Links in Cancer Progression. <i>Cancer Research</i> , 2011, 71, 3-7.	0.9	676
31	m6A mRNA methylation controls T cell homeostasis by targeting the IL-7/STAT5/SOCS pathways. <i>Nature</i> , 2017, 548, 338-342.	27.8	668
32	Module Map of Stem Cell Genes Guides Creation of Epithelial Cancer Stem Cells. <i>Cell Stem Cell</i> , 2008, 2, 333-344.	11.1	652
33	Structural imprints in vivo decode RNA regulatory mechanisms. <i>Nature</i> , 2015, 519, 486-490.	27.8	639
34	Massively parallel single-cell chromatin landscapes of human immune cell development and intratumoral T cell exhaustion. <i>Nature Biotechnology</i> , 2019, 37, 925-936.	17.5	622
35	The NeST Long ncRNA Controls Microbial Susceptibility and Epigenetic Activation of the Interferon- $\hat{1}$ <sup>3</sup> Locus. <i>Cell</i> , 2013, 152, 743-754.	28.9	611
36	Gene regulation in the immune system by long noncoding RNAs. <i>Nature Immunology</i> , 2017, 18, 962-972.	14.5	611

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37	ArchR is a scalable software package for integrative single-cell chromatin accessibility analysis. <i>Nature Genetics</i> , 2021, 53, 403-411.	21.4	610
38	CRISPRi-based genome-scale identification of functional long noncoding RNA loci in human cells. <i>Science</i> , 2017, 355, .	12.6	566
39	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. <i>Cell</i> , 2018, 173, 1535-1548.e16.	28.9	545
40	Hierarchical Mechanisms for Direct Reprogramming of Fibroblasts to Neurons. <i>Cell</i> , 2013, 155, 621-635.	28.9	531
41	Long noncoding RNA in genome regulation. <i>RNA Biology</i> , 2010, 7, 582-585.	3.1	523
42	RNA Duplex Map in Living Cells Reveals Higher-Order Transcriptome Structure. <i>Cell</i> , 2016, 165, 1267-1279.	28.9	520
43	Landscape and variation of RNA secondary structure across the human transcriptome. <i>Nature</i> , 2014, 505, 706-709.	27.8	519
44	Intrinsic retroviral reactivation in human preimplantation embryos and pluripotent cells. <i>Nature</i> , 2015, 522, 221-225.	27.8	507
45	c-Jun overexpression in CAR T cells induces exhaustion resistance. <i>Nature</i> , 2019, 576, 293-300.	27.8	480
46	Long Noncoding RNAs in Cell-Fate Programming and Reprogramming. <i>Cell Stem Cell</i> , 2014, 14, 752-761.	11.1	461
47	Ageing, Rejuvenation, and Epigenetic Reprogramming: Resetting the Ageing Clock. <i>Cell</i> , 2012, 148, 46-57.	28.9	460
48	Deletional Tolerance Mediated by Extrathymic Aire-Expressing Cells. <i>Science</i> , 2008, 321, 843-847.	12.6	421
49	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. <i>Nature Genetics</i> , 2017, 49, 1602-1612.	21.4	419
50	Anatomic Demarcation by Positional Variation in Fibroblast Gene Expression Programs. <i>PLoS Genetics</i> , 2006, 2, e119.	3.5	413
51	Understanding the transcriptome through RNA structure. <i>Nature Reviews Genetics</i> , 2011, 12, 641-655.	16.3	411
52	A mammalian pseudogene lncRNA at the interface of inflammation and anti-inflammatory therapeutics. <i>ELife</i> , 2013, 2, e00762.	6.0	407
53	Atlas of Subcellular RNA Localization Revealed by APEX-Seq. <i>Cell</i> , 2019, 178, 473-490.e26.	28.9	400
54	A Long Noncoding RNA lincRNA-EPS Acts as a Transcriptional Brake to Restrain Inflammation. <i>Cell</i> , 2016, 165, 1672-1685.	28.9	399

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55	Suppression of progenitor differentiation requires the long noncoding RNA ANCR. <i>Genes and Development</i> , 2012, 26, 338-343.	5.9	391
56	Structural organization of the inactive X chromosome in the mouse. <i>Nature</i> , 2016, 535, 575-579.	27.8	369
57	RNA SHAPE analysis in living cells. <i>Nature Chemical Biology</i> , 2013, 9, 18-20.	8.0	366
58	Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. <i>Cell</i> , 2018, 173, 1398-1412.e22.	28.9	362
59	N6-Methyladenosine Modification Controls Circular RNA Immunity. <i>Molecular Cell</i> , 2019, 76, 96-109.e9.	9.7	348
60	Sensing Self and Foreign Circular RNAs by Intron Identity. <i>Molecular Cell</i> , 2017, 67, 228-238.e5.	9.7	346
61	Circular ecDNA promotes accessible chromatin and high oncogene expression. <i>Nature</i> , 2019, 575, 699-703.	27.8	343
62	Structure and Thermodynamics of N <sup>6</sup> -Methyladenosine in RNA: A Spring-Loaded Base Modification. <i>Journal of the American Chemical Society</i> , 2015, 137, 2107-2115.	13.7	331
63	Direct Lineage Conversion of Terminally Differentiated Hepatocytes to Functional Neurons. <i>Cell Stem Cell</i> , 2011, 9, 374-382.	11.1	326
64	Single-cell multiomic analysis identifies regulatory programs in mixed-phenotype acute leukemia. <i>Nature Biotechnology</i> , 2019, 37, 1458-1465.	17.5	321
65	The Mammalian Ribo-interactome Reveals Ribosome Functional Diversity and Heterogeneity. <i>Cell</i> , 2017, 169, 1051-1065.e18.	28.9	314
66	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. <i>Cell</i> , 2021, 184, 2503-2519.e17.	28.9	312
67	Transient rest restores functionality in exhausted CAR-T cells through epigenetic remodeling. <i>Science</i> , 2021, 372, .	12.6	297
68	Genome-Wide Views of Chromatin Structure. <i>Annual Review of Biochemistry</i> , 2009, 78, 245-271.	11.1	292
69	Targeted Disruption of Hotair Leads to Homeotic Transformation and Gene Derepression. <i>Cell Reports</i> , 2013, 5, 3-12.	6.4	289
70	Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers. <i>Nature Genetics</i> , 2020, 52, 891-897.	21.4	273
71	Single-Cell Analyses Identify Brain Mural Cells Expressing CD19 as Potential Off-Tumor Targets for CAR-T Immunotherapies. <i>Cell</i> , 2020, 183, 126-142.e17.	28.9	269
72	Generation of pure GABAergic neurons by transcription factor programming. <i>Nature Methods</i> , 2017, 14, 621-628.	19.0	265

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73	Chromatin Isolation by RNA Purification (ChIRP). <i>Journal of Visualized Experiments</i> , 2012, , .	0.3	259
74	Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. <i>Nature Genetics</i> , 2017, 49, 1522-1528.	21.4	255
75	Discovery of stimulation-responsive immune enhancers with CRISPR activation. <i>Nature</i> , 2017, 549, 111-115.	27.8	247
76	The histone chaperone CAF-1 safeguards somatic cell identity. <i>Nature</i> , 2015, 528, 218-224.	27.8	244
77	Control of differentiation in a self-renewing mammalian tissue by the histone demethylase JMJD3. <i>Genes and Development</i> , 2008, 22, 1865-1870.	5.9	239
78	RNA helicase DDX21 coordinates transcription and ribosomal RNA processing. <i>Nature</i> , 2015, 518, 249-253.	27.8	232
79	Impaired mitochondrial oxidative phosphorylation limits the self-renewal of T cells exposed to persistent antigen. <i>Nature Immunology</i> , 2020, 21, 1022-1033.	14.5	227
80	irCLIP platform for efficient characterization of protein-RNA interactions. <i>Nature Methods</i> , 2016, 13, 489-492.	19.0	222
81	Transcriptional profiling of long non-coding RNAs and novel transcribed regions across a diverse panel of archived human cancers. <i>Genome Biology</i> , 2012, 13, R75.	9.6	221
82	Human B Cell Clonal Expansion and Convergent Antibody Responses to SARS-CoV-2. <i>Cell Host and Microbe</i> , 2020, 28, 516-525.e5.	11.0	219
83	Single-cell epigenomic analyses implicate candidate causal variants at inherited risk loci for Alzheimer's and Parkinson's diseases. <i>Nature Genetics</i> , 2020, 52, 1158-1168.	21.4	217
84	Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks. <i>Cell</i> , 2019, 176, 361-376.e17.	28.9	215
85	Chromatin and gene-regulatory dynamics of the developing human cerebral cortex at single-cell resolution. <i>Cell</i> , 2021, 184, 5053-5069.e23.	28.9	209
86	Age-Dependent Pancreatic Gene Regulation Reveals Mechanisms Governing Human $\beta$ Cell Function. <i>Cell Metabolism</i> , 2016, 23, 909-920.	16.2	205
87	Quantitative analysis of RNA-protein interactions on a massively parallel array reveals biophysical and evolutionary landscapes. <i>Nature Biotechnology</i> , 2014, 32, 562-568.	17.5	202
88	ATAC-seq reveals the accessible genome by transposase-mediated imaging and sequencing. <i>Nature Methods</i> , 2016, 13, 1013-1020.	19.0	199
89	An inducible long noncoding RNA amplifies DNA damage signaling. <i>Nature Genetics</i> , 2016, 48, 1370-1376.	21.4	195
90	Genome-wide Measurement of RNA Folding Energies. <i>Molecular Cell</i> , 2012, 48, 169-181.	9.7	192

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91	Chromatin accessibility dynamics in a model of human forebrain development. <i>Science</i> , 2020, 367, .	12.6	187
92	RNA templating the epigenome. <i>Epigenetics</i> , 2011, 6, 539-543.	2.7	184
93	RNA structure maps across mammalian cellular compartments. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 322-330.	8.2	183
94	Long Noncoding RNAs: Molecular Modalities to Organismal Functions. <i>Annual Review of Biochemistry</i> , 2020, 89, 283-308.	11.1	183
95	Leukemia-Associated Cohesin Mutants Dominantly Enforce Stem Cell Programs and Impair Human Hematopoietic Progenitor Differentiation. <i>Cell Stem Cell</i> , 2015, 17, 675-688.	11.1	177
96	CD44+ Cells in Head and Neck Squamous Cell Carcinoma Suppress T-Cell-Mediated Immunity by Selective Constitutive and Inducible Expression of PD-L1. <i>Clinical Cancer Research</i> , 2016, 22, 3571-3581.	7.0	177
97	Gpr124 is essential for blood-brain barrier integrity in central nervous system disease. <i>Nature Medicine</i> , 2017, 23, 450-460.	30.7	177
98	Essential role of lncRNA binding for WDR5 maintenance of active chromatin and embryonic stem cell pluripotency. <i>ELife</i> , 2014, 3, e02046.	6.0	176
99	Single-cell RNA sequencing in cardiovascular development, disease and medicine. <i>Nature Reviews Cardiology</i> , 2020, 17, 457-473.	13.7	174
100	The conserved RNA helicase YTHDC2 regulates the transition from proliferation to differentiation in the germline. <i>ELife</i> , 2017, 6, .	6.0	167
101	A dermal <i>HOX</i> transcriptional program regulates site-specific epidermal fate. <i>Genes and Development</i> , 2008, 22, 303-307.	5.9	165
102	Revealing long noncoding RNA architecture and functions using domain-specific chromatin isolation by RNA purification. <i>Nature Biotechnology</i> , 2014, 32, 933-940.	17.5	161
103	Long Noncoding RNA in Hematopoiesis and Immunity. <i>Immunity</i> , 2015, 42, 792-804.	14.3	161
104	Physiological roles of long noncoding RNAs: insight from knockout mice. <i>Trends in Cell Biology</i> , 2014, 24, 594-602.	7.9	156
105	Integrative analysis of single-cell genomics data by coupled nonnegative matrix factorizations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7723-7728.	7.1	156
106	DDX5 and its associated lncRNA Rmrp modulate TH17 cell effector functions. <i>Nature</i> , 2015, 528, 517-522.	27.8	154
107	Tandem Stem-Loops in roX RNAs Act Together to Mediate X Chromosome Dosage Compensation in <i>Drosophila</i> . <i>Molecular Cell</i> , 2013, 51, 156-173.	9.7	152
108	Rapid evolutionary turnover underlies conserved lncRNA-genome interactions. <i>Genes and Development</i> , 2016, 30, 191-207.	5.9	152

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109	Transcriptome-wide interrogation of RNA secondary structure in living cells with icSHAPE. <i>Nature Protocols</i> , 2016, 11, 273-290.	12.0	147
110	Mechanisms of an autoimmunity syndrome in mice caused by a dominant mutation in Aire. <i>Journal of Clinical Investigation</i> , 2008, 118, 1712-1726.	8.2	143
111	Discovery and functional interrogation of SARS-CoV-2 RNA-host protein interactions. <i>Cell</i> , 2021, 184, 2394-2411.e16.	28.9	141
112	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. <i>Nature Genetics</i> , 2018, 50, 1140-1150.	21.4	139
113	Chromatin Accessibility Landscape of Cutaneous T Cell Lymphoma and Dynamic Response to HDAC Inhibitors. <i>Cancer Cell</i> , 2017, 32, 27-41.e4.	16.8	136
114	The histone demethylase UTX enables RB-dependent cell fate control. <i>Genes and Development</i> , 2010, 24, 327-332.	5.9	135
115	A novel ATAC-seq approach reveals lineage-specific reinforcement of the open chromatin landscape via cooperation between BAF and p63. <i>Genome Biology</i> , 2015, 16, 284.	8.8	135
116	A TGF $\beta$ -Responsive Gene Signature Is Associated with a Subset of Diffuse Scleroderma with Increased Disease Severity. <i>Journal of Investigative Dermatology</i> , 2010, 130, 694-705.	0.7	132
117	Individuality and Variation of Personal Regulomes in Primary Human T Cells. <i>Cell Systems</i> , 2015, 1, 51-61.	6.2	128
118	Tissue-selective effects of nucleolar stress and rDNA damage in developmental disorders. <i>Nature</i> , 2018, 554, 112-117.	27.8	125
119	Technologies to probe functions and mechanisms of long noncoding RNAs. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 29-35.	8.2	124
120	Transcript-indexed ATAC-seq for precision immune profiling. <i>Nature Medicine</i> , 2018, 24, 580-590.	30.7	124
121	Cerebellar nuclei evolved by repeatedly duplicating a conserved cell-type set. <i>Science</i> , 2020, 370, .	12.6	123
122	ecDNA hubs drive cooperative intermolecular oncogene expression. <i>Nature</i> , 2021, 600, 731-736.	27.8	123
123	Rapid Chromatin Switch in the Direct Reprogramming of Fibroblasts to Neurons. <i>Cell Reports</i> , 2017, 20, 3236-3247.	6.4	121
124	Mechanoresponsive stem cells acquire neural crest fate in jaw regeneration. <i>Nature</i> , 2018, 563, 514-521.	27.8	121
125	RNA-GPS Predicts SARS-CoV-2 RNA Residency to Host Mitochondria and Nucleolus. <i>Cell Systems</i> , 2020, 11, 102-108.e3.	6.2	119
126	Genome-Wide Temporal Profiling of Transcriptome and Open Chromatin of Early Cardiomyocyte Differentiation Derived From hiPSCs and hESCs. <i>Circulation Research</i> , 2017, 121, 376-391.	4.5	118



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127	The road ahead in genetics and genomics. <i>Nature Reviews Genetics</i> , 2020, 21, 581-596.	16.3	118
128	Molecular framework for response to imatinib mesylate in systemic sclerosis. <i>Arthritis and Rheumatism</i> , 2009, 60, 584-591.	6.7	117
129	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	109
130	Structured elements drive extensive circular RNA translation. <i>Molecular Cell</i> , 2021, 81, 4300-4318.e13.	9.7	108
131	B cell-specific XIST complex enforces X-inactivation and restrains atypical B cells. <i>Cell</i> , 2021, 184, 1790-1803.e17.	28.9	105
132	Cryptic activation of an <i>Irf8</i> enhancer governs cDC1 fate specification. <i>Nature Immunology</i> , 2019, 20, 1161-1173.	14.5	100
133	GWAS for systemic sclerosis identifies multiple risk loci and highlights fibrotic and vasculopathy pathways. <i>Nature Communications</i> , 2019, 10, 4955.	12.8	100
134	Single-cell lineage tracing by endogenous mutations enriched in transposase accessible mitochondrial DNA. <i>ELife</i> , 2019, 8, .	6.0	93
135	Identification of a Selective Polymerase Enables Detection of N <sup>6</sup> -Methyladenosine in RNA. <i>Journal of the American Chemical Society</i> , 2013, 135, 19079-19082.	13.7	92
136	7SK-BAF axis controls pervasive transcription at enhancers. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 231-238.	8.2	92
137	Single-cell epigenomic variability reveals functional cancer heterogeneity. <i>Genome Biology</i> , 2017, 18, 15.	8.8	92
138	Dicer-microRNA-Myc circuit promotes transcription of hundreds of long noncoding RNAs. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 585-590.	8.2	90
139	Enhanced safety and efficacy of protease-regulated CAR-T cell receptors. <i>Cell</i> , 2022, 185, 1745-1763.e22.	28.9	88
140	Transcriptome sequencing in Sjögren syndrome identifies Sjögren cell and mycosis fungoides-associated lncRNAs and novel transcripts. <i>Blood</i> , 2012, 120, 3288-3297.	1.4	85
141	Genome-wide mapping of RNA structure using nuclease digestion and high-throughput sequencing. <i>Nature Protocols</i> , 2013, 8, 849-869.	12.0	85
142	Engineering circular RNA for enhanced protein production. <i>Nature Biotechnology</i> , 2023, 41, 262-272.	17.5	83
143	Dynamic Chromatin Localization of Sirt6 Shapes Stress- and Aging-Related Transcriptional Networks. <i>PLoS Genetics</i> , 2011, 7, e1002153.	3.5	82
144	Epigenomics. <i>Circulation Research</i> , 2018, 122, 1191-1199.	4.5	80

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145	An Nfil3- and Zeb2-dependent pathway imposes Irf8 enhancer switching during cDC1 development. <i>Nature Immunology</i> , 2019, 20, 1174-1185.	14.5	80
146	The role of Xist-mediated Polycomb recruitment in the initiation of X-chromosome inactivation. <i>EMBO Reports</i> , 2019, 20, e48019.	4.5	79
147	Landscape of monoallelic DNA accessibility in mouse embryonic stem cells and neural progenitor cells. <i>Nature Genetics</i> , 2017, 49, 377-386.	21.4	76
148	Joint single-cell DNA accessibility and protein epitope profiling reveals environmental regulation of epigenomic heterogeneity. <i>Nature Communications</i> , 2018, 9, 4590.	12.8	76
149	TFAP2C- and p63-Dependent Networks Sequentially Rearrange Chromatin Landscapes to Drive Human Epidermal Lineage Commitment. <i>Cell Stem Cell</i> , 2019, 24, 271-284.e8.	11.1	76
150	Integrated spatial multiomics reveals fibroblast fate during tissue repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	76
151	A Mutation in the Transcription Factor Foxp3 Drives T Helper 2 Effector Function in Regulatory T Cells. <i>Immunity</i> , 2019, 50, 362-377.e6.	14.3	72
152	Dissecting noncoding and pathogen RNA-protein interactomes. <i>Rna</i> , 2015, 21, 135-143.	3.5	71
153	Stress from Nucleotide Depletion Activates the Transcriptional Regulator HEXIM1 to Suppress Melanoma. <i>Molecular Cell</i> , 2016, 62, 34-46.	9.7	71
154	HiChIRP reveals RNA-associated chromosome conformation. <i>Nature Methods</i> , 2019, 16, 489-492.	19.0	70
155	Uncovering the role of genomic "dark matter" in human disease. <i>Journal of Clinical Investigation</i> , 2012, 122, 1589-1595.	8.2	70
156	Systematic reconstruction of RNA functional motifs with high-throughput microfluidics. <i>Nature Methods</i> , 2012, 9, 1192-1194.	19.0	69
157	Rapid chromatin repression by Aire provides precise control of immune tolerance. <i>Nature Immunology</i> , 2018, 19, 162-172.	14.5	69
158	A Transcriptional Program Mediating Entry into Cellular Quiescence. <i>PLoS Genetics</i> , 2007, 3, e91.	3.5	67
159	Decoding the RNA structurome. <i>Current Opinion in Structural Biology</i> , 2016, 36, 142-148.	5.7	66
160	BABEL enables cross-modality translation between multiomic profiles at single-cell resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	66
161	An Activity Switch in Human Telomerase Based on RNA Conformation and Shaped by TCAB1. <i>Cell</i> , 2018, 174, 218-230.e13.	28.9	64
162	Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons. <i>ELife</i> , 2019, 8, .	6.0	64

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163	Comparison of SHAPE reagents for mapping RNA structures inside living cells. <i>Rna</i> , 2017, 23, 169-174.	3.5	62
164	3D ATAC-PALM: super-resolution imaging of the accessible genome. <i>Nature Methods</i> , 2020, 17, 430-436.	19.0	62
165	Medulloblastoma-associated DDX3 variant selectively alters the translational response to stress. <i>Oncotarget</i> , 2016, 7, 28169-28182.	1.8	62
166	HOTAIR: Flight of noncoding RNAs in cancer metastasis. <i>Cell Cycle</i> , 2010, 9, 3391-3392.	2.6	61
167	Long Noncoding RNAs: At the Intersection of Cancer and Chromatin Biology. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2017, 7, a026492.	6.2	60
168	Long non-coding RNA HOTAIR drives EZH2-dependent myofibroblast activation in systemic sclerosis through miRNA 34a-dependent activation of NOTCH. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 507-517.	0.9	60
169	GPC2-CAR T cells tuned for low antigen density mediate potent activity against neuroblastoma without toxicity. <i>Cancer Cell</i> , 2022, 40, 53-69.e9.	16.8	60
170	Mechanistic insights in X-chromosome inactivation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160356.	4.0	59
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