

Howard Y Chang

List of Publications by Year in descending order

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Version: 2024-02-01

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	Engineering circular RNA for enhanced protein production. <i>Nature Biotechnology</i> , 2023, 41, 262-272.	17.5	83
2	Extrachromosomal DNA: An Emerging Hallmark in Human Cancer. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2022, 17, 367-386.	22.4	44
3	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
4	Identification of Protein-RNA Interactions in Mouse Testis Tissue Using fRIP. <i>Bio-protocol</i> , 2022, 12, e4286.	0.4	1
5	Epigenomic priming of immune genes implicates oligodendroglia in multiple sclerosis susceptibility. <i>Neuron</i> , 2022, 110, 1193-1210.e13.	8.1	36
6	Circular RNA migration in agarose gel electrophoresis. <i>Molecular Cell</i> , 2022, 82, 1768-1777.e3.	9.7	13
7	Oncogene Convergence in Extrachromosomal DNA Hubs. <i>Cancer Discovery</i> , 2022, 12, 1195-1198.	9.4	4
8	BRD2 compartmentalizes the accessible genome. <i>Nature Genetics</i> , 2022, 54, 481-491.	21.4	29
9	A Genetic Bottleneck of Mitochondrial DNA During Human Lymphocyte Development. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	18
10	The Mettl3 epitranscriptomic writer amplifies p53 stress responses. <i>Molecular Cell</i> , 2022, 82, 2370-2384.e10.	9.7	22
11	Enhanced safety and efficacy of protease-regulated CAR-T cell receptors. <i>Cell</i> , 2022, 185, 1745-1763.e22.	28.9	88
12	Polycomb-mediated genome architecture enables long-range spreading of H3K27 methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	33
13	ArchR is a scalable software package for integrative single-cell chromatin accessibility analysis. <i>Nature Genetics</i> , 2021, 53, 403-411.	21.4	610
14	B cell-specific XIST complex enforces X-inactivation and restrains atypical B cells. <i>Cell</i> , 2021, 184, 1790-1803.e17.	28.9	105
15	Discovery and functional interrogation of SARS-CoV-2 RNA-host protein interactions. <i>Cell</i> , 2021, 184, 2394-2411.e16.	28.9	141
16	Transient rest restores functionality in exhausted CAR-T cells through epigenetic remodeling. <i>Science</i> , 2021, 372, .	12.6	297
17	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
18	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. <i>Cell</i> , 2021, 184, 2503-2519.e17.	28.9	312

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19	Recruiting T cells in cancer immunotherapy. <i>Science</i> , 2021, 372, 130-131.	12.6	56
20	Profiling chromatin accessibility responses in human neutrophils with sensitive pathogen detection. <i>Life Science Alliance</i> , 2021, 4, e202000976.	2.8	5
21	Personal regulome navigation of cancer. <i>Nature Reviews Cancer</i> , 2021, 21, 609-610.	28.4	3
22	Dynamic chromatin regulatory landscape of human CAR T cell exhaustion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	36
23	LKB1 inactivation modulates chromatin accessibility to drive metastatic progression. <i>Nature Cell Biology</i> , 2021, 23, 915-924.	10.3	26
24	Structured elements drive extensive circular RNA translation. <i>Molecular Cell</i> , 2021, 81, 4300-4318.e13.	9.7	108
25	Chromatin accessibility associates with protein-RNA correlation in human cancer. <i>Nature Communications</i> , 2021, 12, 5732.	12.8	18
26	Locus specific epigenetic modalities of random allelic expression imbalance. <i>Nature Communications</i> , 2021, 12, 5330.	12.8	7
27	fSHAPE, fSHAPE-eCLIP, and SHAPE-eCLIP probe transcript regions that interact with specific proteins. <i>STAR Protocols</i> , 2021, 2, 100762.	1.2	1
28	JUN promotes hypertrophic skin scarring via CD36 in preclinical in vitro and in vivo models. <i>Science Translational Medicine</i> , 2021, 13, eabb3312.	12.4	32
29	NOT-Gated CD93 CAR T Cells Effectively Target AML with Minimized Endothelial Cross-Reactivity. <i>Blood Cancer Discovery</i> , 2021, 2, 648-665.	5.0	37
30	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
31	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
32	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation. <i>Nature Genetics</i> , 2021, 53, 1564-1576.	21.4	45
33	PEPATAC: an optimized pipeline for ATAC-seq data analysis with serial alignments. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab101.	3.2	34
34	Noncoding RNAs: biology and applicationsâ€”a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1506, 118-141.	3.8	13
35	ecDNA hubs drive cooperative intermolecular oncogene expression. <i>Nature</i> , 2021, 600, 731-736.	27.8	123
36	Tracking the immune response with single-cell genomics. <i>Vaccine</i> , 2020, 38, 4487-4490.	3.8	7

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37	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
38	Chromatin Landscape Underpinning Human Dendritic Cell Heterogeneity. <i>Cell Reports</i> , 2020, 32, 108180.	6.4	18
39	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
40	Chromatin accessibility landscapes of skin cells in systemic sclerosis nominate dendritic cells in disease pathogenesis. <i>Nature Communications</i> , 2020, 11, 5843.	12.8	22
41	Footprinting SHAPE-eCLIP Reveals Transcriptome-wide Hydrogen Bonds at RNA-Protein Interfaces. <i>Molecular Cell</i> , 2020, 80, 903-914.e8.	9.7	20
42	Structural modularity of the XIST ribonucleoprotein complex. <i>Nature Communications</i> , 2020, 11, 6163.	12.8	53
43	Prrx1 Fibroblasts Represent a Pro-fibrotic Lineage in the Mouse Ventral Dermis. <i>Cell Reports</i> , 2020, 33, 108356.	6.4	44
44	Endogenous Retrovirus-Derived lncRNA BANCR Promotes Cardiomyocyte Migration in Humans and Non-human Primates. <i>Developmental Cell</i> , 2020, 54, 694-709.e9.	7.0	37
45	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	109
46	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
47	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
48	Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers. <i>Nature Genetics</i> , 2020, 52, 891-897.	21.4	273
49	The road ahead in genetics and genomics. <i>Nature Reviews Genetics</i> , 2020, 21, 581-596.	16.3	118
50	RNA-GPS predicts high-resolution RNA subcellular localization and highlights the role of splicing. <i>Rna</i> , 2020, 26, 851-865.	3.5	15
51	A distal enhancer at risk locus 11q13.5 promotes suppression of colitis by Treg cells. <i>Nature</i> , 2020, 583, 447-452.	27.8	40
52	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
53	Long Noncoding RNAs: Molecular Modalities to Organismal Functions. <i>Annual Review of Biochemistry</i> , 2020, 89, 283-308.	11.1	183
54	Diverse lncRNA mechanisms in brain development and disease. <i>Current Opinion in Genetics and Development</i> , 2020, 65, 42-46.	3.3	43

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55	3D ATAC-PALM: super-resolution imaging of the accessible genome. <i>Nature Methods</i> , 2020, 17, 430-436.	19.0	62
56	Pro-neuronal activity of Myod1 due to promiscuous binding to neuronal genes. <i>Nature Cell Biology</i> , 2020, 22, 401-411.	10.3	38
57	Single-cell RNA sequencing in cardiovascular development, disease and medicine. <i>Nature Reviews Cardiology</i> , 2020, 17, 457-473.	13.7	174
58	CRISPR-engineered T cells in patients with refractory cancer. <i>Science</i> , 2020, 367, .	12.6	872
59	Acetate supplementation restores chromatin accessibility and promotes tumor cell differentiation under hypoxia. <i>Cell Death and Disease</i> , 2020, 11, 102.	6.3	39
60	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
61	Fitness effects of CRISPR/Cas9-targeting of long noncoding RNA genes. <i>Nature Biotechnology</i> , 2020, 38, 573-576.	17.5	27
62	CRISPRpic: fast and precise analysis for CRISPR-induced mutations via refined index counting . <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa012.	3.2	15
63	Chromatin accessibility dynamics in a model of human forebrain development. <i>Science</i> , 2020, 367, .	12.6	187
64	Cerebellar nuclei evolved by repeatedly duplicating a conserved cell-type set. <i>Science</i> , 2020, 370, .	12.6	123
65	Spn links RNA-mediated endogenous retrovirus silencing and X chromosome inactivation. <i>ELife</i> , 2020, 9, .	6.0	33
66	An Nfil3- <i>Zeb2</i> - <i>Id2</i> pathway imposes <i>Irf8</i> enhancer switching during cDC1 development. <i>Nature Immunology</i> , 2019, 20, 1174-1185.	14.5	80
67	Cryptic activation of an <i>Irf8</i> enhancer governs cDC1 fate specification. <i>Nature Immunology</i> , 2019, 20, 1161-1173.	14.5	100
68	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
69	<i>Satb1</i> integrates DNA binding site geometry and torsional stress to differentially target nucleosome-dense regions. <i>Nature Communications</i> , 2019, 10, 3221.	12.8	33
70	Single-cell lineage tracing by endogenous mutations enriched in transposase accessible mitochondrial DNA. <i>ELife</i> , 2019, 8, .	6.0	93
71	Clonal replacement of tumor-specific T cells following PD-1 blockade. <i>Nature Medicine</i> , 2019, 25, 1251-1259.	30.7	974
72	Atlas of Subcellular RNA Localization Revealed by APEX-Seq. <i>Cell</i> , 2019, 178, 473-490.e26.	28.9	400

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73	GWAS for systemic sclerosis identifies multiple risk loci and highlights fibrotic and vasculopathy pathways. <i>Nature Communications</i> , 2019, 10, 4955.	12.8	100
74	The role of <i>Xist</i> -mediated Polycomb recruitment in the initiation of X-chromosome inactivation. <i>EMBO Reports</i> , 2019, 20, e48019.	4.5	79
75	N6-Methyladenosine Modification Controls Circular RNA Immunity. <i>Molecular Cell</i> , 2019, 76, 96-109.e9.	9.7	348
76	Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons. <i>ELife</i> , 2019, 8, .	6.0	64
77	A Mutation in the Transcription Factor <i>Foxp3</i> Drives T Helper 2 Effector Function in Regulatory T Cells. <i>Immunity</i> , 2019, 50, 362-377.e6.	14.3	72
78	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
79	Enhancer Connectome Nominates Target Genes of Inherited Risk Variants from Inflammatory Skin Disorders. <i>Journal of Investigative Dermatology</i> , 2019, 139, 605-614.	0.7	21
80	HiChIRP reveals RNA-associated chromosome conformation. <i>Nature Methods</i> , 2019, 16, 489-492.	19.0	70
81	RNA structure maps across mammalian cellular compartments. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 322-330.	8.2	183
82	Subcellular Spatial Transcriptomes: Emerging Frontier for Understanding Gene Regulation. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2019, 84, 31-45.	1.1	9
83	Circular ecDNA promotes accessible chromatin and high oncogene expression. <i>Nature</i> , 2019, 575, 699-703.	27.8	343
84	c-Jun overexpression in CAR T cells induces exhaustion resistance. <i>Nature</i> , 2019, 576, 293-300.	27.8	480
85	PIRCh-seq: functional classification of non-coding RNAs associated with distinct histone modifications. <i>Genome Biology</i> , 2019, 20, 292.	8.8	20
86	Functional significance of U2AF1 S34F mutations in lung adenocarcinomas. <i>Nature Communications</i> , 2019, 10, 5712.	12.8	27
87	Single-cell multiomic analysis identifies regulatory programs in mixed-phenotype acute leukemia. <i>Nature Biotechnology</i> , 2019, 37, 1458-1465.	17.5	321
88	Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks. <i>Cell</i> , 2019, 176, 361-376.e17.	28.9	215
89	First-in-Human Assessment of Feasibility and Safety of Multiplexed Genetic Engineering of Autologous T Cells Expressing NY-ESO -1 TCR and CRISPR/Cas9 Gene Edited to Eliminate Endogenous TCR and PD-1 (NYCE T cells) in Advanced Multiple Myeloma (MM) and Sarcoma. <i>Blood</i> , 2019, 134, 49-49.	1.4	10
90	The novel lncRNA <i>lnc-NR2F1</i> is pro-neurogenic and mutated in human neurodevelopmental disorders. <i>ELife</i> , 2019, 8, .	6.0	59

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91	Transcript-indexed ATAC-seq for precision immune profiling. <i>Nature Medicine</i> , 2018, 24, 580-590.	30.7	124
92	Epigenomics. <i>Circulation Research</i> , 2018, 122, 1191-1199.	4.5	80
93	Tissue-selective effects of nucleolar stress and rDNA damage in developmental disorders. <i>Nature</i> , 2018, 554, 112-117.	27.8	125
94	Rapid chromatin repression by Aire provides precise control of immune tolerance. <i>Nature Immunology</i> , 2018, 19, 162-172.	14.5	69
95	Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. <i>Cell</i> , 2018, 173, 1398-1412.e22.	28.9	362
96	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. <i>Cell</i> , 2018, 173, 1535-1548.e16.	28.9	545
97	Retinoic acid and BMP4 cooperate with p63 to alter chromatin dynamics during surface epithelial commitment. <i>Nature Genetics</i> , 2018, 50, 1658-1665.	21.4	47
98	The RNA Base-Pairing Problem and Base-Pairing Solutions. <i>Cold Spring Harbor Perspectives in Biology</i> , 2018, 10, a034926.	5.5	31
99	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
100	Mechanoresponsive stem cells acquire neural crest fate in jaw regeneration. <i>Nature</i> , 2018, 563, 514-521.	27.8	121
101	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	12.6	781
102	ChIRP-MS: RNA-Directed Proteomic Discovery. <i>Methods in Molecular Biology</i> , 2018, 1861, 37-45.	0.9	37
103	A Chromatin Basis for Cell Lineage and Disease Risk in the Human Pancreas. <i>Cell Systems</i> , 2018, 7, 310-322.e4.	6.2	38
104	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
105	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. <i>Nature Genetics</i> , 2018, 50, 1140-1150.	21.4	139
106	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
107	Expression of the transcription factor ZBTB46 distinguishes human histiocytic disorders of classical dendritic cell origin. <i>Modern Pathology</i> , 2018, 31, 1479-1486.	5.5	14
108	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

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109	Single-cell epigenomic variability reveals functional cancer heterogeneity. <i>Genome Biology</i> , 2017, 18, 15.	8.8	92
110	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
111	Generation of pure GABAergic neurons by transcription factor programming. <i>Nature Methods</i> , 2017, 14, 621-628.	19.0	265
112	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
113	Sensing Self and Foreign Circular RNAs by Intron Identity. <i>Molecular Cell</i> , 2017, 67, 228-238.e5.	9.7	346
114	The Mammalian Ribo-interactome Reveals Ribosome Functional Diversity and Heterogeneity. <i>Cell</i> , 2017, 169, 1051-1065.e18.	28.9	314
115	Gpr124 is essential for blood-brain barrier integrity in central nervous system disease. <i>Nature Medicine</i> , 2017, 23, 450-460.	30.7	177
116	CRISPRi-based genome-scale identification of functional long noncoding RNA loci in human cells. <i>Science</i> , 2017, 355, .	12.6	566
117	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
118	Mechanistic insights in X-chromosome inactivation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160356.	4.0	59
119	Rapid Chromatin Switch in the Direct Reprogramming of Fibroblasts to Neurons. <i>Cell Reports</i> , 2017, 20, 3236-3247.	6.4	121
120	Gene regulation in the immune system by long noncoding RNAs. <i>Nature Immunology</i> , 2017, 18, 962-972.	14.5	611
121	Discovery of stimulation-responsive immune enhancers with CRISPR activation. <i>Nature</i> , 2017, 549, 111-115.	27.8	247
122	IL-4R α Inhibitor for Atopic Disease. <i>Cell</i> , 2017, 170, 222.	28.9	28
123	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
124	Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. <i>Nature Genetics</i> , 2017, 49, 1522-1528.	21.4	255
125	Challenges and recommendations for epigenomics in precision health. <i>Nature Biotechnology</i> , 2017, 35, 1128-1132.	17.5	19
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	Comparison of SHAPE reagents for mapping RNA structures inside living cells. <i>Rna</i> , 2017, 23, 169-174.	3.5	62
128	LncRNA Seduction of GOT2 Goes Viral. <i>Immunity</i> , 2017, 47, 1021-1023.	14.3	4
129	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
130	Preleukemic Hematopoietic Stem Cells in Human Acute Myeloid Leukemia. <i>Frontiers in Oncology</i> , 2017, 7, 263.	2.8	39
131	The conserved RNA helicase YTHDC2 regulates the transition from proliferation to differentiation in the germline. <i>ELife</i> , 2017, 6, .	6.0	167
132	Transcription coactivator and lncRNA duet evoke Hox genes. <i>PLoS Genetics</i> , 2017, 13, e1006797.	3.5	0
133	Stress from Nucleotide Depletion Activates the Transcriptional Regulator HEXIM1 to Suppress Melanoma. <i>Molecular Cell</i> , 2016, 62, 34-46.	9.7	71
134	Long Noncoding RNAs in Cancer Pathways. <i>Cancer Cell</i> , 2016, 29, 452-463.	16.8	2,584
135	Single-cell profiling of lncRNAs in the developing human brain. <i>Genome Biology</i> , 2016, 17, 68.	8.8	16
136	Age-Dependent Pancreatic Gene Regulation Reveals Mechanisms Governing Human β 2 Cell Function. <i>Cell Metabolism</i> , 2016, 23, 909-920.	16.2	205
137	irCLIP platform for efficient characterization of protein-RNA interactions. <i>Nature Methods</i> , 2016, 13, 489-492.	19.0	222
138	RNA Duplex Map in Living Cells Reveals Higher-Order Transcriptome Structure. <i>Cell</i> , 2016, 165, 1267-1279.	28.9	520
139	An inducible long noncoding RNA amplifies DNA damage signaling. <i>Nature Genetics</i> , 2016, 48, 1370-1376.	21.4	195
140	Understanding RNA-Chromatin Interactions Using Chromatin Isolation by RNA Purification (ChIRP). <i>Methods in Molecular Biology</i> , 2016, 1480, 115-123.	0.9	56
141	Molecular and Neural Functions of Rai1 , the Causal Gene for Smith-Magenis Syndrome. <i>Neuron</i> , 2016, 92, 392-406.	8.1	51
142	lncRNA Structure: Message to the Heart. <i>Molecular Cell</i> , 2016, 64, 1-2.	9.7	43
143	Factors That May Promote an Effective Local Research Environment. <i>Journal of Investigative Dermatology</i> , 2016, 136, 1529-1531.	0.7	1
144	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. <i>Nature Genetics</i> , 2016, 48, 1193-1203.	21.4	952

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145	HiChIP: efficient and sensitive analysis of protein-directed genome architecture. <i>Nature Methods</i> , 2016, 13, 919-922.	19.0	853
146	Structural organization of the inactive X chromosome in the mouse. <i>Nature</i> , 2016, 535, 575-579.	27.8	369
147	ATAC-seq reveals the accessible genome by transposase-mediated imaging and sequencing. <i>Nature Methods</i> , 2016, 13, 1013-1020.	19.0	199
148	A Long Noncoding RNA lincRNA-EP3 Acts as a Transcriptional Brake to Restrain Inflammation. <i>Cell</i> , 2016, 165, 1672-1685.	28.9	399
149	HOXC10 Expression Supports the Development of Chemotherapy Resistance by Fine Tuning DNA Repair in Breast Cancer Cells. <i>Cancer Research</i> , 2016, 76, 4443-4456.	0.9	52
150	Transcriptome-wide interrogation of RNA secondary structure in living cells with icSHAPE. <i>Nature Protocols</i> , 2016, 11, 273-290.	12.0	147
151	Rapid evolutionary turnover underlies conserved lncRNA-genome interactions. <i>Genes and Development</i> , 2016, 30, 191-207.	5.9	152
152	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. <i>Nature Methods</i> , 2016, 13, 245-247.	19.0	44
153	Unique features of long non-coding RNA biogenesis and function. <i>Nature Reviews Genetics</i> , 2016, 17, 47-62.	16.3	2,891
154	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
155	7SK-BAF axis controls pervasive transcription at enhancers. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 231-238.	8.2	92
156	Systematic Characterization of Long Noncoding RNAs Reveals the Contrasting Coordination of <i>Cis</i> - and <i>Trans</i> -Molecular Regulation in Human Fetal and Adult Hearts. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 110-118.	5.1	42
157	Decoding the RNA structurome. <i>Current Opinion in Structural Biology</i> , 2016, 36, 142-148.	5.7	66
158	Genome-Wide Probing of RNA Structures In Vitro Using Nucleases and Deep Sequencing. <i>Methods in Molecular Biology</i> , 2016, 1361, 141-160.	0.9	4
159	Comment on "Hotair Is Dispensable for Mouse Development". <i>PLoS Genetics</i> , 2016, 12, e1006406.	3.5	17
160	Novel Gene Expression Profile of Women with Intrinsic Skin Youthfulness by Whole Transcriptome Sequencing. <i>PLoS ONE</i> , 2016, 11, e0165913.	2.5	11
161	Medulloblastoma-associated DDX3 variant selectively alters the translational response to stress. <i>Oncotarget</i> , 2016, 7, 28169-28182.	1.8	62
162	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

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163	Long Noncoding RNA in Hematopoiesis and Immunity. <i>Immunity</i> , 2015, 42, 792-804.	14.3	161
164	DDX5 and its associated lncRNA Rmrp modulate TH17 cell effector functions. <i>Nature</i> , 2015, 528, 517-522.	27.8	154
165	The histone chaperone CAF-1 safeguards somatic cell identity. <i>Nature</i> , 2015, 528, 218-224.	27.8	244
166	Dissecting noncoding and pathogen RNA-protein interactomes. <i>Rna</i> , 2015, 21, 135-143.	3.5	71
167	Technologies to probe functions and mechanisms of long noncoding RNAs. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 29-35.	8.2	124
168	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
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