

John L Rinn

List of Publications by Year in descending order

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155
papers

80,166
citations

4120

87
h-index

6630

156
g-index

190
all docs

190
docs citations

190
times ranked

85379
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. <i>Nature Protocols</i> , 2012, 7, 562-578.	5.5	11,433
2	The dynamics and regulators of cell fate decisions are revealed by pseudotemporal ordering of single cells. <i>Nature Biotechnology</i> , 2014, 32, 381-386.	9.4	4,652
3	Long non-coding RNA HOTAIR reprograms chromatin state to promote cancer metastasis. <i>Nature</i> , 2010, 464, 1071-1076.	13.7	4,648
4	Functional Demarcation of Active and Silent Chromatin Domains in Human HOX Loci by Noncoding RNAs. <i>Cell</i> , 2007, 129, 1311-1323.	13.5	3,835
5	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. <i>Nature</i> , 2009, 458, 223-227.	13.7	3,801
6	Genome Regulation by Long Noncoding RNAs. <i>Annual Review of Biochemistry</i> , 2012, 81, 145-166.	5.0	3,665
7	Differential analysis of gene regulation at transcript resolution with RNA-seq. <i>Nature Biotechnology</i> , 2013, 31, 46-53.	9.4	3,256
8	The multilayered complexity of ceRNA crosstalk and competition. <i>Nature</i> , 2014, 505, 344-352.	13.7	3,223
9	Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses. <i>Genes and Development</i> , 2011, 25, 1915-1927.	2.7	3,208
10	Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11667-11672.	3.3	2,709
11	Modular regulatory principles of large non-coding RNAs. <i>Nature</i> , 2012, 482, 339-346.	13.7	2,036
12	A Large Intergenic Noncoding RNA Induced by p53 Mediates Global Gene Repression in the p53 Response. <i>Cell</i> , 2010, 142, 409-419.	13.5	1,919
13	lincRNAs act in the circuitry controlling pluripotency and differentiation. <i>Nature</i> , 2011, 477, 295-300.	13.7	1,749
14	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
15	Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. <i>Nature Biotechnology</i> , 2010, 28, 503-510.	9.4	1,251
16	Improving RNA-Seq expression estimates by correcting for fragment bias. <i>Genome Biology</i> , 2011, 12, R22.	13.9	1,164
17	Global Identification of Human Transcribed Sequences with Genome Tiling Arrays. <i>Science</i> , 2004, 306, 2242-2246.	6.0	983
18	Large intergenic non-coding RNA-RoR modulates reprogramming of human induced pluripotent stem cells. <i>Nature Genetics</i> , 2010, 42, 1113-1117.	9.4	902

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19	Control of somatic tissue differentiation by the long non-coding RNA TINCR. <i>Nature</i> , 2013, 493, 231-235.	13.7	810
20	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. <i>Genome Research</i> , 2012, 22, 577-591.	2.4	809
21	Basset: learning the regulatory code of the accessible genome with deep convolutional neural networks. <i>Genome Research</i> , 2016, 26, 990-999.	2.4	790
22	A histone H3 lysine 27 demethylase regulates animal posterior development. <i>Nature</i> , 2007, 449, 689-694.	13.7	718
23	Genome-wide measurement of RNA secondary structure in yeast. <i>Nature</i> , 2010, 467, 103-107.	13.7	713
24	Multiple knockout mouse models reveal lincRNAs are required for life and brain development. <i>ELife</i> , 2013, 2, e01749.	2.8	609
25	Discovery and annotation of long noncoding RNAs. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 5-7.	3.6	581
26	Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 198-206.	3.6	565
27	Localization and abundance analysis of human lincRNAs at single-cell and single-molecule resolution. <i>Genome Biology</i> , 2015, 16, 20.	3.8	565
28	Non-coding RNAs as regulators of embryogenesis. <i>Nature Reviews Genetics</i> , 2011, 12, 136-149.	7.7	558
29	Peptidomic discovery of short open reading frame-encoded peptides in human cells. <i>Nature Chemical Biology</i> , 2013, 9, 59-64.	3.9	529
30	Unbiased Reconstruction of a Mammalian Transcriptional Network Mediating Pathogen Responses. <i>Science</i> , 2009, 326, 257-263.	6.0	473
31	Large non-coding RNAs: missing links in cancer?. <i>Human Molecular Genetics</i> , 2010, 19, R152-R161.	1.4	466
32	Transposable elements reveal a stem cell-specific class of long noncoding RNAs. <i>Genome Biology</i> , 2012, 13, R107.	13.9	462
33	DNMT1-interacting RNAs block gene-specific DNA methylation. <i>Nature</i> , 2013, 503, 371-376.	13.7	446
34	Targeted RNA sequencing reveals the deep complexity of the human transcriptome. <i>Nature Biotechnology</i> , 2012, 30, 99-104.	9.4	437
35	Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1149-1163.	13.5	419
36	Anatomic Demarcation by Positional Variation in Fibroblast Gene Expression Programs. <i>PLoS Genetics</i> , 2006, 2, e119.	1.5	413

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37	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. <i>Nature Genetics</i> , 2015, 47, 469-478.	9.4	409
38	Suppression of progenitor differentiation requires the long noncoding RNA ANCR. <i>Genes and Development</i> , 2012, 26, 338-343.	2.7	391
39	Scaffold function of long non-coding RNA HOTAIR in protein ubiquitination. <i>Nature Communications</i> , 2013, 4, 2939.	5.8	382
40	The Reality of Pervasive Transcription. <i>PLoS Biology</i> , 2011, 9, e1000625.	2.6	380
41	Long noncoding RNAs regulate adipogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3387-3392.	3.3	371
42	Mechanisms of Long Non-coding RNAs in Mammalian Nervous System Development, Plasticity, Disease, and Evolution. <i>Neuron</i> , 2015, 88, 861-877.	3.8	366
43	Chromatin signature of embryonic pluripotency is established during genome activation. <i>Nature</i> , 2010, 464, 922-926.	13.7	340
44	Hierarchical Maintenance of MLL Myeloid Leukemia Stem Cells Employs a Transcriptional Program Shared with Embryonic Rather Than Adult Stem Cells. <i>Cell Stem Cell</i> , 2009, 4, 129-140.	5.2	326
45	Identifying Recent Adaptations in Large-Scale Genomic Data. <i>Cell</i> , 2013, 152, 703-713.	13.5	325
46	Distribution of NF- κ B-binding sites across human chromosome 22. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12247-12252.	3.3	298
47	Lin28a transgenic mice manifest size and puberty phenotypes identified in human genetic association studies. <i>Nature Genetics</i> , 2010, 42, 626-630.	9.4	282
48	Multiplexable, locus-specific targeting of long RNAs with CRISPR-Display. <i>Nature Methods</i> , 2015, 12, 664-670.	9.0	268
49	Integrative analyses reveal a long noncoding RNA-mediated sponge regulatory network in prostate cancer. <i>Nature Communications</i> , 2016, 7, 10982.	5.8	267
50	The transcriptional activity of human Chromosome 22. <i>Genes and Development</i> , 2003, 17, 529-540.	2.7	253
51	DeCoN: Genome-wide Analysis of In Vivo Transcriptional Dynamics during Pyramidal Neuron Fate Selection in Neocortex. <i>Neuron</i> , 2015, 85, 275-288.	3.8	248
52	The histone chaperone CAF-1 safeguards somatic cell identity. <i>Nature</i> , 2015, 528, 218-224.	13.7	244
53	Spontaneous autoimmunity prevented by thymic expression of a single self-antigen. <i>Journal of Experimental Medicine</i> , 2006, 203, 2727-2735.	4.2	240
54	An Integrated Genome-wide CRISPRa Approach to Functionalize lncRNAs in Drug Resistance. <i>Cell</i> , 2018, 173, 649-664.e20.	13.5	238

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55	Ribosome profiling reveals resemblance between long non-coding RNAs and 5' leaders of coding RNAs. <i>Development (Cambridge)</i> , 2013, 140, 2828-2834.	1.2	237
56	A comparison of genetically matched cell lines reveals the equivalence of human iPSCs and ESCs. <i>Nature Biotechnology</i> , 2015, 33, 1173-1181.	9.4	235
57	The long non-coding RNA <i>Morrbid</i> regulates Bim and short-lived myeloid cell lifespan. <i>Nature</i> , 2016, 537, 239-243.	13.7	234
58	Sexual dimorphism in mammalian gene expression. <i>Trends in Genetics</i> , 2005, 21, 298-305.	2.9	231
59	Pint lincRNA connects the p53 pathway with epigenetic silencing by the Polycomb repressive complex 2. <i>Genome Biology</i> , 2013, 14, R104.	13.9	224
60	Programming human pluripotent stem cells into white and brown adipocytes. <i>Nature Cell Biology</i> , 2012, 14, 209-219.	4.6	209
61	Chromatin environment, transcriptional regulation, and splicing distinguish lincRNAs and mRNAs. <i>Genome Research</i> , 2017, 27, 27-37.	2.4	207
62	Integrative Analyses of Human Reprogramming Reveal Dynamic Nature of Induced Pluripotency. <i>Cell</i> , 2015, 162, 412-424.	13.5	206
63	Widespread RNA binding by chromatin-associated proteins. <i>Genome Biology</i> , 2016, 17, 28.	3.8	197
64	Long Noncoding RNAs: Molecular Modalities to Organismal Functions. <i>Annual Review of Biochemistry</i> , 2020, 89, 283-308.	5.0	183
65	<i>Neat1</i> is a p53-inducible lincRNA essential for transformation suppression. <i>Genes and Development</i> , 2017, 31, 1095-1108.	2.7	179
66	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , 2015, 518, 355-359.	13.7	172
67	Genome-Wide Analysis of KAP1 Binding Suggests Autoregulation of KRAB-ZNFs. <i>PLoS Genetics</i> , 2007, 3, e89.	1.5	166
68	A dermal <i>HOX</i> transcriptional program regulates site-specific epidermal fate. <i>Genes and Development</i> , 2008, 22, 303-307.	2.7	165
69	RNA traffic control of chromatin complexes. <i>Current Opinion in Genetics and Development</i> , 2010, 20, 142-148.	1.5	161
70	CREB Binds to Multiple Loci on Human Chromosome 22. <i>Molecular and Cellular Biology</i> , 2004, 24, 3804-3814.	1.1	160
71	Strand-specific RNA sequencing in <i>Plasmodium falciparum</i> malaria identifies developmentally regulated long non-coding RNA and circular RNA. <i>BMC Genomics</i> , 2015, 16, 454.	1.2	160
72	Linking RNA biology to lncRNAs. <i>Genome Research</i> , 2015, 25, 1456-1465.	2.4	158

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73	Spatiotemporal expression and transcriptional perturbations by long noncoding RNAs in the mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6855-6862.	3.3	152
74	Major Molecular Differences between Mammalian Sexes Are Involved in Drug Metabolism and Renal Function. <i>Developmental Cell</i> , 2004, 6, 791-800.	3.1	151
75	Mechanisms of an autoimmunity syndrome in mice caused by a dominant mutation in Aire. <i>Journal of Clinical Investigation</i> , 2008, 118, 1712-1726.	3.9	143
76	Live-cell mapping of organelle-associated RNAs via proximity biotinylation combined with protein-RNA crosslinking. <i>ELife</i> , 2017, 6, .	2.8	143
77	Genetic determinants and epigenetic effects of pioneer-factor occupancy. <i>Nature Genetics</i> , 2018, 50, 250-258.	9.4	139
78	RNA-protein interactions in human health and disease. <i>Seminars in Cell and Developmental Biology</i> , 2011, 22, 359-365.	2.3	131
79	Co-Cat's Cradling the 3D Genome by the Act of LncRNA Transcription. <i>Molecular Cell</i> , 2016, 62, 657-664.	4.5	128
80	DNA methylation and epigenetic control of cellular differentiation. <i>Cell Cycle</i> , 2010, 9, 3880-3883.	1.3	127
81	A global transcriptional analysis of <i>Plasmodium falciparum</i> malaria reveals a novel family of telomere-associated lncRNAs. <i>Genome Biology</i> , 2011, 12, R56.	13.9	124
82	Gene co-regulation by Fezf2 selects neurotransmitter identity and connectivity of corticospinal neurons. <i>Nature Neuroscience</i> , 2014, 17, 1046-1054.	7.1	121
83	<i>linc-HOXA1</i> is a noncoding RNA that represses <i>Hoxa1</i> transcription in <i>cis</i> . <i>Genes and Development</i> , 2013, 27, 1260-1271.	2.7	120
84	Ras/Erk MAPK Signaling in Epidermal Homeostasis and Neoplasia. <i>Cell Cycle</i> , 2007, 6, 2928-2931.	1.3	119
85	RNA and dynamic nuclear organization. <i>Science</i> , 2014, 345, 1240-1241.	6.0	119
86	lncRNAs: Linking RNA to Chromatin. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a018614-a018614.	2.3	118
87	Genome-wide RNA-Seq of Human Motor Neurons Implicates Selective ER Stress Activation in Spinal Muscular Atrophy. <i>Cell Stem Cell</i> , 2015, 17, 569-584.	5.2	108
88	High-throughput functional analysis of lncRNA core promoters elucidates rules governing tissue specificity. <i>Genome Research</i> , 2019, 29, 344-355.	2.4	100
89	High-throughput identification of <i>scp</i> RNA nuclear enrichment sequences. <i>EMBO Journal</i> , 2018, 37, .	3.5	99
90	RNA is essential for PRC2 chromatin occupancy and function in human pluripotent stem cells. <i>Nature Genetics</i> , 2020, 52, 931-938.	9.4	99

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91	Interchromosomal interactions: A genomic love story of kissing chromosomes. <i>Journal of Cell Biology</i> , 2019, 218, 27-38.	2.3	98
92	A TAD boundary is preserved upon deletion of the CTCF-rich Firre locus. <i>Nature Communications</i> , 2018, 9, 1444.	5.8	97
93	InÂVivo Characterization of Linc-p21 Reveals Functional cis -Regulatory DNA Elements. <i>Cell Reports</i> , 2016, 16, 2178-2186.	2.9	94
94	A distant trophoblast-specific enhancer controls HLA-G expression at the maternalâ€fetal interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5364-5369.	3.3	90
95	Transposable elements modulate human RNA abundance and splicing via specific RNA-protein interactions. <i>Genome Biology</i> , 2014, 15, 537.	3.8	88
96	Integrative genomic analysis reveals widespread enhancer regulation by p53 in response to DNA damage. <i>Nucleic Acids Research</i> , 2015, 43, 4447-4462.	6.5	84
97	Single-Cell Profiling of Ebola Virus Disease InÂVivo Reveals Viral and Host Dynamics. <i>Cell</i> , 2020, 183, 1383-1401.e19.	13.5	79
98	A Systems Biology Approach to Anatomic Diversity of Skin. <i>Journal of Investigative Dermatology</i> , 2008, 128, 776-782.	0.3	78
99	Transcriptional silencing of long noncoding RNA GNG12-AS1 uncouples its transcriptional and product-related functions. <i>Nature Communications</i> , 2016, 7, 10406.	5.8	77
100	The Sox2 transcription factor binds RNA. <i>Nature Communications</i> , 2020, 11, 1805.	5.8	77
101	RNase-mediated protein footprint sequencing reveals protein-binding sites throughout the human transcriptome. <i>Genome Biology</i> , 2014, 15, R3.	13.9	76
102	Function and evolution of local repeats in the Firre locus. <i>Nature Communications</i> , 2016, 7, 11021.	5.8	75
103	Spatiotemporal allele organization by allele-specific CRISPR live-cell imaging (SNP-CLING). <i>Nature Structural and Molecular Biology</i> , 2018, 25, 176-184.	3.6	75
104	Genetic Models Reveal cis and trans Immune-Regulatory Activities for lincRNA-Cox2. <i>Cell Reports</i> , 2018, 25, 1511-1524.e6.	2.9	73
105	Visualization of lncRNA by Single-Molecule Fluorescence In Situ Hybridization. <i>Methods in Molecular Biology</i> , 2015, 1262, 3-19.	0.4	68
106	Aligning Single-Cell Developmental and Reprogramming Trajectories Identifies Molecular Determinants of Myogenic Reprogramming Outcome. <i>Cell Systems</i> , 2018, 7, 258-268.e3.	2.9	65
107	p53 regulates enhancer accessibility and activity in response to DNA damage. <i>Nucleic Acids Research</i> , 2017, 45, 9889-9900.	6.5	61
108	The Tug1 lncRNA locus is essential for male fertility. <i>Genome Biology</i> , 2020, 21, 237.	3.8	61

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109	Differential contribution of steady-state <i>scp</i> RNA and active transcription in chromatin organization. <i>EMBO Reports</i> , 2019, 20, e48068.	2.0	61
110	Inter-chromosomal Contact Properties in Live-Cell Imaging and in Hi-C. <i>Molecular Cell</i> , 2018, 69, 1039-1045.e3.	4.5	60
111	The Firre locus produces a trans-acting RNA molecule that functions in hematopoiesis. <i>Nature Communications</i> , 2019, 10, 5137.	5.8	60
112	Group 1 Innate Lymphoid Cell Lineage Identity Is Determined by a cis-Regulatory Element Marked by a Long Non-coding RNA. <i>Immunity</i> , 2017, 47, 435-449.e8.	6.6	57
113	LncRNA requirements for mouse acute myeloid leukemia and normal differentiation. <i>ELife</i> , 2017, 6, .	2.8	54
114	From genotype to phenotype: genetics of mammalian long non-coding RNAs in vivo. <i>Nature Reviews Genetics</i> , 2022, 23, 229-243.	7.7	53
115	To repress or not to repress: This is the guardian's question. <i>Trends in Cell Biology</i> , 2011, 21, 344-353.	3.6	52
116	Diverse Phenotypes and Specific Transcription Patterns in Twenty Mouse Lines with Ablated LincRNAs. <i>PLoS ONE</i> , 2015, 10, e0125522.	1.1	51
117	Computational analysis of noncoding RNAs. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012, 3, 759-778.	3.2	50
118	LINC00520 is induced by Src, STAT3, and PI3K and plays a functional role in breast cancer. <i>Oncotarget</i> , 2016, 7, 81981-81994.	0.8	48
119	A CLK3-HMGA2 Alternative Splicing Axis Impacts Human Hematopoietic Stem Cell Molecular Identity throughout Development. <i>Cell Stem Cell</i> , 2018, 22, 575-588.e7.	5.2	40
120	HOXA3 Modulates Injury-Induced Mobilization and Recruitment of Bone Marrow-Derived Cells. <i>Stem Cells</i> , 2009, 27, 1654-1665.	1.4	37
121	Identification of proteins binding coding and non-coding human RNAs using protein microarrays. <i>BMC Genomics</i> , 2012, 13, 633.	1.2	35
122	Cis and trans effects differentially contribute to the evolution of promoters and enhancers. <i>Genome Biology</i> , 2020, 21, 210.	3.8	35
123	Trans- and cis-acting effects of Firre on epigenetic features of the inactive X chromosome. <i>Nature Communications</i> , 2020, 11, 6053.	5.8	33
124	Diverse epigenetic mechanisms maintain parental imprints within the embryonic and extraembryonic lineages. <i>Developmental Cell</i> , 2021, 56, 2995-3005.e4.	3.1	33
125	'Oming in on RNA-protein interactions. <i>Genome Biology</i> , 2014, 15, 401.	13.9	32
126	RNA-seq as a tool for evaluating human embryo competence. <i>Genome Research</i> , 2019, 29, 1705-1718.	2.4	31

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127	Mitoregulin Controls \hat{I}^2 -Oxidation in Human and Mouse Adipocytes. <i>Stem Cell Reports</i> , 2020, 14, 590-602.	2.3	31
128	Mosaic cis-regulatory evolution drives transcriptional partitioning of HERVH endogenous retrovirus in the human embryo. <i>ELife</i> , 2022, 11, .	2.8	31
129	Resolving mechanisms of immune-mediated disease in primary $\langle scp \rangle CD \langle /scp \rangle$ 4 T cells. <i>EMBO Molecular Medicine</i> , 2020, 12, e12112.	3.3	30
130	Myo2p, a class V myosin in budding yeast, associates with a large ribonucleic acid-protein complex that contains mRNAs and subunits of the RNA-processing body. <i>Rna</i> , 2008, 14, 491-502.	1.6	29
131	Single-cell imaging reveals unexpected heterogeneity of telomerase reverse transcriptase expression across human cancer cell lines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18488-18497.	3.3	27
132	Nuclear compartmentalization of TERT mRNA and TUG1 lncRNA is driven by intron retention. <i>Nature Communications</i> , 2021, 12, 3308.	5.8	25
133	Common variants in signaling transcription-factor-binding sites drive phenotypic variability in red blood cell traits. <i>Nature Genetics</i> , 2020, 52, 1333-1345.	9.4	24
134	'Lnc'-ing enhancers to MYC regulation. <i>Cell Research</i> , 2014, 24, 643-644.	5.7	23
135	Identification of human long noncoding RNAs associated with nonalcoholic fatty liver disease and metabolic homeostasis. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	23
136	Dynamic changes during the treatment of pancreatic cancer. <i>Oncotarget</i> , 2018, 9, 14764-14790.	0.8	21
137	Enhancers in the Peril lincRNA locus regulate distant but not local genes. <i>Genome Biology</i> , 2018, 19, 219.	3.8	20
138	Expression of Shal potassium channel subunits in the adult and developing cochlear nucleus of the mouse. <i>Hearing Research</i> , 2000, 147, 31-45.	0.9	18
139	In vivo Firre and Dxz4 deletion elucidates roles for autosomal gene regulation. <i>ELife</i> , 2019, 8, .	2.8	18
140	Illuminating Genomic Dark Matter with RNA Imaging. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032094.	2.3	17
141	Reorganization of $\langle i \rangle$ inter $\hat{a} \langle /i \rangle$ chromosomal interactions in the 2q37-deletion syndrome. <i>EMBO Journal</i> , 2018, 37, .	3.5	13
142	Noncoding RNAs: biology and applications-a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1506, 118-141.	1.8	13
143	Genome-wide CRISPR interference screen identifies long non-coding RNA loci required for differentiation and pluripotency. <i>PLoS ONE</i> , 2021, 16, e0252848.	1.1	12
144	Linking long noncoding RNA to drug resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21963-21965.	3.3	11

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145	Myosin 7b is a regulatory long noncoding RNA (lncMYH7b) in the human heart. <i>Journal of Biological Chemistry</i> , 2021, 296, 100694.	1.6	11
146	Silent pericentromeric repeats speak out. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15008-15009.	3.3	8
147	Evolutionary divergence of Firre localization and expression. <i>Rna</i> , 2022, , rna.079070.121.	1.6	8
148	Poly-combing the genome for RNA. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1344-1346.	3.6	6
149	Sixty years of genome biology. <i>Genome Biology</i> , 2013, 14, 113.	13.9	6
150	An in vivo screen of noncoding loci reveals that <i>Daedalus</i> is a gatekeeper of an Ikaros-dependent checkpoint during haematopoiesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	2
151	Defective insulin receptor signaling in hPSCs skews pluripotency and negatively perturbs neural differentiation. <i>Journal of Biological Chemistry</i> , 2021, 296, 100495.	1.6	2
152	Genome-wide binding analysis of 195 DNA binding proteins reveals a reservoir of promoters and human specific SVA-repeat family regulation. <i>PLoS ONE</i> , 2021, 16, e0237055.	1.1	2
153	The Emerging Non-Coding RNA World. <i>Molecular Medicine and Medicinal</i> , 2010, , 17-49.	0.4	1
154	Design Issues in Implementing a Portable Sample Tracking and Analysis Research Support (STARS) System for PCR Based Microarray Research. , 2006, , .		0
155	As we come to the end of 2011, several members of the Genome Biology Editorial Board give their views on the state of play in genomics. <i>Genome Biology</i> , 2011, 12, 137.	13.9	0